

; PRIOR APPLICATION NUMBER: US/09/657,346  
; PRIOR FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 175  
; SEQ ID NO 32  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-293-783-32

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2275 GGTTTCACCGTGTAGCCAG 2294  
||| ||||| ||||| |||||  
Db 1 GGTTTCACCATGTGTGCAG 20

RESULT 1520  
US-10-293-783-33  
; Sequence 33, Application US/10293783  
; Publication No. US20030130222A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXP  
; FILE REFERENCE: ISPH-0544  
; CURRENT APPLICATION NUMBER: US/10/293,783  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US/09/800,631  
; PRIOR FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US/09/657,346  
; PRIOR FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 175  
; SEQ ID NO 33  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-293-783-33

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2146 TCTTGGCTCACTCAAGCTC 2165  
||| ||||| ||||| |||||  
Db 1 TCTCGGCTCACTCAACCTC 20

RESULT 1521  
US-10-293-783-49  
; Sequence 49, Application US/10293783  
; Publication No. US20030130222A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXP  
; FILE REFERENCE: ISPH-0544  
; CURRENT APPLICATION NUMBER: US/10/293,783  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US/09/800,631  
; PRIOR FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US/09/657,346  
; PRIOR FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 175  
; SEQ ID NO 49  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-293-783-49

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGC 2361  
||| ||||| ||||| |||||  
Db 1 AAGTAGCTGGGATTACAGGC 20

RESULT 1522  
US-10-293-783-66  
; Sequence 66, Application US/10293783  
; Publication No. US20030130222A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXE  
; FILE REFERENCE: ISPH-0544  
; CURRENT APPLICATION NUMBER: US/10/293,783  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US/09/800,631  
; PRIOR FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US/09/657,346  
; PRIOR FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 175  
; SEQ ID NO 66  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-293-783-66

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGCTCG 2304  
||| ||||| ||||| |||||  
Db 1 TGTGGCCAGGGTGTCTCG 20

RESULT 1523  
US-10-119-431-42  
; Sequence 42, Application US/10119431  
; Publication No. US20030152939A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Zhong, Mei  
; APPLICANT: Khrantsov, Nikolai  
; APPLICANT: Li, Li  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Padigaru, Muraidhara  
; APPLICANT: Anderson, David  
; APPLICANT: Shimkets, Richard A.  
; TITLE OF INVENTION: NOVEL SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING  
; TITLE OF INVENTION: THEM  
; FILE REFERENCE: Cura-29 CIP1  
; CURRENT APPLICATION NUMBER: US/10/119,431  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: 60/103,195  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/282,548  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/412,231  
; PRIOR FILING DATE: 1999-10-05  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Chemically
; OTHER INFORMATION: Synthesized
US-10-119-431-42

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2104 CCGAGTCTTGCTGCTTACC 2123
      |||||
Db 1 CAGAGTCTTGCTGCTTCC 20

RESULT 1524
US-10-345-092-62/c
; Sequence 62, Application US/10345092
; Publication No. US20030165506A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; TITLE OF INVENTION: No. US20030165506A1el alpha-catenin expressed in heart and testis
; FILE REFERENCE: FVR/atc/V067
; CURRENT APPLICATION NUMBER: US/10/345,092
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 00202472.7
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,309
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: lower primer
US-10-345-092-62

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2095 TTTTGGACCGAGTCTTGC 2114
      |||||
Db 20 TTTTGGACCGAGTCTGC 1

RESULT 1525
US-10-210-951-198/c
; Sequence 198, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/210,951
```

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; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe.
US-10-210-951-198

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 48 TCGAAAGATGGAGCAAGAA 67
      |||||
Db 20 TCGAGGGATGGAGAAAGAA 1

RESULT 1526
US-10-289-845-16
; Sequence 16, Application US/10289845
; Publication No. US20030170679A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Linda
; APPLICANT: Wagner, Susanne
; APPLICANT: Parodi, Luis
; TITLE OF INVENTION: Single Nucleotide Polymorphisms in GH-1
; FILE REFERENCE: 00791.US1
; CURRENT APPLICATION NUMBER: US/10/289,845
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-289-845-16

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2176 GGCTTCGACCATTCCTCG 2195
      |||||
Db 1 GGATTCACGCCATTCCTCG 20

RESULT 1527
US-10-211-884-198/c
```



```
/ Sequence 199, Application US/10211884
/ Publication No. US20030175900A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Marsters, Scot A.
/ APPLICANT: Pan, James
/ APPLICANT: Pitti, Robert M.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stone, Donna M.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
/ FILE REFERENCE: P2931R1C1
/ CURRENT APPLICATION NUMBER: US/10/211,884
/ CURRENT FILING DATE: 2002-08-02
/ PRIOR APPLICATION NUMBER: 60/014699
/ PRIOR FILING DATE: 1996-04-01
/ PRIOR APPLICATION NUMBER: 60/026943
/ PRIOR FILING DATE: 1996-09-23
/ PRIOR APPLICATION NUMBER: 60/059121
/ PRIOR FILING DATE: 1997-07-17
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/062037
/ PRIOR FILING DATE: 1997-10-10
/ PRIOR APPLICATION NUMBER: 60/063755
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063045
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/066511
/ PRIOR FILING DATE: 1997-11-24
/ PRIOR APPLICATION NUMBER: 60/066772
/ PRIOR FILING DATE: 1997-11-24
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 258
/ SEQ ID NO 198
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Oligonucleotide Probe.
/ US-10-211-884-198

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 48 TCGGAAGATGGAGCAAGAA 67
Db 20 TCGGAGCGATGGAGAAAGAA 1

RESULT 1528
US-10-331-907-78
/ Sequence 78, Application US/10331907
/ Publication No. US20030181660A1
/ GENERAL INFORMATION:
/ APPLICANT: Todd, John A
/ APPLICANT: Hess, John W
/ APPLICANT: Caskey, Charles T
/ APPLICANT: Cox, Roger D
/ APPLICANT: Gerhold, David
/ APPLICANT: Hammond, Holly
/ APPLICANT: Hey, Patricia
/ APPLICANT: Kawaguchi, Yoshihiko
/ APPLICANT: Merriman, Tony R
/ APPLICANT: Metzker, Michael L
/ TITLE OF INVENTION: No. US20030181660A1 LDL-Receptor
/ NUMBER OF SEQUENCES: 455
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nixon and Vanderhye
/ STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
/ CITY: Arlington

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2293 AGGATGCTCTCGATCTCCTG 2312
Db 1 AGGCTGCTCTCAACTCCTG 20

RESULT 1529
US-10-331-907-240/c
/ Sequence 240, Application US/10331907
/ Publication No. US20030181660A1
/ GENERAL INFORMATION:
/ APPLICANT: Todd, John A
/ APPLICANT: Hess, John W
/ APPLICANT: Caskey, Charles T
/ APPLICANT: Cox, Roger D
/ APPLICANT: Gerhold, David
/ APPLICANT: Hammond, Holly
/ APPLICANT: Hey, Patricia
/ APPLICANT: Kawaguchi, Yoshihiko
/ APPLICANT: Merriman, Tony R
/ APPLICANT: Metzker, Michael L
/ TITLE OF INVENTION: No. US20030181660A1 LDL-Receptor
/ NUMBER OF SEQUENCES: 455
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nixon and Vanderhye
/ STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
/ CITY: Arlington
```

STATE: Virginia  
COUNTRY: US  
ZIP: VA 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/331,907  
FILING DATE: 31-Dec-2002  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,923A  
FILING DATE: 14-Feb-2001  
APPLICATION NUMBER: PCT/GB98/01102  
FILING DATE: 15-APR-1998  
APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: B.J. Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-81  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 240:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 240:  
US-10-331-907-240

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTGCTCTGTTC 2122  
||| ||||| ||||| |||||  
Db 20 ACAGGGTCTGCTCTGTTC 1

RESULT 1530  
US-10-005-344-341/c  
; Sequence 341, Application US/10005344  
; Publication No. US20030203862A1  
; GENERAL INFORMATION:  
; APPLICANT: Loren J. Miraglia  
; APPLICANT: Pamela Nero  
; APPLICANT: Mark J. Graham  
; APPLICANT: Brett P. Monia  
; APPLICANT: Erich Koller  
; APPLICANT: Mingyi Chiang  
; APPLICANT: Mano Manoharan  
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.  
; FILE REFERENCE: ISPH-0622  
; CURRENT APPLICATION NUMBER: US/10/005,344  
; PRIORITY FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: US 09/048,810  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/280,805  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 379  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 341  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-446-373-98

US-10-005-344-341

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 978 GATCTTGATGCTGCTGTAAG 997  
||||| ||||| ||||| |||||  
Db 20 GATCTTGACGATGCGTAAG 1

RESULT 1531  
US-10-005-344-351/c  
; Sequence 351, Application US/10005344  
; Publication No. US20030203862A1  
; GENERAL INFORMATION:  
; APPLICANT: Loren J. Miraglia  
; APPLICANT: Pamela Nero  
; APPLICANT: Mark J. Graham  
; APPLICANT: Brett P. Monia  
; APPLICANT: Erich Koller  
; APPLICANT: Mingyi Chiang  
; APPLICANT: Mano Manoharan  
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.  
; FILE REFERENCE: ISPH-0622  
; CURRENT APPLICATION NUMBER: US/10/005,344  
; CURRENT FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: US 09/048,810  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/280,805  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 379  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 351  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-005-344-351

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1638 GGTGACCTAAATAATGTTG 1657  
||| ||||| ||||| |||||  
Db 20 GGGCGGCTAAATAATGCTG 1

RESULT 1532  
US-10-446-373-98  
; Sequence 98, Application US/10446373  
; Publication No. US20030204076A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE EXPRESSION  
; FILE REFERENCE: RTS-0232  
; CURRENT APPLICATION NUMBER: US/10/446,373  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: US/09/953,318  
; PRIOR FILING DATE: 2001-09-13  
; NUMBER OF SEQ ID NOS: 154  
; SEQ ID NO 98  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-446-373-98

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2234 CACACACCTGGCTAATTTT 2253  
||||| ||| ||||| |||||  
Db 1 CACATGCCCGCTAATTTT 20

RESULT 1533  
US-10-211-858-198/c  
; Sequence 198, Application US/10211858  
; Publication No. US20030211096A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Marsters, Scot A.  
; APPLICANT: Pan, James  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stone, Donna M.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
; FILE REFERENCE: P2931R1C1  
; CURRENT APPLICATION NUMBER: US/10/211,858  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/014699  
; PRIOR FILING DATE: 1996-04-01  
; PRIOR APPLICATION NUMBER: 60/026943  
; PRIOR FILING DATE: 1996-09-23  
; PRIOR APPLICATION NUMBER: 60/059121  
; PRIOR FILING DATE: 1997-07-17  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/062037  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066772  
; PRIOR FILING DATE: 1997-11-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 258  
; SEQ ID NO 198  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide Probe.  
US-10-211-858-198

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 48 TCGAAAGATGGACAGAA 67  
||||| ||||| |||||  
Db 20 TCGAGGGATGGAGAA 1

RESULT 1534  
US-10-181-875-71/c  
; Sequence 71, Application US/10181875

; Publication No. US20030216333A1  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Brett P. Monia  
; APPLICANT: Robert McKay  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPRESSION  
; FILE REFERENCE: RTSP-0356  
; CURRENT APPLICATION NUMBER: US/10/181,875  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: 09/488,856  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 71  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-181-875-71

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2146 TCTTGCTCACTGCAAGCTC 2165  
||||| ||||| ||||| |||||  
Db 20 TCTCGGGTCACTGCAACCTC 1

RESULT 1535  
US-10-094-749-3312  
; Sequence 3312, Application US/10094749  
; Publication No. US20030219741A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOHIKO  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOYUKI  
; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASUHO, YASUHIKO  
; FILE REFERENCE: 084335/0160  
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA  
; CURRENT APPLICATION NUMBER: US/10/094,749  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/350,435  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: JP 2001-328381  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 3381  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3312  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized primer sequence  
US-10-094-749-3312

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2086 TTTTGAGACCGAGCTTGCT 2115  
 |||||  
 Db 1 TTTTGAGACAGATTGCGT 20

RESULT 1536  
 US-10-282-174-215  
 ; Sequence 215, Application US/10282174  
 ; Publication No. US20030224380A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Becker, Kenneth David  
 ; APPLICANT: Velicelebi, Gonul  
 ; APPLICANT: Elliot, Kathryn J.  
 ; APPLICANT: Wang, Xin  
 ; APPLICANT: Tanzi, Rudolph E.  
 ; APPLICANT: Bertram, Lars  
 ; APPLICANT: Saunders, Aleister J.  
 ; APPLICANT: Mullin, Kristina M.  
 ; APPLICANT: Sampson, Andrew Johnson  
 ; APPLICANT: Blacker, Deborah Lynne  
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10  
 ; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER  
 ; FILE REFERENCE: 37481-3308  
 ; CURRENT APPLICATION NUMBER: US/10/282,174  
 ; PRIOR FILING DATE: 2002-10-25  
 ; PRIOR APPLICATION NUMBER: US 60/339,525  
 ; PRIOR FILING DATE: 2001-10-25  
 ; PRIOR APPLICATION NUMBER: US 60/338,010  
 ; PRIOR FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/336,929  
 ; PRIOR FILING DATE: 2001-11-09  
 ; PRIOR APPLICATION NUMBER: US 60/338,363  
 ; PRIOR FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: US 60/337,052  
 ; PRIOR FILING DATE: 2002-03-28  
 ; NUMBER OF SEQ ID NOS: 564  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 215  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 US-10-282-174-215

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2344 AGTGTGGGATTACAGCAT 2363  
 |||||  
 Db 1 AGTGTGGGATTATAGGCTT 20

RESULT 1537  
 US-10-282-174-234  
 ; Sequence 234, Application US/10282174  
 ; Publication No. US20030224380A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Becker, Kenneth David  
 ; APPLICANT: Velicelebi, Gonul  
 ; APPLICANT: Elliot, Kathryn J.  
 ; APPLICANT: Wang, Xin  
 ; APPLICANT: Tanzi, Rudolph E.  
 ; APPLICANT: Bertram, Lars  
 ; APPLICANT: Saunders, Aleister J.

; APPLICANT: Mullin, Kristina M.  
 ; APPLICANT: Sampson, Andrew Johnson  
 ; APPLICANT: Blacker, Deborah Lynne  
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10  
 ; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER  
 ; FILE REFERENCE: 37481-3308  
 ; CURRENT APPLICATION NUMBER: US/10/282,174  
 ; PRIOR FILING DATE: 2002-10-25  
 ; PRIOR APPLICATION NUMBER: US 60/339,525  
 ; PRIOR FILING DATE: 2001-10-25  
 ; PRIOR APPLICATION NUMBER: US 60/338,010  
 ; PRIOR FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/336,929  
 ; PRIOR FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/338,363  
 ; PRIOR FILING DATE: 2001-11-09  
 ; PRIOR APPLICATION NUMBER: US 60/337,052  
 ; PRIOR FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: US 60/368,919  
 ; PRIOR FILING DATE: 2002-03-28  
 ; NUMBER OF SEQ ID NOS: 564  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 234  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 US-10-282-174-234

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2321 ATCCGCCACCTGGCGCTCC 2340  
 |||||  
 Db 1 ATCCGCCACCTGGGACTTC 20

RESULT 1538  
 US-10-160-807-22  
 ; Sequence 22, Application US/10160807  
 ; Publication No. US20030224514A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: William Gaarde  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Andrew T. Watt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION  
 ; FILE REFERENCE: RTS-0189  
 ; CURRENT APPLICATION NUMBER: US/10/160,807  
 ; PRIOR FILING DATE: 2002-05-31  
 ; NUMBER OF SEQ ID NOS: 296  
 ; SEQ ID NO 22  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-160-807-22

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2341 CAAAGTGGGATTACAGG 2360  
 |||||  
 Db 1 CAAAGTGGGATTACAGG 20

RESULT 1539  
 US-10-160-807-175/c  
 ; Sequence 175, Application US/10160807

```

; Publication No. US20030224514A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/160,807
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 175
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-160-807-175

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
Db 20 CAAGTAGCTGGGATTACAGG 1

RESULT 1540
US-10-388-263-680
; Sequence 680, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 680
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-680

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2275 GGTTTCACCGTGTAGCCAG 2294
Db 1 GGTTTCACCATGTGGTCAG 20

RESULT 1541
US-10-388-263-681
; Sequence 681, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.

```

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; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 681
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-681

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2146 TCTTGGCTCACTGCAAGCTC 2165
Db 1 TCTCGGCTCACTACAACCTC 20

RESULT 1542
US-10-388-263-697
; Sequence 697, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-697

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGC 2361
Db 1 AAGTAGCTGGGATTACAGC 20

```

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RESULT 1543
US-10-388-263-714
; Sequence 714, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowbert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeill, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Saemor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 714
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-714

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGGTCTCG 2304
||||| ||||| ||||| |||||
Db 1 TGTGGCCAGGTTGGTCTGG 20

RESULT 1544
US-10-177-798-40/c
; Sequence 40, Application US/10177798
; Publication No. US20030235912A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ORPHAN G-PROTEIN COUPLED RECEPTOR GPRC5B
; FILE REFERENCE: PTD-0047
; CURRENT APPLICATION NUMBER: US/10/177,798
; CURRENT FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 70
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-798-40

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 981 CTTGATCGTGGTGAAGTGA 1000
||||| ||||| ||||| |||||
Db 20 CCTGATGCTGGTGAAGTCA 1

RESULT 1545
US-10-199-676-54/c
; Sequence 54, Application US/10199676
```

```
; Publication No. US20040014051A1
; GENERAL INFORMATION:
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF BREAST CANCER-1 EXPRESSION
; FILE REFERENCE: PTD-0017
; CURRENT APPLICATION NUMBER: US/10/199,676
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-199-676-54

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTTGCTC 2116
||||| ||||| ||||| |||||
Db 20 TTTGAGACAGGGTCTTACTC 1

RESULT 1546
US-10-199-676-79
; Sequence 79, Application US/10199676
; Publication No. US20040014051A1
; GENERAL INFORMATION:
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF BREAST CANCER-1 EXPRESSION
; FILE REFERENCE: PTD-0017
; CURRENT APPLICATION NUMBER: US/10/199,676
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-199-676-79

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTTGCTC 2116
||||| ||||| ||||| |||||
Db 1 TTTGAGACAGGGTCTTACTC 20

RESULT 1547
US-10-210-556-77
; Sequence 77, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowbert
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION
; FILE REFERENCE: PTD-0015
; CURRENT APPLICATION NUMBER: US/10/210,556
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 77
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

## US-10-210-556-77

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2292 CAGGATCGTCTCGATCTCCT 2311  
|||||  
DB 1 CAGGCTGGTTTCGAACCTCT 20

## RESULT 1548

US-10-210-556-195/c  
; Sequence 195, Application US/10210556  
; Publication No. US20040023904A1  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowart  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION  
; FILE REFERENCE: PTS-0015  
; CURRENT APPLICATION NUMBER: US/10/210,556  
; CURRENT FILING DATE: 2002-07-31  
; NUMBER OF SEQ ID NOS: 227  
; SEQ ID NO 195  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-210-556-195

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2292 CAGGATCGTCTCGATCTCCT 2311  
|||||  
DB 20 CAGGCTGGTTTCGAACCTCT 1

## RESULT 1549

US-10-237-614-17/c  
; Sequence 17, Application US/10237614  
; Publication No. US20040048259A1  
; GENERAL INFORMATION:  
; APPLICANT: SOMIARI, RICHARD IDEM  
; APPLICANT: SOMIARI, STELLA BASSEY  
; APPLICANT: JACOBS, F. NICHOLAS  
; APPLICANT: JORDAN, RICK  
; TITLE OF INVENTION: MULTIPLE-GENE DIAGNOSTIC PROBES AND ASSAY KITS AND  
; TITLE OF INVENTION: METHOD FOR THE ASSESSMENT OF MULTIPLE MARKERS FOR  
; TITLE OF INVENTION: BREAST CANCER PROGNOSIS  
; FILE REFERENCE: 13168.0006  
; CURRENT APPLICATION NUMBER: US/10/237,614  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-237-614-17

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2236 CCACACCTGGCTAATTTT 2255  
|||||  
DB 20 CCAGACTTGGCTAATTTAT 1

## RESULT 1550

US-10-147-299A-11  
; Sequence 11, Application US/10147299A  
; Publication No. US20040058323A1  
; GENERAL INFORMATION:  
; APPLICANT: KO, ALBERT I.  
; APPLICANT: HAAKE, DAVID A.  
; APPLICANT: REIS, MITERMAYER GALVAO  
; APPLICANT: MATSUNAGA, JAMES  
; APPLICANT: CRODA, JULIO HENRIQUE ROSA  
; APPLICANT: SIQUEIRA, ISADORA CRISTINA  
; APPLICANT: RILEY, LEE W.  
; APPLICANT: BAROCCHI, MICHELE  
; APPLICANT: YOUNG, TRACY ANN  
; TITLE OF INVENTION: PROTEINS WITH REPETITIVE BACTERIAL-IG-LIKE (BIG)  
; FILE REFERENCE: 3673-19  
; CURRENT APPLICATION NUMBER: US/10/147,299A  
; CURRENT FILING DATE: 2002-05-17  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: probe  
US-10-147-299A-11

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1446 GATGATAAAATTACACAAGC 1465  
|||||  
DB 1 GATTTTAAAGTTACACAAGC 20

## RESULT 1551

US-10-655-847-22  
; Sequence 22, Application US/10655847  
; Publication No. US20040063129A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION  
; FILE REFERENCE: RTS-0189  
; CURRENT APPLICATION NUMBER: US/10/655,847  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US/10/160,807  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 296  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-655-847-22

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2341 CAAAGTGTGGGATTACAGS 2360  
|||||  
DB 1 CAAGTAGCTGGGATTACAGG 20

## RESULT 1552

```
US-10-655-847-175/c
; Sequence 175, Application US/10655847
; Publication No. US20040063129A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/655,847
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US/10/160,807
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 175
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-655-847-175

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2341 CAAAGTGTCTGGGATTACAGG 2360
Db 20 CAAAGTGTCTGGGATTACAGG 1

RESULT 1553
US-10-683-386-42/c
; Sequence 42, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, VOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOKOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-42

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2048 TTTTTCCTTAATATGAT 2067
Db 20 TTTTTCCTTAATATATAT 1

RESULT 1554
US-10-728-509-150

; Sequence 150, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 150
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-150

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGCATGAG 2366
Db 1 GCTGGGATTAAAGCGTGGC 20

RESULT 1555
US-10-304-116-92
; Sequence 92, Application US/10304116
; Publication No. US20040101857A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF CYTOKINE-INDUCIBLE KINASE EXPRESSION
; FILE REFERENCE: RTS-0397
; CURRENT APPLICATION NUMBER: US/10/304,116
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-116-92

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTTGCTCTGT 2119
Db 1 GAGATGGAGTCTCGCTCTGT 20

RESULT 1556
US-10-304-116-138/c
; Sequence 138, Application US/10304116
; Publication No. US20040101857A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF CYTOKINE-INDUCIBLE KINASE EXPRESSION
; FILE REFERENCE: RTS-0397
; CURRENT APPLICATION NUMBER: US/10/304,116
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 138
; LENGTH: 20
; TYPE: DNA
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; ORGANISM: H. sapiens
; FEATURE:
US-10-304-116-138

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTGTCTGT 2119
|||||
Db 20 GAGATGGAGTCTGCTCTGT 1

RESULT 1557
US-10-303-325-84
; Sequence 84, Application US/10303325
; Publication No. US20040102395A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: MODULATION OF IAP-LIKE EXPRESSION
; FILE REFERENCE: RTS-0434
; CURRENT APPLICATION NUMBER: US/10/303,325
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 84
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-325-84

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2109 TCTTGCTCTGTACCCAGGC 2128
|||||
Db 1 TCTCGCTCTGTACCCGGGC 20

RESULT 1558
US-10-303-325-150/c
; Sequence 150, Application US/10303325
; Publication No. US20040102395A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: MODULATION OF IAP-LIKE EXPRESSION
; FILE REFERENCE: RTS-0434
; CURRENT APPLICATION NUMBER: US/10/303,325
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 150
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-303-325-150

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2109 TCTTGCTCTGTACCCAGGC 2128
|||||
Db 20 TCTCGCTCTGTACCCGGGC 1

RESULT 1559
US-10-688-706-682/c
; Sequence 682, Application US/10688706
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```
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 682
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-682

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1346 CAAACTGGAAACTCAACAC 1365
|||||
Db 20 CAAACTGTAAGACTTAAAC 1

RESULT 1560
US-10-318-819A-74
; Sequence 74, Application US/10318819A
; Publication No. US20040115645A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DRAK2 EXPRESSION
; FILE REFERENCE: PTS-0069
; CURRENT APPLICATION NUMBER: US/10/318,819A
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 133
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-318-819A-74

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2107 AGTCTTGCTCTGTACCCAG 2126
|||||
Db 1 AGTGTGCTCTGTGCGCCAG 20

RESULT 1561
US-10-318-819A-126/c
; Sequence 126, Application US/10318819A
; Publication No. US20040115645A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DRAK2 EXPRESSION
; FILE REFERENCE: PTS-0069
; CURRENT APPLICATION NUMBER: US/10/318,819A
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 133
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
```

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; ORGANISM: H. sapiens
; FEATURE:
US-10-318-819A-126

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2107 AGCTTGCTCTGTTACCCAG 2126
Db 20 AGTGTGCTCTGTCGCCAG 1

RESULT 1562
US-10-671-395-656/c
; Sequence 656, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 656
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-656

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2150 GGCTCACTGCAAGCTCTGCC 2169
Db 20 GGCTCACTGCAAGCTCTGCC 1

RESULT 1563
US-10-671-395-668/c
; Sequence 668, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 668
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-668

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2107 AGCTTGCTCTGTTACCCAG 2126
Db 20 AGTGTGCTCTGTCGCCAG 1

RESULT 1562
US-10-671-395-656/c
; Sequence 656, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 656
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-656

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2150 GGCTCACTGCAAGCTCTGCC 2169
Db 20 GGCTCACTGCAAGCTCTGCC 1

RESULT 1563
US-10-671-395-668/c
; Sequence 668, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 668
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-668

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2149 TGGCTCACTGCAAGCTCTGC 2168
Db 20 TGGCTCACTGCAAGCTCTGC 1

RESULT 1564
US-10-671-395-696/c
; Sequence 696, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 696
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-696

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCAC 2370
Db 20 GGATGACAGGCATGAATCAC 1

RESULT 1565
US-10-671-395-863/c
; Sequence 863, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 863
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-863

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2235 ACCACACCTGGCTAATTTT 2254
Db 20 ACCATACCCAGCTAATTTT 1

RESULT 1566
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1261
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1261

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2118 GTTACCCAGGCTGGAGTGCA 2137
Db 20 GTTGCCCAAGCTGGAGTGAA 1

RESULT 1571
US-10-671-395-1269/c
; Sequence 1269, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1269
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1269

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2350 GGGATTACGCGCATGACCCA 2369
Db 20 GGGATGACGCGCATGAATCA 1

RESULT 1572
US-10-671-395-1448/c
; Sequence 1448, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1448
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1448

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2195 GCCTCAGCCTCCCAATTAGC 2214
Db 20 GCCTCAGCCTCCTGAGTAGC 1

RESULT 1573
US-10-671-395-1453/c
; Sequence 1453, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1453
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1453

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2196 CCTCAGCCTCCCAATTAGCT 2215
Db 20 CCTCAGCCTCCTGAGTAGCT 1

RESULT 1574
US-10-671-395-1517/c
; Sequence 1517, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1517
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1517

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2319 TGATCGCCACCTCGGCCT 2338
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/ APPLICANT: Gierse, James K
/ TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
/ TITLE OF INVENTION: EXPRESSION
/ FILE REFERENCE: 1179/1/US
/ CURRENT APPLICATION NUMBER: US/10/671,395
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: 60/413,549
/ PRIOR FILING DATE: 2002-09-25
/ NUMBER OF SEQ ID NOS: 1809
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1745
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: Human PGE2 antisense
US-10-671-195-1745

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```
Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2285 TGTTAGCCAGGATGGTCTCG 2304
    ||||| ||||| ||||| ||||| |||||
Db 20 TGTTGCCAGGAGGGTCTCG 1

RESULT 1584
US-10-671-395-1751/c
; Sequence 1751, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671.395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1751
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1751

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2322 TCGGCCACCTCGGCTCC 2341
    ||||| ||||| ||||| ||||| |||||
Db 20 TCCACGGCTCGGCTCCC 1

RESULT 1585
US-10-819-244-87/c
; Sequence 87, Application US/10819244
; Publication No. US20040171575A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERFERON GAMMA RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0235
; CURRENT APPLICATION NUMBER: US/10/819,244
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: US/09/843,377
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-819-244-87

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2108 GTCTTGCTCTGTACCCAGG 2127
    ||||| ||||| ||||| ||||| |||||
Db 20 GTCTTGCACTGTGCCCCAGG 1
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RESULT 1586
US-10-819-244-89
; Sequence 89, Application US/10819244
; Publication No. US20040171575A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERFERON GAMMA RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0235
; CURRENT APPLICATION NUMBER: US/10/819,244
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: US/09/843,377
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 89
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-819-244-89

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2189 TCTCTGCTCGCTCAGCTCCCA 2208
    ||||| ||||| ||||| ||||| |||||
Db 1 TCTCTTGCACTCAGCTCTCA 20

RESULT 1587
US-10-776-013-45
; Sequence 45, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-776-013-45

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
```

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1460 ACAAGCTTCACATCACAAG 1479  
Db 1 ACAAGCTTCATGGTCACAAG 20

## RESULT 1588

US-10-010-802-81  
; Sequence 81, Application US/10010802  
; Publication No. US20030078220A1  
; GENERAL INFORMATION:  
; APPLICANT: Genaisance Pharmaceuticals  
; APPLICANT: Chew, Anne  
; APPLICANT: Denton, R. Rex  
; APPLICANT: Duda, Amy  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Stephens, J. Claiborne  
; APPLICANT: Windemuth, Andreas  
; TITLE OF INVENTION: Drug Target Isoenes: Polymorphisms in the Interleukin  
; FILE REFERENCE: MWH-0002US2 IL4R alpha  
; CURRENT APPLICATION NUMBER: US/10/010,802  
; CURRENT FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: PCT/US00/19094  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 81  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-010-802-81

Query Match 0.6%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2126 GCCTGGAGTCAGTG 2140  
Db 1 GCCTGGAGTCAGTG 15

## RESULT 1589

US-10-092-885-46/c  
; Sequence 46, Application US/10092885  
; Publication No. US20030190618A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMAL, BABRU  
; APPLICANT: LI, YUAN  
; APPLICANT: HERMIDA, LEANDRO C.  
; APPLICANT: HOPPA, NANCY L.  
; APPLICANT: JOHE, KARL K.  
; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG  
; FILE REFERENCE: 0109015/026  
; CURRENT APPLICATION NUMBER: US/10/092,885  
; CURRENT FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-092-885-46

Query Match 0.6%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGCT 2349  
Db 15 GCCTCCCAAGTGCT 1

RESULT 1590  
US-10-092-885-48/c  
; Sequence 48, Application US/10092885  
; Publication No. US20030190618A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMAL, BABRU  
; APPLICANT: LI, YUAN  
; APPLICANT: HERMIDA, LEANDRO C.  
; APPLICANT: HOPPA, NANCY L.  
; APPLICANT: JOHE, KARL K.  
; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG  
; FILE REFERENCE: 0109015/026  
; CURRENT APPLICATION NUMBER: US/10/092,885  
; CURRENT FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 48  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-092-885-48

Query Match 0.6%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGCT 2349  
Db 15 GCCTCCCAAGTGCT 1

## RESULT 1591

US-10-156-306-1660  
; Sequence 1660, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1660  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-1660

Query Match 0.6%; Score 15; DB 1; Length 17;  
Best Local Similarity 73.3%; Pred. No. 1.5e+03;  
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2147 CTTGGCTCACTGCAA 2161  
Db 1 CUUGGCUCACUGCAA 15

## RESULT 1592

US-10-156-306-1670  
; Sequence 1670, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBHB01-664-A (400/050)



; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1670  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-1670

Query Match 0.6%; Score 15; DB 1; Length 17;  
Best Local Similarity 66.7%; Pred. No. 1.5e+03;  
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2187 ATTCTCCTGCTCAG 2201  
||:||||:||||  
Db 3 AUUCCUGCCUCAG 17

RESULT 1593  
US-10-156-306-1674  
; Sequence 1674, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Leve  
; FILE REFERENCE: MH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1674  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-1674

Query Match 0.6%; Score 15; DB 1; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2192 CCTGCTCAGCCCTCC 2206  
||:||||:||||  
Db 1 CCUGCCUCAGCCUCC 15

RESULT 1594  
US-10-156-306-2408  
; Sequence 2408, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: MH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2408  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-2408

Query Match 0.6%; Score 15; DB 1; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2269 AGACAGGGTTTCACC 2283

Db 2 AGACAGGGUUCACC 16  
|||||||:||||

RESULT 1595  
US-10-238-700-664  
; Sequence 664, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve  
; FILE REFERENCE: 400/057 (MH01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 664  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-664

Query Match 0.6%; Score 15; DB 1; Length 17;  
Best Local Similarity 73.3%; Pred. No. 1.5e+03;  
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1228 CTTTCATGCAATGAAA 1242  
||:||||:||||  
Db 3 CUUAGGCAUGAAA 17

RESULT 1596  
US-10-238-700-698  
; Sequence 698, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve  
; FILE REFERENCE: 400/057 (MH01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 698  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-698

Query Match 0.6%; Score 15; DB 1; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGGC 2361  
||:||||:||||  
Db 3 GCUGGGAUACAGGC 17

RESULT 1597  
US-10-061-201-696  
; Sequence 696, Application US/10061201  
; Publication No. US20030166229A1  
; GENERAL INFORMATION:

```
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 696
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-696
```

```
Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 913 TAATAAGGGAGATAT 927
Db 2 TAATAAGGGAGATAT 16
```

```
RESULT 1598
US-10-061-201-697
; Sequence 697, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
```

```
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 697
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-697
```

```
Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 913 TAATAAGGGAGATAT 927
Db 1 TAATAAGGGAGATAT 15
```

```
RESULT 1599
US-10-336-472-138
; Sequence 138, Application US/10336472
; Publication No. US20040043929A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Ballinger, Robert A.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Chant, John S.
; APPLICANT: Berghs, Constance
; APPLICANT: Gangolli, Baha A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gilbert, Jennifer A.
; APPLICANT: Gunther, Erik
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Mishra, Vishnu
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Stone, David J.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Ort, Tatiana
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-533C
; CURRENT APPLICATION NUMBER: US/10/336,472
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: 09/746,491
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 10/005,041
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 10/023,681
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 10/024,212
; PRIOR FILING DATE: 2001-12-18
```

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; PRIOR APPLICATION NUMBER: 10/055,569
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/092,900
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 10/136,826
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 10/236,417
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/345,092
; PRIOR FILING DATE: 2002-01-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: CuraSegList version 0.1
; SEQ ID NO 138
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-336-472-138

Query Match          0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 CCTGGCCCGGAGAGT 186
Db 1 CCTGGCCCGGAGAGT 15

RESULT 1600
US-10-255-434-9
; Sequence 9, Application US/10255434
; Publication No. US20030129626A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Kirsten V.
; APPLICANT: Hyldig-Nielsen, Jens J.
; APPLICANT: Williams, Brett F.
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly
; TITLE OF INVENTION: Distributed Repeat Sequences In Genomic Nucleic Acid
; FILE REFERENCE: BP0101-US
; CURRENT APPLICATION NUMBER: US/10/255,434
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic
; OTHER INFORMATION: Oligomer Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe
US-10-255-434-9

Query Match          0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGGC 2361
Db 3 GCTGGGATTACAGGC 17

RESULT 1601
US-10-255-434-21/c
; Sequence 21, Application US/10255434
; Publication No. US20030129626A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Kirsten V.
; APPLICANT: Hyldig-Nielsen, Jens J.
; APPLICANT: Williams, Brett F.
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly
; TITLE OF INVENTION: Distributed Repeat Sequences In Genomic Nucleic Acid
; FILE REFERENCE: BP0101-US
; CURRENT APPLICATION NUMBER: US/10/255,434
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic
; OTHER INFORMATION: Oligomer Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe
US-10-255-434-21

Query Match          0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGGC 2361
Db 16 GCTGGGATTACAGGC 2

RESULT 1602
US-10-108-260A-5312/c
; Sequence 5312, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5312
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized
US-10-108-260A-5312

Query Match          0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 TTCAGGAGAGAAAC 750
Db 18 TTCAGGAGAGAAAC 4

RESULT 1603
US-10-007-078-84/c
; Sequence 84, Application US/10007078
; Publication No. US20030105042A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF EIF2C1 EXPRESSION
; FILE REFERENCE: RTS-0236
; CURRENT APPLICATION NUMBER: US/10/007,078
; CURRENT FILING DATE: 2001-11-08
```

```
/ NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 84
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-007-078-84

Query Match          0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2144 GATCTTGGCTCACTG 2158
Db      |||||
        15 GATCTGGCTCACTG 1

RESULT 1604
US-10-349-143-8216
; Sequence 8216, Application US/10349143
; Publication No. US2004000584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Il'ya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8216
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-14468 for SEQ 351, in complete
US-10-349-143-8216

Query Match          0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 829 ATGAATTATCTCGTG 843
Db      |||||
        1 ATGAATTATCTCGTG 15

RESULT 1605
US-10-671-395-1324/c
; Sequence 1324, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; OTHER INFORMATION: Human PGE2 antisense

QY 2347 GCTGGGATTACAGGC 2361
Db      |||||
        15 GCTGGGATTACAGGC 2

RESULT 1606
US-10-671-395-1390/c
; Sequence 1390, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1390
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1390

Query Match          0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGGC 2361
Db      |||||
        16 GCTGGGATTACAGGC 2

RESULT 1607
US-10-671-395-1438/c
; Sequence 1438, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1438
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
```

US-10-671-395-1438

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361  
Db 17 GCTGGGATTACAGC 3

RESULT 1608

US-10-671-395-1511/c  
; Sequence 1511, Application US/10671395  
; Publication No. US20040132063A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Gierse, James K  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE  
; FILE REFERENCE: 1179/1/US  
; CURRENT APPLICATION NUMBER: US/10/671,395  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: 60/413,549  
; PRIOR FILING DATE: 2002-09-25  
; NUMBER OF SEQ ID NOS: 1809  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1511  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Human PGE2 antisense  
US-10-671-395-1511

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361  
Db 18 GCTGGGATTACAGC 4

RESULT 1609

US-10-671-395-1558/c  
; Sequence 1558, Application US/10671395  
; Publication No. US20040132063A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Gierse, James K  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE  
; FILE REFERENCE: 1179/1/US  
; CURRENT APPLICATION NUMBER: US/10/671,395  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: 60/413,549  
; PRIOR FILING DATE: 2002-09-25  
; NUMBER OF SEQ ID NOS: 1809  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1558  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Human PGE2 antisense  
US-10-671-395-1558

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361

Db 19 GCTGGGATTACAGC 5  
|||||

RESULT 1610

US-10-671-395-1568/c  
; Sequence 1568, Application US/10671395  
; Publication No. US20040132063A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Gierse, James K  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE  
; FILE REFERENCE: 1179/1/US  
; CURRENT APPLICATION NUMBER: US/10/671,395  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: 60/413,549  
; PRIOR FILING DATE: 2002-09-25  
; NUMBER OF SEQ ID NOS: 1809  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1568  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Human PGE2 antisense  
US-10-671-395-1568

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361  
Db 20 GCTGGGATTACAGC 6

RESULT 1611

US-09-784-423-69/c  
; Sequence 69, Application US/09784423  
; Patent No. US20020012924A1  
; GENERAL INFORMATION:  
; APPLICANT: Schumm, James W.  
; Bacher, Jeffery W.  
; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Promega Corporation  
; STREET: 2800 Woods Hollow Road  
; CITY: Madison  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53711-5399  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Word 97 (DOS text format)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/784,423  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/018,584  
; FILING DATE: 04-Feb-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Grady J. Frenchick  
; REGISTRATION NUMBER: 29,018  
; REFERENCE/DOCKET NUMBER: 16026.9180  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 257-3501

TELEFAX: (608) 257-2275  
INFORMATION FOR SEQ ID NO: 69  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: Nucleic Acid  
STRANDNESS: Single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID  
US-09-784-423-69

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 1612
US-09-935-223-7
; Sequence 7, Application US/09935223
; Publication No. US20020086983A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
; FILE REFERENCE: TJU3499
; CURRENT APPLICATION NUMBER: US/09/935,223
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 09/723,450
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
; US-09-935-223-7

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RESULT 1613  
US-09-982-262B-4/c  
Sequence 4, Application US/09982262B  
Publication NO. US20030077565A1  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Christopher K. Mirabelli  
TITLE OF INVENTION: OLIGONUCLEOTIDE MODULATION OF CELL ADHESION  
FILE REFERENCE: ISPH-0612  
CURRENT APPLICATION NUMBER: US/09/982,262B  
CURRENT FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 09/659,288  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 09/128,496  
PRIOR FILING DATE: 1998-08-03  
PRIOR APPLICATION NUMBER: 08/440,740  
PRIOR FILING DATE: 1995-05-12  
PRIOR APPLICATION NUMBER: 08/063,167

```

; PRIOR FILING DATE: 1993-05-17
; PRIOR APPLICATION NUMBER: 07/969,151
; PRIOR FILING DATE: 1993-02-10
; PRIOR APPLICATION NUMBER: 08/007,997
; PRIOR FILING DATE: 1993-01-21
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-982-262B-4

```

```

RESULT 1614
US-10-351-951-71/c
, Sequence 71, Application US/10351951
, Publication NO. US2003020380A1
, GENERAL INFORMATION:
, APPLICANT: Stefansson, Stefan E.
, TITLE OF INVENTION: GENE LINKED TO OSTEOARTHRITIS
, FILE REFERENCE: 2345.2043-004
, CURRENT APPLICATION NUMBER: US/10/351,951
, CURRENT FILING DATE: 2003-01-24
, PRIOR APPLICATION NUMBER: 10/057,312
, PRIOR FILING DATE: 2002-01-25
, PRIOR APPLICATION NUMBER: 60/431,538
, PRIOR FILING DATE: 2002-12-05
, NUMBER OF SEQ ID NOS: 132
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 71
, LENGTH: 18
, TYPE: DNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: primer that hybridizes to the human MATN3 gene
US-10-351-951-71

```

RESULT 1615  
US-10-454-663-4/c  
; Sequence 4, Application US/10454663  
; Publication No. US20040033977A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Christopher K. Mirabelli  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MODULATION OF CELL ADHESION  
; FILE REFERENCE: ISPH-0744  
; CURRENT APPLICATION NUMBER: US/10/454,663  
; CURRENT FILING DATE: 2003-06-04  
; PRIOR APPLICATION NUMBER: 09/982,262  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/659,288  
; PRIOR FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 09/128,496  
; PRIOR FILING DATE: 1998-08-03

; PRIOR APPLICATION NUMBER: 08/440,740  
; PRIOR FILING DATE: 1995-05-12  
; PRIOR APPLICATION NUMBER: 08/063,167  
; PRIOR FILING DATE: 1993-05-17  
; PRIOR APPLICATION NUMBER: 07/969,151  
; PRIOR FILING DATE: 1993-02-10  
; PRIOR APPLICATION NUMBER: 08/007,997  
; PRIOR FILING DATE: 1993-01-21  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 4  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-454-663-4

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2322 TCGCCACCTCGGCCTC 2339  
||| ||||| |||||  
Db 18 TCTCCACCTCAGCCTC 1

RESULT 1616  
US-10-627-757-40  
; Sequence 40, Application US/10627757  
; Publication No. US20040091914A1  
; GENERAL INFORMATION:  
; APPLICANT: KOUCHI YASUHIRO  
; APPLICANT: MASASGO AKINORI  
; APPLICANT: TAKAHATI TAKAYUKI  
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK  
; FILE REFERENCE: Q76319  
; CURRENT APPLICATION NUMBER: US/10/627,757  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: JP P2002-226612  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Designed DNA based on OPTN gene  
US-10-627-757-40

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2321 ATCGCCACCTCGGCCT 2338  
||| ||||| |||||  
Db 1 ATCACCACCTCGACCT 18

RESULT 1617  
US-10-473-126-613/c  
; Sequence 613, Application US/10473126  
; Publication No. US20040234973A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell  
; FILE REFERENCE: proliferative disorders  
; CURRENT APPLICATION NUMBER: US/10/473,126  
; CURRENT FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 1258  
; SEQ ID NO 613  
; LENGTH: 18

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Detection oligonucleotide for CDH3  
US-10-473-126-613

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2235 ACCACACCTGGCTAATTT 2252  
||| ||||| |||||  
Db 18 ACCACACCTGGCTAATTT 1

RESULT 1618  
US-09-784-423-64/c  
; Sequence 64, Application US/09784423  
; Patent No. US20020012924A1  
; GENERAL INFORMATION:  
; APPLICANT: Schumm, James W.  
; Bacher, Jeffery W.  
; TITLE OF INVENTION: MATERIALS AND METHODS FOR  
IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM  
REPEAT DNA MARKERS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Promega Corporation  
; STREET: 2800 Woods Hollow Road  
; CITY: Madison  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53711-5399  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb  
; COMPUTER: IBM compatible PC  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Word 97 (DOS text format)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/784,423  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/018,584  
; FILING DATE: 04-Feb-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Grady J. Frenchick  
; REGISTRATION NUMBER: 29,018  
; REFERENCE/DOCKET NUMBER: 16026.9180  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 257-3501  
; TELEFAX: (608) 257-2275  
; INFORMATION FOR SEQ ID NO: 64  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 64  
US-09-784-423-64

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2106 GAGTCTGCTGTTTACC 2123  
||| ||||| |||||  
Db 19 GAGTCTGCTGTTTACC 2

RESULT 1619  
US-10-444-925-599/c  
; Sequence 599, Application US/10444925

Publication No. US20040009946A1  
GENERAL INFORMATION:  
APPLICANT: Lewis, Stephen Patrick  
APPLICANT: Klinghoffer, Richard  
APPLICANT: Wilson, Linda K.  
TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION  
FILE REFERENCE: 200125.441  
CURRENT APPLICATION NUMBER: US/10/444,925  
NUMBER OF SEQ ID NOS: 599  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 599  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Small interfering RNA  
US-10-444-925-599

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 802 CAATTAGTGAGACAGAAG 819  
| | | | | | | | | | | | | | | | | | |  
Db 19 CCATTAGTGAGACACAAG 2

RESULT 1620  
US-10-636-065-128  
Sequence 128, Application US/10636065  
Publication No. US20040127694A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: LaCasse, Eric  
APPLICANT: Baird, Stephen  
APPLICANT: Holcik, Martin  
APPLICANT: Young, Sean  
TITLE OF INVENTION: Antisense TAP Nucleic Acids and Uses  
TITLE OF INVENTION: Thereof  
FILE REFERENCE: 07891/025005  
CURRENT APPLICATION NUMBER: US/10/636,065  
CURRENT FILING DATE: 2003-08-07  
PRIOR APPLICATION NUMBER: 09/672,717  
PRIOR FILING DATE: 2000-09-28  
NUMBER OF SEQ ID NOS: 231  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 128  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: based on Homo sapiens  
US-10-636-065-128

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1093 TTAGTGAAGAGGACAAG 1110  
| | | | | | | | | | | | | | | | | | |  
Db 2 TTAGTGAAGAGGACAAG 19

RESULT 1621  
US-10-670-011-10  
Sequence 10, Application US/10670011  
Publication No. US20040209832A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: McSwiggen, James  
APPLICANT: Beigelman, Leonid

APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: 400/132 (MBHB02-742-G)  
CURRENT APPLICATION NUMBER: US/10/670,011  
CURRENT FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: PCT/US03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US60/399,348  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US60/440,129  
PRIOR FILING DATE: 2003-01-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 427  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 10  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re  
US-10-670-011-10

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 27.8%; Pred. No. 1.5e+03;  
Matches 5; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Qy 2046 TTTTCTTCTTAATAT 2063  
| | | | | | | | | | | | | | | | | | |  
Db 2 UUCUUUUUUUAAACAU 19

RESULT 1622  
US-10-670-011-106/c  
Sequence 106, Application US/10670011  
Publication No. US20040209832A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: McSwiggen, James  
APPLICANT: Beigelman, Leonid  
APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: 400/132 (MBHB02-742-G)  
CURRENT APPLICATION NUMBER: US/10/670,011  
CURRENT FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: PCT/US03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US60/399,348



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; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 427
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-670-011-106

Query Match          0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2046 TTTTTCCTCTAAATAT 2063
      |||||||||
Db  18  TTCTTTTCTTAAACAT 1

RESULT 1623
US-09-764-887-575/c
; Sequence 575, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PALL3
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 575
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-575

Query Match          0.6%; Score 14.8; DB 1; Length 66;
Best Local Similarity 59.5%; Pred. No. 9.6e+02;
Matches 25; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy  1031 AGTTTCAGATCAGTTTGTAGTGTAGNATTTGAAGTTGAATCTCT 1072
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  58  AGTTTGACACGCGCTGTGTAATATGTTGTAACCCCGTCTCT 17

RESULT 1624
US-10-073-961-575/c
; Sequence 575, Application US/10073961
; Publication No. US20030077602A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PALL3C1
; CURRENT APPLICATION NUMBER: US/10/073,961
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/764,887
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
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; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
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;  
; PRIOR FILING DATE: 1999-07-21

US-10-212-872-962/c

; PRIOR APPLICATION NUMBER: 09/383,316  
; PRIOR FILING DATE: 1999-08-25  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-739-909-5

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2146 TCTGGCTCACTGCAA 2161  
||| |||||  
DB 1 TCTGGCTCACTGCAA 16

## RESULT 1630

US-09-739-909-6  
; Sequence 6, Application US/09739909  
; Publication No. US20030022163A1  
; GENERAL INFORMATION:  
; APPLICANT: Mandrekar, Michelle N.  
; APPLICANT: Tereba, Allan  
; APPLICANT: Shultz, John W.  
; TITLE OF INVENTION: Detection of Repetitive Nucleic Acid Sequences  
; FILE REFERENCE: US CIP of PRO-104.0  
; CURRENT APPLICATION NUMBER: US/09/739,909  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 09/358,972  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 09/383,316  
; PRIOR FILING DATE: 1999-08-25  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-739-909-6

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGCGTGAG 2366  
||| |||||  
DB 1 GGATTACAGCGTGAG 16

## RESULT 1631

US-10-255-434-5/c  
; Sequence 5, Application US/10255434  
; Publication No. US20030129626A1  
; GENERAL INFORMATION:  
; APPLICANT: Nielsen, Kirsten V.  
; APPLICANT: Hyldig-Nielsen, Jens J.  
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The  
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly  
; TITLE OF INVENTION: Distributed Repeat Sequences In Genomic Nucleic Acid  
; FILE REFERENCE: BP0101-US  
; CURRENT APPLICATION NUMBER: US/10/255,434  
; CURRENT FILING DATE: 2002-09-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic  
; OTHER INFORMATION: Oligomer Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe  
; OTHER INFORMATION: Sequence  
US-10-255-434-5

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCTCCC 2341  
||| |||||  
DB 1 CCGGCTCGGCTCCC 1

## RESULT 1632

US-10-255-434-17  
; Sequence 17, Application US/10255434  
; Publication No. US20030129626A1  
; GENERAL INFORMATION:  
; APPLICANT: Nielsen, Kirsten V.  
; APPLICANT: Hyldig-Nielsen, Jens J.  
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The  
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly  
; TITLE OF INVENTION: Distributed Repeat Sequences In Genomic Nucleic Acid  
; FILE REFERENCE: BP0101-US  
; CURRENT APPLICATION NUMBER: US/10/255,434  
; CURRENT FILING DATE: 2002-09-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic  
; OTHER INFORMATION: Oligomer Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe  
; OTHER INFORMATION: Sequence  
US-10-255-434-17

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCTCCC 2341  
||| |||||  
DB 1 CCGGCTCGGCTCCC 16

## RESULT 1633

US-10-091-281-60  
; Sequence 60, Application US/10091281  
; Publication No. US20030190617A1  
; GENERAL INFORMATION:  
; APPLICANT: RAYMOND, VINCENT  
; APPLICANT: SI, ERWIN  
; APPLICANT: MORISSETTE, JEAN  
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF  
; FILE REFERENCE: 13587.338  
; CURRENT APPLICATION NUMBER: US/10/091,281  
; CURRENT FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 60  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Putative B2TF/E2.01 motif

US-10-091-281-60

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 285 AAACCCCGGATGGTGA 300  
DB 1 AAACCCCGGATGGTGA 16

RESULT 1634

US-10-092-885-43/c

; Sequence 43, Application US/10092885

; Publication No. US20030190618A1

; GENERAL INFORMATION:

; APPLICANT: SAMAL, BABRU

; APPLICANT: LI, YUAN

; APPLICANT: HERMIDA, LEANDRO C.

; APPLICANT: HOPPA, NANCY L.

; APPLICANT: JOHE, KARL K.

; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG

; FILE REFERENCE: LIBRARIES OF CDNAS

; CURRENT APPLICATION NUMBER: 0109015/026

; CURRENT FILING DATE: 2002-03-06

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 43

; LENGTH: 16

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-092-885-43

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2352 GATTACAGCGTGAGC 2367  
DB 16 GATTACAGCGTGAGC 1

RESULT 1635

US-10-092-885-55/c

; Sequence 55, Application US/10092885

; Publication No. US20030190618A1

; GENERAL INFORMATION:

; APPLICANT: SAMAL, BABRU

; APPLICANT: LI, YUAN

; APPLICANT: HERMIDA, LEANDRO C.

; APPLICANT: HOPPA, NANCY L.

; APPLICANT: JOHE, KARL K.

; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG

; FILE REFERENCE: LIBRARIES OF CDNAS

; CURRENT APPLICATION NUMBER: 0109015/026

; CURRENT FILING DATE: 2002-03-06

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 55

; LENGTH: 16

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-092-885-55

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGCGG 2275  
DB 16 TTTTAGTAGACAGCGG 1

RESULT 1636

US-09-866-108-7367

; Sequence 7367, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/006666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/006670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 7367

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-7367

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 818 AGAAATTCAGATGAA 833  
DB 2 AGAAATTCAGTGA 17

RESULT 1637

US-09-866-108-7369

; Sequence 7369, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AROMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 7369  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7369

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 819 GAAAATTCAGATGAAT 834  
|||||:|||||  
Db 1 GAAAATTCAGTGAAT 16

RESULT 1638  
US-09-776-474-380  
; Sequence 380, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boother, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Fattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK  
; FILE REFERENCE: MHB00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 380  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-380

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 1.6e+03;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAGAAGCAGTAGCAGT 950  
|||||:|||||  
Db 2 AAGACAGUCGAGU 17

RESULT 1639  
US-09-776-474-692  
; Sequence 692, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boother, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Fattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK  
; FILE REFERENCE: MHB00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 692  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-692

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 1.6e+03;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 938 AAGCAGTAGCAGTGAA 953  
|||||:|||||  
Db 1 AAGCAGUCGAGUGAA 16

RESULT 1640  
US-10-060-998-413/c  
; Sequence 413, Application US/10060998  
; Publication No. US20030104530A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1  
; FILE REFERENCE: PB01108  
; CURRENT APPLICATION NUMBER: US/10/060,998  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/343,331  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 3056

; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 413  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-998-413

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1766 TGTGCTAACTTATTC 1781  
DB 17 TGTGCTGACTTATTC 2

RESULT 1641  
US-10-060-998-415/c  
; Sequence 415, Application US/10060998  
; Publication No. US20030104530A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1  
; FILE REFERENCE: PB01108  
; CURRENT APPLICATION NUMBER: US/10/060,998  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/343,331  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 3056  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 415  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-998-415

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1765 TTGTGCTAACTTATTT 1780  
DB 16 TTGTGCTGACTTATTT 1

RESULT 1642  
US-10-156-306-524  
; Sequence 524, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 524  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-524

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 18.8%; Pred. No. 1.6e+03;  
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2045 TTTTTCCTTTCTTAAA 2060  
DB 2 UUUUUUUUUUUUUAAA 17

RESULT 1643  
US-10-156-306-525  
; Sequence 525, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 525  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-525

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 18.8%; Pred. No. 1.6e+03;  
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2045 TTTTTCCTTTCTTAAA 2060  
DB 1 UUUUUUUUUUUUUAAA 16

RESULT 1644  
US-10-156-306-534  
; Sequence 534, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 534  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-534

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 68.8%; Pred. No. 1.6e+03;  
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2113 GCTCTGTTATCCAGGC 2128  
DB 2 GCUCUGUCCCGAGGC 17

RESULT 1645  
US-10-156-306-573  
; Sequence 573, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; FILE REFERENCE: MBH01-664-A (400/050)





; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2404  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-2404

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 1.6e+03;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2356 ACAGGCGATGAGCCACC 2371  
|||||||:|||||  
DB 1 ACAGGCAUGGCCACC 16

RESULT 1651  
US-10-238-700-364/c  
; Sequence 364, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/057 (MBHB01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 364  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-364

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 450 ACTTATCTATGAAAG 465  
|||||||:|||||  
DB 16 AGTTACTATGAAAG 1

RESULT 1652  
US-10-238-700-712  
; Sequence 712, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/057 (MBHB01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 712  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-712

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTCACC 2283  
|||||||:|||||  
DB 1 GAGACGGGGUUCACC 16

RESULT 1653  
US-10-061-201-693  
; Sequence 693, Application US/10061201  
; Publication No. US20030166229A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/328,205  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 693  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-061-201-693

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 910 GTGTAATAAGGAGAT 925  
|||||||:|||||  
DB 2 GTTTAATAAGGAGAT 17

RESULT 1654  
US-10-339-793-52  
; Sequence 52, Application US/10339793  
; Publication No. US20030180764A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Shang, Jin  
; APPLICANT: Bowen, Benjamin  
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS  
; FILE REFERENCE: 37-000310US  
; CURRENT APPLICATION NUMBER: US/10/339,793  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 443  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 17  
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-339-793-52

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2320 GATCGGCCACCTCGG 2335
      ||||| ||||| |||||
Db 1 GATCCACCCACCTCGG 16

RESULT 1655
US-10-723-361-7367
; Sequence 7367, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; NUMBER OF SEQ ID NOS: 15755
; SEQ ID NO 7367
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7369

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 819 GAAATTCAGATGAAT 834
      ||||| ||||| |||||
Db 1 GAAATTCAGTTGAAT 16

RESULT 1657
US-10-498-462-2243
; Sequence 2243, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2243
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-2243

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 818 AGAAATTCAGATGAA 833
      ||||| ||||| |||||
Db 2 AGAAATTCAGTTGAA 17

RESULT 1656
US-10-723-361-7369
; Sequence 7369, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
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; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART A
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; NUMBER OF SEQ ID NOS: 15755
; SEQ ID NO 7369
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7369

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 819 GAAATTCAGATGAAT 834
      ||||| ||||| |||||
Db 1 GAAATTCAGTTGAAT 16

RESULT 1657
US-10-498-462-2243
; Sequence 2243, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2243
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-2243

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 38 GCCCTGTGTGCGGAA 53  
 |||||  
 Db 2 GCCCTGTGTGCGGAA 17

## RESULT 1658

US-10-498-462-2245  
 ; Sequence 2245, Application US/10498462  
 ; Publication No. US20040259175A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guo, Jinjiao  
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1  
 ; FILE REFERENCE: PB01102  
 ; CURRENT APPLICATION NUMBER: US/10/498,462  
 ; CURRENT FILING DATE: 2004-06-10  
 ; PRIOR APPLICATION NUMBER: US 60/339,764  
 ; PRIOR FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: PCT/US02/37506  
 ; PRIOR FILING DATE: 2002-11-22  
 ; NUMBER OF SEQ ID NOS: 3320  
 ; SOFTWARE: Aesomica Sequence Listing Engine  
 ; SEQ ID NO 2245  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-498-462-2245

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 CCCTGTGTGCGGAA 54  
 |||||  
 Db 1 CCCTGTGTGCGGAA 16

## RESULT 1659

US-09-881-012-1/c  
 ; Sequence 1, Application US/09881012  
 ; Publication No. US20020192655A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ginns, Edward I.  
 ; APPLICANT: Egeland, Janice A.  
 ; APPLICANT: Paul, Steven M.  
 ; APPLICANT: The Government of the United States of America  
 ; APPLICANT: as represented by The Secretary of the  
 ; APPLICANT: Department of Health and Human Services  
 ; TITLE OF INVENTION: Susceptibility and Resistance Genes for  
 ; TITLE OF INVENTION: Bipolar Affective Disorder  
 ; FILE REFERENCE: 015280-248110US  
 ; CURRENT APPLICATION NUMBER: US/09/881,012  
 ; CURRENT FILING DATE: 2001-06-13  
 ; PRIOR APPLICATION NUMBER: US/09/175,158  
 ; PRIOR FILING DATE: 1998-10-19  
 ; PRIOR APPLICATION NUMBER: US 60/062,924  
 ; PRIOR FILING DATE: 1997-10-20  
 ; NUMBER OF SEQ ID NOS: 240  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: D6S344 forward primer  
 US-09-881-012-1

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2118 GTTACCCAGGCTGGAG 2133  
 |||||  
 Db 16 GTGACCCAGGCTGGAG 1

RESULT 1660  
 US-09-881-012-1/c  
 ; Sequence 1, Application US/09881012  
 ; Publication No. US20040248086A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ginns, Edward I.  
 ; APPLICANT: Egeland, Janice A.  
 ; APPLICANT: Paul, Steven M.  
 ; APPLICANT: The Government of the United States of America  
 ; APPLICANT: as represented by The Secretary of the  
 ; APPLICANT: Department of Health and Human Services  
 ; TITLE OF INVENTION: Susceptibility and Resistance Genes for  
 ; TITLE OF INVENTION: Bipolar Affective Disorder  
 ; FILE REFERENCE: 015280-248110US  
 ; CURRENT APPLICATION NUMBER: US/09/881,012  
 ; CURRENT FILING DATE: 2001-06-13  
 ; PRIOR APPLICATION NUMBER: US/09/175,158  
 ; PRIOR FILING DATE: 1998-10-19  
 ; PRIOR APPLICATION NUMBER: US 60/062,924  
 ; PRIOR FILING DATE: 1997-10-20  
 ; NUMBER OF SEQ ID NOS: 240  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: D6S344 forward primer  
 US-09-881-012-1

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 1.6e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2118 GTTACCCAGGCTGGAG 2133  
 |||||  
 Db 16 GTGACCCAGGCTGGAG 1

## RESULT 1661

US-09-881-012-83/c  
 ; Sequence 83, Application US/09881012  
 ; Publication No. US20020192655A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ginns, Edward I.  
 ; APPLICANT: Egeland, Janice A.  
 ; APPLICANT: Paul, Steven M.  
 ; APPLICANT: The Government of the United States of America  
 ; APPLICANT: as represented by The Secretary of the  
 ; APPLICANT: Department of Health and Human Services  
 ; TITLE OF INVENTION: Susceptibility and Resistance Genes for  
 ; TITLE OF INVENTION: Bipolar Affective Disorder  
 ; FILE REFERENCE: 015280-248110US  
 ; CURRENT APPLICATION NUMBER: US/09/881,012  
 ; CURRENT FILING DATE: 2001-06-13  
 ; PRIOR APPLICATION NUMBER: US/09/175,158  
 ; PRIOR FILING DATE: 1998-10-19  
 ; PRIOR APPLICATION NUMBER: US 60/062,924  
 ; PRIOR FILING DATE: 1997-10-20  
 ; NUMBER OF SEQ ID NOS: 240  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 83  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: D4S422 forward primer  
 ; NAME/KEY: modified base  
 ; LOCATION: (8)...(8)  
 ; OTHER INFORMATION: n = g,a,c or t  
 US-09-881-012-83

```
Query Match          0.6%; Score 14.4; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2098 TTGAGACCGAGTCTTGC 2114
Db 18 TTGAGACGGAGTCTTGC 2

RESULT 1662
US-09-881-012-83/c
; Sequence 83, Application US/09881012
; Publication No. US20040248086A9
; GENERAL INFORMATION:
; APPLICANT: Ginns, Edward I.
; APPLICANT: Egeland, Janice A.
; APPLICANT: Paul, Steven M.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Susceptibility and Resistance Genes for
; TITLE OF INVENTION: Bipolar Affective Disorder
; FILE REFERENCE: 015280-248110US
; CURRENT APPLICATION NUMBER: US/09/881,012
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US/09/175,158
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: US 60/062,924
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D4S422 forward primer
; NAME/KEY: modified base
; LOCATION: (8)...(8)
; OTHER INFORMATION: n = g,a,c or t
US-09-881-012-83

Query Match          0.6%; Score 14.4; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2098 TTGAGACCGAGTCTTGC 2114
Db 18 TTGAGACGGAGTCTTGC 2

RESULT 1663
US-09-775-479-9
; Sequence 9, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: LECLERC, Guy
; APPLICANT: MARTEL, R,m1
; TITLE OF INVENTION: RADIOLABELLED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIOLABELLED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 12168-1US-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 18

Query Match          0.6%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2045 TTTTCTTTTCTTAAA 2060
Db 3 TTTTCTTTTCTTAAA 18

RESULT 1664
US-10-351-951-123
; Sequence 123, Application US/10351951
; Publication No. US2003020390A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Stefan E.
; TITLE OF INVENTION: GENE LINKED TO OSTEOARTHRITIS
; FILE REFERENCE: 2345.2043-004
; CURRENT APPLICATION NUMBER: US/10/351,951
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 10/057,312
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/431,538
; PRIOR FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer that hybridizes to the human MATN3 gene
US-10-351-951-123

Query Match          0.6%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2356 ACAGGCATGCGCAC 2371
Db 1 ACAGGCATGCGCAC 16

RESULT 1665
US-09-242-772-30/c
; Sequence 30, Application US/09242772
; Publication No. US20020009720A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie
; TITLE OF INVENTION: PLAG gene family and tumorigenesis
; FILE REFERENCE: VIB-011-US
; CURRENT APPLICATION NUMBER: US/09/242,772
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: EP 96202229.6
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: EP 97200130.9
; PRIOR FILING DATE: 1997-01-17
; PRIOR APPLICATION NUMBER: PCT/EP97/04759
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; FEATURE:
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! NAME/KEY: misc feature  
! OTHER INFORMATION: antisense primer D8S1828  
US-09-242-772-30

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2099 TGACCGAGCTCTGCC 2114  
||||| |||||  
Db 16 TGACACAGAGCTCTGC 1

RESULT 1666  
US-10-320-646-20/C  
! Sequence 20, Application US/10320646  
! Publication No. US20030143687A1  
! GENERAL INFORMATION:  
! APPLICANT: MAGAININ PHARMACEUTICALS, INC.  
! TITLE OF INVENTION: Biological Variability of Asthma  
! Associated Factors Useful in Treating and Diagnosing  
! Atopic Allergies Including Asthma and Related Disorders  
! NUMBER OF SEQUENCES: 36  
! CORRESPONDENCE ADDRESS:  
! ADDRESSEE: Morgan, Lewis & Bockius LLP  
! STREET: 1800 M St., NW  
! CITY: Washington  
! STATE: DC  
! COUNTRY: USA  
! ZIP: 20036  
! COMPUTER READABLE FORM:  
! MEDIUM TYPE: Floppy disk  
! COMPUTER: IBM PC compatible  
! OPERATING SYSTEM: PC-DOS/MS-DOS  
! SOFTWARE: Patent In Release #1.0, Version #1.30  
! CURRENT APPLICATION DATA:  
! APPLICATION NUMBER: US/10/320,646  
! FILING DATE: 17-Dec-2002  
! PRIOR APPLICATION DATA:  
! APPLICATION NUMBER: US/09/596,377  
! FILING DATE: 16-Jun-2000  
! APPLICATION NUMBER: US 60/032,224  
! FILING DATE: 02-DEC-1996  
! APPLICATION NUMBER: US 08/980,872  
! FILING DATE: 01-DEC-1997  
! APPLICATION NUMBER: PCT/US97/21992  
! FILING DATE: 02-DEC-1997  
! ATTORNEY/AGENT INFORMATION:  
! NAME: Michael S. Tuscan  
! REGISTRATION NUMBER: 43,210  
! REFERENCE/DOCKET NUMBER: 36870-5057-US  
! TELECOMMUNICATION INFORMATION:  
! TELEPHONE: 202 467 7000  
! TELEFAX: 202 467 7176  
! INFORMATION FOR SEQ ID NO: 20:  
! SEQUENCE CHARACTERISTICS:  
! LENGTH: 19 base pairs  
! TYPE: nucleic acid  
! STRANDEDNESS: single  
! TOPOLOGY: linear  
! MOLECULE TYPE: other nucleic acid  
! SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-320-646-20

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2322 TCCGCCCACTCTCGCC 2337  
||||| |||||  
Db 18 TCCGCCCACTCTCGCC 3

RESULT 1667  
US-10-294-228-24  
! Sequence 24, Application US/10294228  
! Publication No. US20040018176A1  
! GENERAL INFORMATION:  
! APPLICANT: Tolentino, Michael J.  
! APPLICANT: Reich, Samuel Jotham  
! TITLE OF INVENTION: Compositions and Methods for siRNA  
! TITLE OF INVENTION: Inhibition of Angiogenesis  
! FILE REFERENCE: 43826-1  
! CURRENT APPLICATION NUMBER: US/10/294,228  
! CURRENT FILING DATE: 2002-11-14  
! PRIOR APPLICATION NUMBER: US 60/398,417  
! PRIOR FILING DATE: 2002-07-24  
! NUMBER OF SEQ ID NOS: 80  
! SOFTWARE: FastSeq for Windows Version 4.0  
! SEQ ID NO 24  
! LENGTH: 19  
! TYPE: DNA  
! ORGANISM: Artificial Sequence  
! FEATURE:  
! OTHER INFORMATION: Targeting Sequence  
US-10-294-228-24

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 GAAAGATGGAGCAAGA 66  
||||| |||||  
Db 2 GAAAGATAGAGCAAGA 17

RESULT 1668  
US-10-294-228-25  
! Sequence 25, Application US/10294228  
! Publication No. US20040018176A1  
! GENERAL INFORMATION:  
! APPLICANT: Tolentino, Michael J.  
! APPLICANT: Reich, Samuel Jotham  
! TITLE OF INVENTION: Compositions and Methods for siRNA  
! TITLE OF INVENTION: Inhibition of Angiogenesis  
! FILE REFERENCE: 43826-1  
! CURRENT APPLICATION NUMBER: US/10/294,228  
! CURRENT FILING DATE: 2002-11-14  
! PRIOR APPLICATION NUMBER: US 60/398,417  
! PRIOR FILING DATE: 2002-07-24  
! NUMBER OF SEQ ID NOS: 80  
! SOFTWARE: FastSeq for Windows Version 4.0  
! SEQ ID NO 25  
! LENGTH: 19  
! TYPE: DNA  
! ORGANISM: Artificial Sequence  
! FEATURE:  
! OTHER INFORMATION: Targeting Sequence  
US-10-294-228-25

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 GAAAGATGGAGCAAGA 66  
||||| |||||  
Db 1 GAAAGATAGAGCAAGA 16

RESULT 1669  
US-10-674-124A-27098/C  
! Sequence 27098, Application US/10674124A  
! Publication No. US20040197979A1  
! GENERAL INFORMATION:  
! APPLICANT: INOKO, Hidetoshi  
! APPLICANT: TAMIYA, Gen

; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE  
; FILE OF INVENTION: GENETIC POLYMORPHISM MARKERS  
; FILE REFERENCE: ORIN-003CIP  
; CURRENT APPLICATION NUMBER: US/10/674,124A  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 10/257,511  
; PRIOR FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: PCT/JP00/07621  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: JP2000-112699  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: JP2002-327516  
; PRIOR FILING DATE: 2002-09-28  
; PRIOR APPLICATION NUMBER: JP2002-383869  
; PRIOR FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 27110  
; SEQ ID NO 27098  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-10-674-124A-27098

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2231 TGCACCCACACCTGGC 2246  
Db 16 TGCACCCACATCTGGC 1

Search completed: January 26, 2005, 12:41:49  
Job time : 60 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 25, 2005, 16:20:19 ; Search time 100 Seconds  
(without alignments)  
3.683 Million cell updates/sec

Title: US-09-966-724B-2-COPY

Perfect score: 2372

Sequence: 1 GCACCGCGGAGCTGGCTG.....ATTACAGGCATGAGCCACCG 2372

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 3105 seqs, 77640 residues

Total number of hits satisfying chosen parameters: 6210

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2000 summaries

Database : rng.db.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	88.8	3.7	100	1	AAK73008 Human immune/haema
C 2	88.8	3.7	100	1	AAL03022 Human reproductive
C 3	87.8	3.7	100	1	AAK69883 Human immune/haema
C 4	86.4	3.6	100	1	AAC13296 Human secreted pro
C 5	86.4	3.6	100	1	AAC14608 Human secreted pro
C 6	85.2	3.6	98	1	AAL07382 Human reproductive
C 7	85.2	3.6	98	1	AAL07385 Human reproductive
C 8	85.2	3.6	98	1	ABL98854 Human testicular a
C 9	85.2	3.6	98	1	ABL98851 Human testicular a
C 10	83.6	3.5	99	1	AAS34440 Human DNA for a no
C 11	82.6	3.5	100	1	AAS28286 Genomic sequence #
C 12	82.6	3.5	100	1	ADG41482 Human respiratory
C 13	81.6	3.4	96	1	AAK85166 Human immune/haema
C 14	81.5	3.4	100	1	AAK90852 Human digestive sy
C 15	81.4	3.4	99	1	AAK72850 Human immune/haema
C 16	81.2	3.4	94	1	AAC23951 Human secreted pro
C 17	80.6	3.4	95	1	AAC28711 Human secreted pro
C 18	80	3.4	100	1	AAC11043 Human secreted pro
C 19	78.4	3.3	88	1	ADJ12759 DNA fragment of a
C 20	78.4	3.3	90	1	AAC23570 Human secreted pro
C 21	78	3.3	86	1	AAC14994 Human secreted pro
C 22	75.8	3.2	87	1	ABL37410 Human musculoskele
C 23	75.8	3.2	87	1	ABX60398 CDNA encoding nove
C 24	75.8	3.2	87	1	ADJ31148 Human musculoskele
C 25	74.2	3.1	87	1	AAK79823 Human immune/haema
C 26	73	3.1	73	1	AAK35141 Nucleotide sequenc
C 27	73	3.1	73	1	AAD65023 Human mouse double
C 28	72.8	3.1	76	1	AAC13689 Human secreted pro
C 29	72.6	3.1	87	1	AAK75687 Human immune/haema
C 30	72.6	3.1	87	1	AAK76817 Human immune/haema
C 31	72.6	3.1	87	1	AAK82025 Human immune/haema
C 32	72.6	3.1	87	1	AAK75689 Human immune/haema
C 33	72.6	3.1	87	1	AAK76646 Human immune/haema

C	34	72.6	3.1	87	1	AAK75688 Human immune/haema
C	35	72.6	3.1	87	1	AAS28528 Genomic sequence #
C	36	72.6	3.1	87	1	ADG41724 Human respiratory
C	37	71.4	3.0	84	1	AAC12517 Human secreted pro
C	38	71	3.0	79	1	AAC24033 Human secreted pro
C	39	71	3.0	87	1	AAI99210 Human excretory re
C	40	71	3.0	87	1	AAI99210 Human excretory re
C	41	71	3.0	87	1	AAI99211 Human immune/haema
C	42	71	3.0	87	1	AAK87263 Human immune/haema
C	43	71	3.0	87	1	AAK84994 Human immune/haema
C	44	71	3.0	87	1	AAK87262 Human immune/haema
C	45	71	3.0	87	1	AAK78040 Human immune/haema
C	46	71	3.0	87	1	AAK84995 Human immune/haema
C	47	71	3.0	87	1	AAK68262 Human immune/haema
C	48	71	3.0	87	1	AAK84992 Human immune/haema
C	49	71	3.0	87	1	AAK68855 Human immune/haema
C	50	71	3.0	87	1	AAK68854 Human immune/haema
C	51	71	3.0	87	1	AAS28332 Genomic sequence #
C	52	71	3.0	87	1	AAI63561 Human kidney relat
C	53	71	3.0	87	1	AAI63558 Human kidney relat
C	54	71	3.0	87	1	AAI63560 Human kidney relat
C	55	71	3.0	87	1	ABZ74272 Secreted protein g
C	56	71	3.0	87	1	ADA98801 Human secreted pro
C	57	71	3.0	87	1	ADG41528 Human respiratory
C	58	71	3.0	87	1	ABZ67838 Human secreted pro
C	59	70.8	3.0	84	1	ABK45727 cDNA encoding colo
C	60	70.2	3.0	92	1	AAC11340 Human secreted pro
C	61	69.4	2.9	87	1	AAS36366 Human cardiovascular
C	62	69.4	2.9	87	1	AAK91304 Human digestive sy
C	63	69.4	2.9	87	1	AAK91305 Human digestive sy
C	64	69.4	2.9	87	1	AAK91307 Human digestive sy
C	65	69.4	2.9	87	1	AAK86755 Human immune/haema
C	66	69.4	2.9	87	1	AAK75934 Human immune/haema
C	67	69.4	2.9	87	1	AAK81974 Human immune/haema
C	68	69.4	2.9	87	1	AAK81975 Human immune/haema
C	69	69.4	2.9	87	1	AAK75935 Human immune/haema
C	70	69.4	2.9	87	1	AAK81973 Human immune/haema
C	71	69.4	2.9	87	1	AAK83799 Human immune/haema
C	72	69.4	2.9	87	1	AAK86753 Human immune/haema
C	73	69.4	2.9	87	1	AAI36467 Human musculoskele
C	74	69.4	2.9	87	1	AAI36466 Human musculoskele
C	75	69.4	2.9	87	1	AAI36464 Human musculoskele
C	76	69.4	2.9	87	1	AAI02848 Human reproductive
C	77	69.4	2.9	87	1	AAI02849 Human reproductive
C	78	69.4	2.9	87	1	AAI07338 Human reproductive
C	79	69.4	2.9	87	1	AAS32132 Human liver associ
C	80	69.4	2.9	87	1	AAS32134 Human liver associ
C	81	69.4	2.9	87	1	AAS32131 Human liver associ
C	82	69.4	2.9	87	1	ABN90487 Human liver antige
C	83	69.4	2.9	87	1	ABN90489 Human liver antige
C	84	69.4	2.9	87	1	ABN90486 Human liver antige
C	85	69.4	2.9	87	1	ABX59456 CDNA encoding nove
C	86	69.4	2.9	87	1	ABX59455 CDNA encoding nove
C	87	69.4	2.9	87	1	ABX59452 CDNA encoding nove
C	88	69.4	2.9	87	1	ADJ47060 Human cardiovascular
C	89	69.4	2.9	87	1	ADJ15402 Human liver-relate
C	90	69.4	2.9	87	1	ADJ15399 Human liver-relate
C	91	69.4	2.9	87	1	ADJ15400 Human liver-relate
C	92	69.4	2.9	87	1	ADJ30205 Human musculoskele
C	93	69.4	2.9	87	1	ADJ30202 Human musculoskele
C	94	69.4	2.9	87	1	ADJ30204 Human musculoskele
C	95	68.3	2.9	90	1	AAK83861 Human immune/haema
C	96	68.3	2.9	90	1	AAK85686 Human immune/haema
C	97	67.8	2.9	87	1	AAK90874 Human digestive sy
C	98	67.8	2.9	87	1	ABA15851 Human nervous syst
C	99	67.8	2.9	87	1	ABA15852 Human nervous syst
C	100	66.2	2.8	87	1	AAK65876 Human immune/haema
C	101	66.2	2.8	87	1	AAK65878 Human immune/haema
C	102	66	2.8	82	1	AAK76883 Human immune/haema
C	103	64.4	2.7	80	1	ADJ12544 Mutant human BRCA1
C	104	62.2	2.6	81	1	AAC11941 Human secreted pro
C	105	60	2.5	60	1	ABN39842 Human spliced tran
C	106	60	2.5	61	1	ABZ09613 Human oligonucleot

C 107	60	2.5	68	1	ABZ73066	Tumour suppression
C 108	58.4	2.5	68	1	ABZ09678	Human oligonucleot
C 109	58.4	2.5	68	1	ABZ73131	Tumour suppression
C 110	56.8	2.4	68	1	ABZ09289	Human oligonucleot
C 111	56.8	2.4	68	1	ABZ78742	Tumour suppression
C 112	56.2	2.4	69	1	AA557672	cDNA #348 encoding
C 113	54.4	2.3	65	1	AAAC12925	Human secreted pro
C 114	52	2.2	60	1	ABZ09729	Human oligonucleot
C 115	52	2.2	60	1	ABZ79182	Tumour suppression
C 116	52	2.2	60	1	AD112543	Mutant human BRCA1
C 117	51.6	2.2	66	1	AAK91064	Human digestive sy
C 118	51.6	2.2	66	1	AAAS32099	Human liver associ
C 119	51.6	2.2	66	1	ABN90454	Human liver antige
C 120	51.6	2.2	66	1	ADJ15367	Human liver-relate
C 121	51	2.2	64	1	AAAC11032	Human secreted pro
C 122	50.2	2.1	64	1	AAAC15723	Human secreted pro
C 123	50	2.1	50	1	ABZ04758	Human leukocyte ge
C 124	50	2.1	50	1	ADP10274	50-mer oligonucleo
C 125	50	2.1	63	1	AAI69056	Activated T-cell d
C 126	49.4	2.1	51	1	AAAL32116	Human SNP oligonuc
C 127	48.4	2.0	51	1	AAAT7488	Human Alu subfam
C 128	47.8	2.0	51	1	AAI77877	Human silent SNP c
C 129	47.8	2.0	51	1	AAI79838	Human nonconservat
C 130	47.8	2.0	51	1	AAI79700	Human conservative
C 131	47.8	2.0	51	1	AAH89466	Human coding seque
C 132	47.6	2.0	63	1	AAK85885	Human immune/haema
C 133	47.6	2.0	63	1	AAK85681	Human immune/haema
C 134	47.2	2.0	52	1	ABZ09432	Human oligonucleot
C 135	47.2	2.0	52	1	ABZ78885	Tumour suppression
C 136	47	2.0	47	1	AAZ69526	Human map-related
C 137	46.8	2.0	51	1	AAA77489	Human Alu subfam
C 138	46.8	2.0	59	1	ABK45620	cDNA encoding colo
C 139	46.6	2.0	47	1	ABK41287	Human USF2 gene bi
C 140	46.4	2.0	54	1	AAI68926	Activated T-cell d
C 141	46.2	1.9	51	1	AAI77876	Human silent SNP c
C 142	46.2	1.9	51	1	AAI79701	Human conservative
C 143	46.2	1.9	51	1	AAI79839	Human nonconservat
C 144	46.2	1.9	51	1	AAH89467	Human coding seque
C 145	46.2	1.9	51	1	AAH40328	Human SNP flanking
C 146	46.2	1.9	51	1	ABL00161	Human silent nonco
C 147	45.8	1.9	51	1	AAH39992	Human SNP flanking
C 148	45.8	1.9	57	1	AAAC29627	Human secreted pro
C 149	45.6	1.9	57	1	AAK83961	Human immune/haema
C 150	45.2	1.9	51	1	AAI77324	Human silent SNP c
C 151	45.2	1.9	51	1	AAI79589	Human silent SNP c
C 152	44.6	1.9	51	1	AAH89302	Human coding seque
C 153	44.6	1.9	51	1	AAH40072	Human SNP flanking
C 154	44.2	1.9	49	1	AD112542	Mutant human BRCA1
C 155	43.6	1.8	51	1	AAI79588	Human silent SNP c
C 156	43.6	1.8	51	1	AAI77325	Human silent SNP c
C 157	43.2	1.8	51	1	AAI73532	Human silent SNP c
C 158	43	1.8	51	1	AAA77442	Human Alusubfamily
C 159	43	1.8	51	1	AAA76988	Human clone cg4292
C 160	43	1.8	51	1	AAI76185	Human silent SNP c
C 161	43	1.8	51	1	AAI76192	Human silent SNP c
C 162	43	1.8	51	1	AAI79867	Human nonconservat
C 163	43	1.8	51	1	AAI79689	Human conservative
C 164	43	1.8	51	1	AAH90176	Human clone cg4286
C 165	43	1.8	51	1	AAH89484	Human coding seque
C 166	43	1.8	51	1	AAH89506	Human coding seque
C 167	43	1.8	51	1	AAH89303	Human coding seque
C 168	43	1.8	51	1	ADK19860	Human mannosyl tra
C 169	42.6	1.8	49	1	AAK65537	Human immune/haema
C 170	42.6	1.8	49	1	AAK62905	Human genomic DNA
C 171	42.2	1.8	51	1	AAI79513	Human silent SNP c
C 172	42	1.8	50	1	ADG84273	Human TMD0621 prom
C 173	42	1.8	51	1	AAI75515	Human silent SNP c
C 174	42	1.8	51	1	AAI73069	Human silent SNP c
C 175	42	1.8	51	1	AAI79770	Human nonconservat
C 176	41.6	1.8	51	1	AAI79646	Human silent SNP c
C 177	41.6	1.8	51	1	AAI73533	Human silent SNP c
C 178	41.6	1.8	52	1	AAAC22417	Human secreted pro
C 179	41.4	1.7	51	1	AAA77443	Human Alusubfamily
C 180	41.4	1.7	51	1	AAA76989	Human clone cg4292
C 181	41.4	1.7	51	1	AAA77230	Human clone cg4397
C 182	41.4	1.7	51	1	AAI73071	Human silent SNP c
C 183	41.4	1.7	51	1	AAI76193	Human silent SNP c
C 184	41.4	1.7	51	1	AAI79866	Human nonconservat
C 185	41.4	1.7	51	1	AAI74978	Human silent SNP c
C 186	41.4	1.7	51	1	AAI74450	Human silent SNP c
C 187	41.4	1.7	51	1	AAI75457	Human silent SNP c
C 188	41.4	1.7	51	1	AAI76650	Human silent SNP c
C 189	41.4	1.7	51	1	AAI75653	Human silent SNP c
C 190	41.4	1.7	51	1	AAI76184	Human silent SNP c
C 191	41.4	1.7	51	1	AAI79688	Human conservative
C 192	41.4	1.7	51	1	AAH90585	Human clone cg4308
C 193	41.4	1.7	51	1	AAH90175	Human clone cg4286
C 194	41.4	1.7	51	1	AAH89507	Human coding seque
C 195	41.4	1.7	51	1	AAH89485	Human coding seque
C 196	41.4	1.7	51	1	AAH89308	Human coding seque
C 197	41.4	1.7	51	1	AAH89304	Human coding seque
C 198	41.4	1.7	51	1	AAH89519	Human coding seque
C 199	41.4	1.7	51	1	ABL00076	Human silent nonco
C 200	41.4	1.7	51	1	ADK19850	Human mannosyl tra
C 201	41.2	1.7	47	1	AAZ66299	Human map-related
C 202	41.2	1.7	47	1	AAZ69248	Sample member clus
C 203	41.2	1.7	51	1	AAAL31459	Human SNP oligonuc
C 204	41.2	1.7	51	1	AAI79699	Human conservative
C 205	41.2	1.7	51	1	AAH37800	Human SNP flanking
C 206	40.8	1.7	51	1	AAI78300	Human silent SNP c
C 207	40.8	1.7	52	1	ABZ09024	Human oligonucleot
C 208	40.8	1.7	52	1	ABZ78477	Tumour suppression
C 209	40.6	1.7	51	1	AAI78039	Human silent SNP c
C 210	40.6	1.7	51	1	AAI79512	Human silent SNP c
C 211	40.4	1.7	50	1	AAH89833	Human coding seque
C 212	40.4	1.7	51	1	AAZ77228	Human clone cg4397
C 213	40.4	1.7	51	1	ADCI6930	Human single nucle
C 214	40.4	1.7	51	1	AAI79771	Human nonconservat
C 215	40.4	1.7	51	1	AAI75514	Human silent SNP c
C 216	40.4	1.7	51	1	AAI73068	Human silent SNP c
C 217	40	1.7	48	1	ADB73481	Human breakpoint r
C 218	40	1.7	51	1	AAI79647	Human silent SNP c
C 219	40	1.7	51	1	AAI73305	Human silent SNP c
C 220	40	1.7	51	1	AAH39524	Human SNP flanking
C 221	40	1.7	51	1	ABZ09598	Human oligonucleot
C 222	40	1.7	51	1	ABZ79051	Tumour suppression
C 223	39.8	1.7	51	1	AAZ77231	Human clone cg4397
C 224	39.8	1.7	51	1	AAAC14922	Human secreted pro
C 225	39.8	1.7	51	1	AAI74451	Human silent SNP c
C 226	39.8	1.7	51	1	AAI75652	Human silent SNP c
C 227	39.8	1.7	51	1	AAI75456	Human silent SNP c
C 228	39.8	1.7	51	1	AAI77410	Human silent SNP c
C 229	39.8	1.7	51	1	AAI75454	Human silent SNP c
C 230	39.8	1.7	51	1	AAI77409	Human silent SNP c
C 231	39.8	1.7	51	1	AAI74979	Human silent SNP c
C 232	39.8	1.7	51	1	AAI73070	Human silent SNP c
C 233	39.8	1.7	51	1	AAH90586	Human clone cg4308
C 234	39.8	1.7	51	1	AAH89305	Human coding seque
C 235	39.8	1.7	51	1	AAH89317	Human coding seque
C 236	39.8	1.7	51	1	AAH89553	Human coding seque
C 237	39.8	1.7	51	1	AAH89518	Human coding seque
C 238	39.8	1.7	51	1	AAH89309	Human coding seque
C 239	39.8	1.7	51	1	AAH89566	Human coding seque
C 240	39.8	1.7	51	1	ABL00112	Human silent nonco
C 241	39.6	1.7	51	1	AAI79698	Human conservative
C 242	39.4	1.7	41	1	ABZ20666	Human G protein su
C 243	39.4	1.7	41	1	ABZ49551	Human glutathione-
C 244	39.4	1.7	41	1	ABZ43959	Human glutathione-
C 245	39.4	1.7	51	1	AAI79580	Human silent SNP c
C 246	39.4	1.7	51	1	AAH89818	Human coding seque
C 247	39.2	1.7	44	1	AD112541	Mutant human BRCA1
C 248	39.2	1.7	51	1	AAI78301	Human silent SNP c
C 249	39	1.6	49	1	AD112532	Mutant human BRCA1
C 250	39	1.6	51	1	AAI78038	Human silent SNP c
C 251	38.9	1.6	51	1	AAI77874	Human silent SNP c
C 252	38.9	1.6	51	1	AAI77875	Human silent SNP c

253	38.8	1.6	51	1	AAAT7229	Human clone c94397	C 326	32	1.3	41	1	ADL81463	Gene 216 single nu
c 254	38.8	1.6	51	1	AAAT75651	Human silent SNP C	C 327	31.4	1.3	41	1	ABH49727	Human DNA mismatch
255	38.8	1.6	51	1	AAAT79075	Human silent SNP C	C 328	31.4	1.3	41	1	ABV74811	Signalase 11.22 pr
256	38.8	1.6	51	1	AAAT74819	Human silent SNP C	C 329	31.4	1.3	41	1	ABL40963	Transcription regu
257	38.8	1.6	51	1	AAAT79530	Human silent SNP C	C 330	31.4	1.3	41	1	ABL40964	Transcription regu
258	38.8	1.6	51	1	AAAT74884	Human silent SNP C	C 331	31.4	1.3	41	1	ABZ47125	Human ATP-binding
c 259	38.8	1.6	51	1	AAAT74965	Human silent SNP C	C 332	31.4	1.3	41	1	ABZ43249	Human ATP-binding
c 260	38.8	1.6	51	1	ADK19818	Human mannosyl tra	C 333	31.4	1.3	41	1	ABZ49403	Human UDP glycosyl
c 261	38.6	1.6	51	1	AAAT75542	Human silent SNP C	C 334	31.4	1.3	41	1	ABZ49403	Human UDP glycosyl
c 262	38.4	1.6	40	1	AAAT19044	Alu PCR primer 1.	C 335	31.2	1.3	41	1	AAAL51683	PC6 protease 9-9 (
c 263	38.4	1.6	40	1	AAAT76559	Human MDM2 40mer P	C 336	31.2	1.3	41	1	AAAT88864	Saccharophosphotra
c 264	38.4	1.6	40	1	ABLS9100	Nucleotide sequenc	C 337	31.2	1.3	41	1	ADCS9512	Polypeptide-respir
c 265	38.4	1.6	40	1	ABLS9100	Human MDM2 mRNA fr	C 338	31.2	1.3	41	1	ADCS9512	Polypeptide-respir
c 266	38.4	1.6	50	1	AAAT76503	Human silent SNP C	C 339	31	1.3	31	1	ABZ57501	Ser/thr protein ki
c 267	38.4	1.6	51	1	AAAT73304	Human silent SNP C	C 340	31	1.3	33	1	ADK66044	Standardized polyn
c 268	38.4	1.6	51	1	AAAT76814	Human silent SNP C	C 341	31	1.3	40	1	ABZ48532	Human mdm-2 probe
c 269	37.8	1.6	41	1	ABZ20667	Human G protein su	C 342	31	1.3	41	1	ABQ83633	Human oligopeptide
c 270	37.8	1.6	41	1	ABZ43958	Human glutathione-	C 343	31	1.3	41	1	ABQ83634	Human mper3-10.01
c 271	37.8	1.6	41	1	ABZ44160	Human NDUFS5 gene	C 344	31	1.3	41	1	ABQ83634	Human mper3-10.01
c 272	37.8	1.6	41	1	ABZ49550	Human NDUFS5 gene	C 345	30.8	1.3	41	1	ABQ83634	CAMP dependent kin
c 273	37.8	1.6	41	1	ABZ49631	Human glutathione-	C 346	29.8	1.3	36	1	ABQ83634	Human retinoblasto
c 274	37.8	1.6	41	1	ABZ43598	Human sulphotransf	C 347	29	1.2	33	1	ACC84461	Genetic analysis m
c 275	37.8	1.6	41	1	ABZ50172	Human NDUFS5 gene	C 348	29	1.2	33	1	ACC84461	NTP peptide encodi
c 276	37.8	1.6	42	1	ADL12523	Human BRCAL DNA ju	C 349	28.8	1.2	29	1	ABL60508	Human MDM2 hybridi
c 277	37.4	1.6	47	1	AAZ68649	Human map-related	C 350	28.8	1.2	32	1	AAK91040	Human digestive sy
c 278	36.2	1.5	41	1	ABA94091	Human tumour suppr	C 351	28.8	1.2	32	1	AAK91040	Human digestive sy
c 279	36.2	1.5	42	1	ADL12521	Human BRCAL DNA ju	C 352	28.8	1.2	32	1	AAK91040	Human liver associ
c 280	35.4	1.5	45	1	AAK91006	Human digestive sy	C 353	28.4	1.2	30	1	AAJ47196	Human liver-relate
c 281	35.4	1.5	45	1	AAK96862	Human immune/haema	C 354	28.4	1.2	30	1	AAJ47196	Human liver-relate
c 282	35.4	1.5	45	1	AAK96862	Human immune/haema	C 355	28.4	1.2	30	1	AAJ47196	Human liver-relate
c 283	35.4	1.5	45	1	AAK96862	Human immune/haema	C 356	28.4	1.2	30	1	AAJ47196	Human liver-relate
c 284	35.4	1.5	45	1	AAK96862	Human immune/haema	C 357	28	1.2	28	1	AAK97658	Human MDM2 gene ta
c 285	35.4	1.5	45	1	AAK96862	Human immune/haema	C 358	28	1.2	28	1	AAK97658	Human MDM2 gene ta
c 286	35.4	1.5	45	1	AAK96862	Human immune/haema	C 359	28	1.2	28	1	AAK97658	Human MDM2 gene ta
c 287	35.4	1.5	45	1	AAK96862	Human immune/haema	C 360	28	1.2	28	1	AAK97658	Human MDM2 gene ta
c 288	35.4	1.5	45	1	AAK96862	Human immune/haema	C 361	28	1.2	28	1	AAK97658	Human MDM2 gene ta
c 289	35.4	1.5	45	1	AAK96862	Human immune/haema	C 362	27.8	1.2	33	1	AAI62688	Human MDM2 mRNA fr
c 290	35.4	1.5	45	1	AAK96862	Human immune/haema	C 363	27.8	1.2	33	1	AAI62688	Human MDM2 mRNA fr
c 291	35.4	1.5	45	1	AAK96862	Human immune/haema	C 364	27.6	1.2	35	1	AAH91537	Taqman probe of th
c 292	35.2	1.5	44	1	AAI76391	Human liver-relate	C 365	27.4	1.2	31	1	AAH91537	Human breast or ov
c 293	34.6	1.5	41	1	ABA94092	Human silent SNP C	C 366	27.4	1.2	31	1	AAQ73572	Human inflammatory
c 294	34.6	1.5	41	1	ABA94092	Human silent SNP C	C 367	27.4	1.2	31	1	AAQ73572	Enhancer element e
c 295	34.6	1.5	41	1	ABA94092	Human silent SNP C	C 368	27	1.1	29	1	AAQ73572	Inter-Alu specific
c 296	34.6	1.5	41	1	ADL64133	Human sulphotransf	C 369	27	1.1	29	1	AAQ73572	Inter-Alu specific
c 297	34.2	1.4	39	1	ACC84472	NTP peptide encodi	C 370	26.8	1.1	32	1	AAZ37740	Polymorphic fragme
c 298	34	1.4	42	1	ACC84458	NTP peptide encodi	C 371	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 299	33.6	1.4	41	1	AAK99206	Human-homo autoimm	C 372	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 300	33.6	1.4	41	1	AAK99207	Human-homo autoimm	C 373	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 301	33.6	1.4	41	1	ABZ45793	Human carbohydrate	C 374	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 302	33.6	1.4	41	1	ABZ46192	Human organic anio	C 375	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 303	33.6	1.4	41	1	ABZ48356	Human organic anio	C 376	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 304	33.6	1.4	44	1	AAI76390	Human silent SNP C	C 377	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 305	33.4	1.4	35	1	AAQ27391	Inter-Alu specific	C 378	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 306	33.4	1.4	41	1	AAI59551	Human proteolytic	C 379	26	1.1	26	1	AAZ37740	Polymorphic fragme
c 307	33.4	1.4	41	1	AAI59550	Human proteolytic	C 380	25.8	1.1	29	1	AAA04303	Enhancer element e
c 308	33	1.4	33	1	ADP12341	Taqman probe set 2	C 381	25.4	1.1	30	1	AAA04303	Enhancer element e
c 309	33	1.4	41	1	ABZ50127	Human NDUFS1 gene	C 382	25.4	1.1	29	1	AAA04303	Human signal pepti
c 310	33	1.4	41	1	ABZ44117	Human NDUFS1 gene	C 383	25.4	1.1	29	1	AAA04303	Human transfer dow
c 311	33	1.4	41	1	ADP75520	Human ADAM19 gene	C 384	25.4	1.1	29	1	AAA04303	Human mdm2 real-ti
c 312	33	1.4	41	1	ADL64280	Human single nucle	C 385	25.2	1.1	32	1	AAQ73570	Human mdm2 real-ti
c 313	32.8	1.4	41	1	ABA96570	Human tyrosinase 9	C 386	25.2	1.1	32	1	AAQ73570	SNP specific SNPE
c 314	32.8	1.4	41	1	ABA96571	Human tyrosinase 9	C 387	25.2	1.1	33	1	ABK50423	Human Alu sequence
c 315	32.8	1.4	41	1	ADCS9511	Polypeptide-respir	C 388	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 316	32.6	1.4	40	1	AAH51207	Human inflammatory	C 389	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 317	32.6	1.4	41	1	ABL60966	Human retinoblasto	C 390	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 318	32.4	1.4	41	1	ABZ97057	Human 2-hydroxy ac	C 391	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 319	32.4	1.4	41	1	ABA97056	Human 2-hydroxy ac	C 392	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 320	32.2	1.4	38	1	AAH91831	Human inflammatory	C 393	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 321	32	1.3	41	1	ABZ72304	Gene 216 SNP refer	C 394	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 322	32	1.3	41	1	ABZ49727	Human sulphotransf	C 395	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 323	32	1.3	41	1	ABZ43574	Human sulphotransf	C 396	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 324	32	1.3	41	1	ABX75157	Human gene 216 DNA	C 397	25	1.1	25	1	AAH51700	Human MDM2 scannin
c 325	32	1.3	41	1	ADJ36885	Gene 216 single nu	C 398	25	1.1	25	1	AAH51700	Human MDM2 scannin







C 837	20	0.8	20	1	AAZ37605	Human mdm2 phospho	910	20	0.8	20	1	AAZ35102	Antisense oligonuc
C 838	20	0.8	20	1	AAZ37629	Human mdm2 phospho	911	20	0.8	20	1	AAZ35106	Antisense oligonuc
C 839	20	0.8	20	1	AAZ37631	Human mdm2 phospho	912	20	0.8	20	1	AAZ35112	Antisense oligonuc
C 840	20	0.8	20	1	AAZ37641	Human mdm2 phospho	C 913	20	0.8	20	1	AAZ35131	Antisense oligonuc
C 841	20	0.8	20	1	AAZ37684	Human mdm2 phospho	914	20	0.8	20	1	AAZ35115	Antisense oligonuc
C 842	20	0.8	20	1	AAZ37686	Human mdm2 phospho	915	20	0.8	20	1	AAZ35107	Antisense oligonuc
C 843	20	0.8	20	1	AAZ37700	Human mdm2 phospho	C 916	20	0.8	20	1	AAZ35124	Antisense oligonuc
C 844	20	0.8	20	1	AAZ37708	Human mdm2 phospho	C 917	20	0.8	20	1	AAZ35133	Antisense oligonuc
C 845	20	0.8	20	1	AAZ37728	Human mdm2 phospho	918	20	0.8	20	1	AAZ35109	Antisense oligonuc
C 846	20	0.8	20	1	AAZ37735	Human mdm2 phospho	919	20	0.8	20	1	AAZ35105	Antisense oligonuc
C 847	20	0.8	20	1	AAZ37743	Human mdm2 phospho	920	20	0.8	20	1	AAZ35108	Antisense oligonuc
C 848	20	0.8	20	1	AAZ37474	Human mdm2 phospho	C 921	20	0.8	20	1	AAZ35128	Antisense oligonuc
C 849	20	0.8	20	1	AAZ37503	Human mdm2 phospho	C 922	20	0.8	20	1	AAZ35129	Antisense oligonuc
C 850	20	0.8	20	1	AAZ37514	Human mdm2 phospho	C 923	20	0.8	20	1	AAZ35135	Antisense oligonuc
C 851	20	0.8	20	1	AAZ37518	Human mdm2 phospho	C 924	20	0.8	20	1	AAZ43383	Alzheimer's diseas
C 852	20	0.8	20	1	AAZ37520	Human mdm2 phospho	C 925	20	0.8	20	1	AAZ96410	Primer used to amp
C 853	20	0.8	20	1	AAZ37521	Human mdm2 phospho	926	20	0.8	20	1	AAZ89373	Human mdm-2 PCR pr
C 854	20	0.8	20	1	AAZ37531	Human mdm2 phospho	927	20	0.8	20	1	AAZ28013	Uncoupling protein
C 855	20	0.8	20	1	AAZ37532	Human mdm2 phospho	C 928	20	0.8	20	1	AAA14945	PCR primer SRI use
C 856	20	0.8	20	1	AAZ37543	Human mdm2 phospho	C 929	20	0.8	20	1	AAZ97667	Human MDM2 PCR pri
C 857	20	0.8	20	1	AAZ37555	Human mdm2 phospho	C 930	20	0.8	20	1	AAZ97654	Human MDM2-targett
C 858	20	0.8	20	1	AAZ37557	Human mdm2 phospho	C 931	20	0.8	20	1	AAZ97657	Human MDM2-targett
C 859	20	0.8	20	1	AAZ37562	Human mdm2 phospho	C 932	20	0.8	20	1	AAZ97656	Human MDM2-targett
C 860	20	0.8	20	1	AAZ37564	Human mdm2 phospho	C 933	20	0.8	20	1	AAZ97665	Human MDM2 PCR pri
C 861	20	0.8	20	1	AAZ37567	Human mdm2 phospho	C 934	20	0.8	20	1	AAZ97669	Human MDM2 PCR pri
C 862	20	0.8	20	1	AAZ37613	Human mdm2 phospho	C 935	20	0.8	20	1	AAZ97655	Human MDM2-targett
C 863	20	0.8	20	1	AAZ37626	Human mdm2 phospho	C 936	20	0.8	20	1	AAZ97666	Human MDM2 PCR pri
C 864	20	0.8	20	1	AAZ37628	Human mdm2 phospho	C 937	20	0.8	20	1	AAZ97668	Human MDM2 PCR pri
C 865	20	0.8	20	1	AAZ37644	Human mdm2 phospho	938	20	0.8	20	1	AAZ14808	Human glycogen syn
C 866	20	0.8	20	1	AAZ37646	Human mdm2 phospho	C 939	20	0.8	20	1	AAZ95176	Human cDNA clone-s
C 867	20	0.8	20	1	AAZ37698	Human mdm2 phospho	C 940	20	0.8	20	1	AAZ23807	Oligo #7 used to p
C 868	20	0.8	20	1	AAZ37711	Human mdm2 phospho	C 941	20	0.8	20	1	AAZ80627	Human mdm2 phospho
C 869	20	0.8	20	1	AAZ37718	Human mdm2 phospho	C 942	20	0.8	20	1	AAZ80629	Human mdm2 phospho
C 870	20	0.8	20	1	AAZ37725	Human mdm2 phospho	C 943	20	0.8	20	1	AAZ80643	Human mdm2 phospho
C 871	20	0.8	20	1	AAZ37732	Human mdm2 phospho	C 944	20	0.8	20	1	AAZ80681	Human mdm2 phospho
C 872	20	0.8	20	1	AAZ37504	Human mdm2 phospho	C 945	20	0.8	20	1	AAZ80687	Human mdm2 phospho
C 873	20	0.8	20	1	AAZ37561	Human mdm2 phospho	C 946	20	0.8	20	1	AAZ80688	Human mdm2 phospho
C 874	20	0.8	20	1	AAZ37563	Human mdm2 phospho	C 947	20	0.8	20	1	AAZ80700	Human mdm2 phospho
C 875	20	0.8	20	1	AAZ37578	Human mdm2 phospho	C 948	20	0.8	20	1	AAZ80705	Human mdm2 phospho
C 876	20	0.8	20	1	AAZ37590	Human mdm2 phospho	C 949	20	0.8	20	1	AAZ80710	Human mdm2 phospho
C 877	20	0.8	20	1	AAZ37594	Human mdm2 phospho	C 950	20	0.8	20	1	AAZ80720	Human mdm2 phospho
C 878	20	0.8	20	1	AAZ37618	Human mdm2 phospho	C 951	20	0.8	20	1	AAZ80727	Human mdm2 phospho
C 879	20	0.8	20	1	AAZ37655	Human mdm2 phospho	C 952	20	0.8	20	1	AAZ80728	Human mdm2 phospho
C 880	20	0.8	20	1	AAZ37688	Human mdm2 phospho	C 953	20	0.8	20	1	AAZ80733	Human mdm2 phospho
C 881	20	0.8	20	1	AAZ37692	Human mdm2 phospho	C 954	20	0.8	20	1	AAZ80795	Human mdm2 phospho
C 882	20	0.8	20	1	AAZ37697	Human mdm2 phospho	C 955	20	0.8	20	1	AAZ80798	Human mdm2 phospho
C 883	20	0.8	20	1	AAZ37730	Human mdm2 phospho	C 956	20	0.8	20	1	AAZ80888	Human mdm2 phospho
C 884	20	0.8	20	1	AAZ37737	Human mdm2 phospho	C 957	20	0.8	20	1	AAZ80641	Human mdm2 phospho
C 885	20	0.8	20	1	AAZ35125	Antisense oligonuc	C 958	20	0.8	20	1	AAZ80689	Human mdm2 phospho
C 886	20	0.8	20	1	AAZ35120	Antisense oligonuc	C 959	20	0.8	20	1	AAZ80718	Human mdm2 phospho
C 887	20	0.8	20	1	AAZ35130	Antisense oligonuc	C 960	20	0.8	20	1	AAZ80735	Human mdm2 phospho
C 888	20	0.8	20	1	AAZ35110	Antisense oligonuc	C 961	20	0.8	20	1	AAZ80778	Human mdm2 phospho
C 889	20	0.8	20	1	AAZ35113	Antisense oligonuc	C 962	20	0.8	20	1	AAZ80784	Human mdm2 phospho
C 890	20	0.8	20	1	AAZ35132	Antisense oligonuc	C 963	20	0.8	20	1	AAZ80788	Human mdm2 phospho
C 891	20	0.8	20	1	AAZ35100	Antisense oligonuc	C 964	20	0.8	20	1	AAZ80789	Human mdm2 phospho
C 892	20	0.8	20	1	AAZ35101	Antisense oligonuc	C 965	20	0.8	20	1	AAZ80791	Human mdm2 phospho
C 893	20	0.8	20	1	AAZ35103	Antisense oligonuc	C 966	20	0.8	20	1	AAZ80801	Human mdm2 phospho
C 894	20	0.8	20	1	AAZ35137	Antisense oligonuc	C 967	20	0.8	20	1	AAZ80817	Human mdm2 phospho
C 895	20	0.8	20	1	AAZ35139	Antisense oligonuc	C 968	20	0.8	20	1	AAZ80826	Human mdm2 phospho
C 896	20	0.8	20	1	AAZ35122	Antisense oligonuc	C 969	20	0.8	20	1	AAZ80836	Human mdm2 phospho
C 897	20	0.8	20	1	AAZ35134	Antisense oligonuc	C 970	20	0.8	20	1	AAZ80839	Human mdm2 phospho
C 898	20	0.8	20	1	AAZ35094	Antisense oligonuc	C 971	20	0.8	20	1	AAZ80842	Human mdm2 phospho
C 899	20	0.8	20	1	AAZ35099	Antisense oligonuc	C 972	20	0.8	20	1	AAZ80845	Human mdm2 phospho
C 900	20	0.8	20	1	AAZ35116	Antisense oligonuc	C 973	20	0.8	20	1	AAZ80848	Human mdm2 phospho
C 901	20	0.8	20	1	AAZ35121	Antisense oligonuc	C 974	20	0.8	20	1	AAZ80860	Human mdm2 phospho
C 902	20	0.8	20	1	AAZ35126	Antisense oligonuc	C 975	20	0.8	20	1	AAZ80892	Human mdm2 phospho
C 903	20	0.8	20	1	AAZ35096	Antisense oligonuc	C 976	20	0.8	20	1	AAZ80638	Human mdm2 phospho
C 904	20	0.8	20	1	AAZ35127	Antisense oligonuc	C 977	20	0.8	20	1	AAZ80674	Human mdm2 phospho
C 905	20	0.8	20	1	AAZ35111	Antisense oligonuc	C 978	20	0.8	20	1	AAZ80745	Human mdm2 phospho
C 906	20	0.8	20	1	AAZ35123	Antisense oligonuc	C 979	20	0.8	20	1	AAZ80755	Human mdm2 phospho
C 907	20	0.8	20	1	AAZ35095	Antisense oligonuc	C 980	20	0.8	20	1	AAZ80763	Human mdm2 phospho
C 908	20	0.8	20	1	AAZ35119	Antisense oligonuc	C 981	20	0.8	20	1	AAZ80767	Human mdm2 phospho
C 909	20	0.8	20	1	AAZ35138	Antisense oligonuc	C 982	20	0.8	20	1	AAZ80785	Human mdm2 phospho









C1421	20	0.8	20	1	AAS29403	Human mdm2 antisense	C1494	20	0.8	20	1	ADD21485	Human mdm2 antisense
C1422	20	0.8	20	1	AAS29489	Human mdm2 antisense	C1495	20	0.8	20	1	ADD21486	Human mdm2 antisense
C1423	20	0.8	20	1	AAS29496	Human mdm2 antisense	C1496	20	0.8	20	1	ADD21522	Human mdm2 antisense
C1424	20	0.8	20	1	AAS29246	Human mdm2 antisense	C1497	20	0.8	20	1	ADD21553	Human mdm2 antisense
C1425	20	0.8	20	1	AAS29304	Human mdm2 antisense	C1498	20	0.8	20	1	ADD21554	Human mdm2 antisense
C1426	20	0.8	20	1	AAS29305	Human mdm2 antisense	C1499	20	0.8	20	1	ADD21555	Human mdm2 antisense
C1427	20	0.8	20	1	AAS29314	Human mdm2 antisense	C1500	20	0.8	20	1	ADD21567	Human mdm2 antisense
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C1430	20	0.8	20	1	AAS29342	Human mdm2 antisense	C1503	20	0.8	20	1	ADD21596	Human mdm2 antisense
C1431	20	0.8	20	1	AAS29374	Human mdm2 antisense	C1504	20	0.8	20	1	ADD21616	Human mdm2 antisense
C1432	20	0.8	20	1	AAS29376	Human mdm2 antisense	C1505	20	0.8	20	1	ADD21634	Human mdm2 antisense
C1433	20	0.8	20	1	AAS29389	Human mdm2 antisense	C1506	20	0.8	20	1	ADD21641	Human mdm2 antisense
C1434	20	0.8	20	1	AAS29396	Human mdm2 antisense	C1507	20	0.8	20	1	ADD21646	Human mdm2 antisense
C1435	20	0.8	20	1	AAS29429	Human mdm2 antisense	C1508	20	0.8	20	1	ADD21650	Human mdm2 antisense
C1436	20	0.8	20	1	AAS29444	Human mdm2 antisense	C1509	20	0.8	20	1	ADD21702	Human mdm2 antisense
C1437	20	0.8	20	1	AAS29468	Human mdm2 antisense	C1510	20	0.8	20	1	ADD21712	Human mdm2 antisense
C1438	20	0.8	20	1	AAS29428	Human mdm2 antisense	C1511	20	0.8	20	1	ADD21719	Human mdm2 antisense
C1439	20	0.8	20	1	AAS29283	Human mdm2 antisense	C1512	20	0.8	20	1	ADD21734	Human mdm2 antisense
C1440	20	0.8	20	1	AAS29309	Human mdm2 antisense	C1513	20	0.8	20	1	ADD21748	Human mdm2 antisense
C1441	20	0.8	20	1	AAS29330	Human mdm2 antisense	C1514	20	0.8	20	1	ADD21750	Human mdm2 antisense
C1442	20	0.8	20	1	AAS29371	Human mdm2 antisense	C1515	20	0.8	20	1	ADD21750	Human mdm2 antisense
C1443	20	0.8	20	1	AAS29386	Human mdm2 antisense	C1516	20	0.8	20	1	ADD21438	Human mdm2 antisense
C1444	20	0.8	20	1	AAS29402	Human mdm2 antisense	C1517	20	0.8	20	1	ADD21451	Human mdm2 antisense
C1445	20	0.8	20	1	AAS29415	Human mdm2 antisense	C1518	20	0.8	20	1	ADD21495	Human mdm2 antisense
C1446	20	0.8	20	1	AAS29423	Human mdm2 antisense	C1519	20	0.8	20	1	ADD21566	Human mdm2 antisense
C1447	20	0.8	20	1	AAS29426	Human mdm2 antisense	C1520	20	0.8	20	1	ADD21569	Human mdm2 antisense
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C1449	20	0.8	20	1	AAS29455	Human mdm2 antisense	C1522	20	0.8	20	1	ADD21627	Human mdm2 antisense
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C1457	20	0.8	20	1	AAS29311	Human mdm2 antisense	C1530	20	0.8	20	1	ADD21445	Human mdm2 antisense
C1458	20	0.8	20	1	AAS29341	Human mdm2 antisense	C1531	20	0.8	20	1	ADD21478	Human mdm2 antisense
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C1462	20	0.8	20	1	AAS29417	Human mdm2 antisense	C1535	20	0.8	20	1	ADD21533	Human mdm2 antisense
C1463	20	0.8	20	1	AAS29436	Human mdm2 antisense	C1536	20	0.8	20	1	ADD21540	Human mdm2 antisense
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C1471	20	0.8	20	1	AAS29289	Human mdm2 antisense	C1544	20	0.8	20	1	ADD21637	Human mdm2 antisense
C1472	20	0.8	20	1	AAS29327	Human mdm2 antisense	C1545	20	0.8	20	1	ADD21668	Human mdm2 antisense
C1473	20	0.8	20	1	AAS29343	Human mdm2 antisense	C1546	20	0.8	20	1	ADD21685	Human mdm2 antisense
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C1476	20	0.8	20	1	AAS29419	Human mdm2 antisense	C1549	20	0.8	20	1	ADD21741	Human mdm2 antisense
C1477	20	0.8	20	1	AAS29441	Human mdm2 antisense	C1550	20	0.8	20	1	ADD21743	Human mdm2 antisense
C1478	20	0.8	20	1	AAS29464	Human mdm2 antisense	C1551	20	0.8	20	1	ADD21450	Human mdm2 antisense
C1479	20	0.8	20	1	AAS29469	Human mdm2 antisense	C1552	20	0.8	20	1	ADD21460	Human mdm2 antisense
C1480	20	0.8	20	1	AAS29481	Human mdm2 antisense	C1553	20	0.8	20	1	ADD21476	Human mdm2 antisense
C1481	20	0.8	20	1	AAS29494	Human mdm2 antisense	C1554	20	0.8	20	1	ADD21477	Human mdm2 antisense
C1482	20	0.8	20	1	ABL40351	Human caspase 6 an	C1555	20	0.8	20	1	ADD21521	Human mdm2 antisense
C1483	20	0.8	20	1	ABL44004	Human chromosome 1	C1556	20	0.8	20	1	ADD21570	Human mdm2 antisense
C1484	20	0.8	20	1	ABL44438	Human chromosome 1	C1557	20	0.8	20	1	ADD21585	Human mdm2 antisense
C1485	20	0.8	20	1	ABA92187	Polymorphism 506B1	C1558	20	0.8	20	1	ADD21593	Human mdm2 antisense
C1486	20	0.8	20	1	ABA92208	Reverse PCR primer	C1559	20	0.8	20	1	ADD21614	Human mdm2 antisense
C1487	20	0.8	20	1	ABK86101	Human MDM-2 Oligon	C1560	20	0.8	20	1	ADD21618	Human mdm2 antisense
C1488	20	0.8	20	1	ABK60510	Human MDM2 mRNA fr	C1561	20	0.8	20	1	ADD21620	Human mdm2 antisense
C1489	20	0.8	20	1	ABK91100	PCR primer Alu3, f	C1562	20	0.8	20	1	ADD21630	Human mdm2 antisense
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C1491	20	0.8	20	1	ACD27753	Peptide linked oli	C1564	20	0.8	20	1	ADD21647	Human mdm2 antisense
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C1722	20	0.8	20	1	ADD21629	Human mdm2 antisense	c1795	20	0.8	20	1	AD866781	GATA primer #1. H
C1723	20	0.8	20	1	ADD21636	Human mdm2 antisense	1796	20	0.8	20	1	AD864979	Human mouse double
C1724	20	0.8	20	1	ADD21640	Human mdm2 antisense	c1797	20	0.8	20	1	AD865012	Human mouse double
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C1769	20	0.8	20	1	ADD21538	Human mdm2 antisense	c1842	20	0.8	20	1	AD865578	Human Y chromosome
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c1860	20	0.8	20	1	ADP12093	Set 2 right PCR pr	1933	19.2	0.8	24	1	ABA01638	Human tyrosinase 1
1861	20	0.8	20	1	ADP12093	Set 1 left PCR pr	1934	19.2	0.8	24	1	ABK90209	Human transcriptio
c1862	20	0.8	20	1	ADP11268	Set 1 right PCR pr	1935	19.2	0.8	24	1	ABV74685	Human SOX3 protein
c1863	20	0.8	20	1	ADN30395	Human Notch2 DNA a	c1936	19.2	0.8	24	1	AAI19678	RT-PCR primer #2 f
c1864	20	0.8	20	1	ADQ75057	Ligand conjugated	1937	19.2	0.8	24	1	ABK12883	Ras GTP activator
c1865	20	0.8	22	1	AAF84350	Human CYP2C18i PCR	1938	19.2	0.8	24	1	ABA05003	Human tyrosine kin
1866	20	0.8	22	1	AAI11629	Human CYP2B6 allele	1939	19.2	0.8	24	1	ABA95476	Human dihydroorota
1867	20	0.8	25	1	ADB04761	Human MD27 scannin	1940	19.2	0.8	24	1	ADC48698	Human dihydropyrra
c1868	20	0.8	26	1	ABL60500	Human MDM2 mRNA fr	1941	19.2	0.8	24	1	ABZ57061	Human epilepsia as
1869	19.8	0.8	23	1	AAH37414	SNP specific lower	1942	19.2	0.8	24	1	ADG83872	Excitatory amino a
1870	19.8	0.8	23	1	ABZ83516	Toxicologically re	1943	19.2	0.8	25	1	ADB04577	Human SLC6A14 forw
c1871	19.8	0.8	24	1	AAI71673	Human myosin heavy	1944	19.2	0.8	25	1	ADB04583	Human MD27 scannin
1872	19.8	0.8	24	1	AAI00333	PCR primer #2, use	1945	19.2	0.8	25	1	ADB04677	Human MD27 scannin
1873	19.8	0.8	24	1	AAI42696	Primer #2 used to	1946	19.2	0.8	25	1	ADB04586	Human MD27 scannin
1874	19.8	0.8	24	1	ABL50916	Human dihydropyrra	1947	19.2	0.8	25	1	ADB04747	Human MD27 scannin
1875	19.8	0.8	24	1	ABV74727	Human clathrin lig	1948	19	0.8	19	1	AAI94763	Human progesterone
1876	19.8	0.8	25	1	ADB04581	Human MD27 scannin	1949	19	0.8	19	1	AAI94754	FISH primer for hu
1877	19.8	0.8	25	1	ADB04735	Human MD27 scannin	1950	19	0.8	19	1	AAH38677	SNP specific upper
1878	19.8	0.8	25	1	ADB04662	Human MD27 scannin	1951	19	0.8	19	1	AAH38221	SNP specific upper
1879	19.8	0.8	25	1	ADB04580	Human MD27 scannin	c1952	19	0.8	19	1	ABL44474	Human chromosome 1
c1880	19.8	0.8	26	1	ABZ22656	Human PEPT1 PCR pr	c1953	19	0.8	19	1	ADK41249	Human chromosome 1
c1881	19.6	0.8	26	1	AAA39394	Alu repeat 3' end	c1954	19	0.8	19	1	ADK41375	Human chromosome 1
c1882	19.6	0.8	26	1	AAI62473	Human SPCX 2826468	1955	19	0.8	19	1	ADO23055	Human p53-binding
c1883	19.6	0.8	26	1	AAI64089	Primer #13. Homo	1956	19	0.8	19	1	ADO23052	Human p53-binding
c1884	19.6	0.8	26	1	AAH22716	Human secreted pro	1957	19	0.8	19	1	ADO23051	Human p53-binding
c1885	19.6	0.8	26	1	ABK61474	Human NOV3 Exon 11	1958	19	0.8	19	1	ADO23053	Human p53-binding
1886	19.6	0.8	26	1	ABX97292	Human NOV-associat	1959	19	0.8	19	1	ADO22917	Human p53-binding
1887	19.6	0.8	26	1	ADN62195	Human NOV20a RTQ-P	1960	19	0.8	19	1	ADO23054	Human p53-binding
1888	19.6	0.8	21	1	AAV40598	Human TSC gene exo	1961	19	0.8	19	1	ADO80008	CENPC1 extend prim
1889	19.4	0.8	21	1	AAH86419	PCR primer PDZK5.6	1962	19	0.8	19	1	ADQ61537	Anti-MDM2 siRNA re
1890	19.4	0.8	21	1	AAH38522	SNP specific lower	1963	19	0.8	19	1	ADQ61535	Anti-MDM2 siRNA re
1891	19.4	0.8	21	1	AAH40070	SNP specific lower	1964	19	0.8	19	1	ADQ61536	Anti-MDM2 siRNA re
c1892	19.4	0.8	21	1	AAH24567	Human Alu sequence	1965	19	0.8	19	1	ADQ61538	Human CAS gene ant
1893	19.4	0.8	21	1	AAQ74069	Microsatellite typ	c1966	19	0.8	20	1	ABS59253	Human MDM2 mRNA fr
1894	19.4	0.8	21	1	ABS98158	Human multidrug re	c1967	19	0.8	20	1	ABL60514	Human MDM2 mRNA fr
1895	19.4	0.8	21	1	ABS97183	Human CYP4501A2 pr	c1968	19	0.8	20	1	ABL60513	Human MDM2 mRNA fr
c1896	19.4	0.8	21	1	ABS98107	Human multidrug re	c1969	19	0.8	20	1	ABL60512	Human MDM2 mRNA fr
1897	19.4	0.8	21	1	ABS98163	Human multidrug re	c1970	19	0.8	20	1	ABL60511	Human MDM2 mRNA fr
c1898	19.4	0.8	21	1	ABS98105	Human multidrug re	c1971	19	0.8	20	1	ADD21777	Mouse mdm2 antisen
c1899	19.4	0.8	21	1	ADE14130	Optineurin promote	c1972	19	0.8	20	1	ADP47745	Human 5-HT7 recept
c1900	19.4	0.8	21	1	ADH59601	Non-nucleotide pro	c1973	19	0.8	20	1	ADMI4508	Human mPGES-1 chim
1901	19.4	0.8	21	1	ADH59613	Non-nucleotide pro	c1974	19	0.8	20	1	ADM15268	Human mPGES-1 chim
1902	19.4	0.8	21	1	ADI23739	Human LPDLR PCR pr	c1975	19	0.8	22	1	AAH38422	SNP specific lower
1903	19.4	0.8	21	1	ADM65580	Human Y chromosome	1976	19	0.8	23	1	ADO47348	Human SORBS1 gene
1904	19.4	0.8	21	1	ADO55495	HIV gene expressio	c1977	19	0.8	24	1	AAI66603	Human ubiquitin-li
c1905	19.4	0.8	22	1	AAI09910	Human biallelic po	c1978	19	0.8	25	1	AAF24672	PCR primer for exo
c1906	19.4	0.8	22	1	AAF29797	Preseniline-1 gene	1979	19	0.8	25	1	ADB04760	Human MD27 scannin
1907	19.4	0.8	22	1	ADC24360	PCR primer for amp	c1980	18.8	0.8	22	1	AAQ82257	Chromosome 11 (loc
c1908	19.4	0.8	23	1	ADH13395	Human malignant ne	c1981	18.8	0.8	22	1	AAI71928	Primer detects mar
1909	19.4	0.8	24	1	ABS56410	Human DNA mismatch	c1982	18.8	0.8	22	1	AAI71925	Primer detects mar
1910	19.4	0.8	24	1	ABK14172	Insulin like growt	c1983	18.8	0.8	22	1	AAI72000	Primer detects mar
c1911	19.4	0.8	24	1	ABV76761	Ras GTP enzyme-act	c1984	18.8	0.8	22	1	AAI71997	Primer detects mar
1912	19.4	0.8	24	1	ABL42193	PCR primer #2 for	c1985	18.8	0.8	22	1	AAZ32938	Sequence tagged si
1913	19.4	0.8	24	1	ABS55854	Human SOX3 protein	c1986	18.8	0.8	22	1	AAH38401	SNP specific upper
1914	19.4	0.8	24	1	ABZ24886	High-mobility comp	1987	18.8	0.8	22	1	AAF62067	Reverse PCR primer
1915	19.2	0.8	20	1	AAI63214	Primer Alu 5' used	1988	18.8	0.8	22	1	AAI46346	Human M30 protein
c1916	19.2	0.8	23	1	ADL72189	Alu-specific prime	c1989	18.8	0.8	22	1	ACA88980	Selection and ampl
c1917	19.2	0.8	24	1	AAV52725	Hepatocyte nuclear	1990	18.8	0.8	24	1	AAH77082	Human vesicular tr
1918	19.2	0.8	24	1	AAZ27978	PCR primer for B18	c1991	18.8	0.8	24	1	AAH91382	Human inflammatory
1919	19.2	0.8	24	1	AAI27181	Reverse primer P2	1992	18.8	0.8	24	1	ABK49351	RNA polymerase II
c1920	19.2	0.8	24	1	AAH92846	Human ABC1 transcr	1993	18.8	0.8	24	1	ABA04737	Human alkylation D
c1921	19.2	0.8	24	1	AAH40034	SNP specific lower	1994	18.8	0.8	24	1	ABZ21179	Human transforme-
1922	19.2	0.8	24	1	AAI66532	Human pterin-molyb	1995	18.8	0.8	24	1	ABZ79587	Hydrogenase 9.46 r
c1923	19.2	0.8	24	1	ABA82841	Human protective D	c1996	18.8	0.8	24	1	AAI55813	RT-PCR primer 1 to
1924	19.2	0.8	24	1	ABL41332	Human mitochondria	c1997	18.8	0.8	24	1	ADC56863	RT-PCR primer Seq
1925	19.2	0.8	24	1	ABS56119	Human mitochondria	c1998	18.8	0.8	25	1	AAI96023	H7A HLA-C gene PCR
1926	19.2	0.8	24	1	ABS56756	RT-PCR primer #2 f	1999	18.8	0.8	25	1	AAI65600	Primer for microsa
1927	19.2	0.8	24	1	ABK52730	DNA topoisomerase	2000	18.8	0.8	25	1	ADB04582	Human MD27 scannin
1928	19.2	0.8	24	1	ABQ77952	Human Mch2 protein							
1929	19.2	0.8	24	1	ABL41338	Mitochondrial tran							
1930	19.2	0.8	24	1	ABK89466	Human large protei							
1931	19.2	0.8	24	1	ABA94088	Human tumour suppr							

ALIGNMENTS

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RESULT 1
AAK73008/c
ID AAK73008 standard; DNA; 100 BP.
XX
XX
AC AAK73008;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27820.
DE
DE DE
DE DE
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
KW

Query Match 3.7%; Score 88.8; DB 1; Length 100;
Best Local Similarity 93.0%; Pred. No. 1.4;
Matches 93; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2266 TAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCCG 2325
Db 100 TAGAGATGGTGTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCCG 41

QY 2326 CCCACCTCGGCCTCCCAAGTGTGGATTACAGGCATGA 2365
Db 40 CCAGCCTCGGCCTCCCAAGTGTGGATTACAGGCATGA 1

RESULT 2
AAL03022/c
ID AAL03022 standard; DNA; 100 BP.
XX
XX
AC AAL03022;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5710.
DE
DE DE
DE DE
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
KW

Query Match 3.7%; Score 88.8; DB 1; Length 100;
Best Local Similarity 93.0%; Pred. No. 1.4;
Matches 93; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2266 TAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCCG 2325
Db 100 TAGAGATGGTGTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCCG 41

QY 2326 CCCACCTCGGCCTCCCAAGTGTGGATTACAGGCATGA 2365
Db 40 CCAGCCTCGGCCTCCCAAGTGTGGATTACAGGCATGA 1

RESULT 3
AAK69883/c
ID AAK69883 standard; DNA; 100 BP.
XX
XX
AC AAK69883;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24695.
DE
DE DE
DE DE
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
KW

Query Match 3.7%; Score 87.8; DB 1; Length 100;
Best Local Similarity 92.9%; Pred. No. 1.6;
Matches 92; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGT 2319
Db 99 TTTTAGTAGACAGAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGT 40
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QY 2320 GATCCGCCACCTCGGCCTCCCAAGTGTGGATTACA 2358
Db 39 GATCTGCCCGCTCGGCCTCCCAAGTGTGGATTACA 1

RESULT 4
AAC13296
ID AAC13296 standard; cDNA; 100 BP.
XX
XX
AC AAC13296;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 17371.
DE
DE DE
DE DE
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
KW

Query Match 3.6%; Score 86.4; DB 1; Length 100;
Best Local Similarity 93.8%; Pred. No. 1.9;
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2233 CCACACACCTGGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTCCCGTGTAGCC 2292
Db 3 CCACCATGCCCGCTAAATTTTGTATTTTGTAGTAGACAGGGTTTCCAGTGTAGCC 62

QY 2293 AGGATGGTCTCGATCTCCTGACCTCGTGATCCGCC 2328
Db 63 AGGATGGTCTTGATCTCTGACCTCGTGATCCGCC 98

RESULT 5
AAC14608
ID AAC14608 standard; cDNA; 100 BP.
XX
XX
AC AAC14608;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 18683.
DE
DE DE
DE DE
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
KW

Query Match 3.6%; Score 86.4; DB 1; Length 100;
Best Local Similarity 93.8%; Pred. No. 1.9;
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2233 CCACACACCTGGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTCCCGTGTAGCC 2292
Db 3 CCACCATGCCCGCTAAATTTTGTATTTTGTAGTAGACAGGGTTTCCAGTGTAGCC 62

QY 2293 AGGATGGTCTCGATCTCCTGACCTCGTGATCCGCC 2328
Db 63 AGGATGGTCTTGATCTCTGACCTCGTGATCCGCC 98

RESULT 6
AAL07382
ID AAL07382 standard; DNA; 98 BP.
XX
XX
AC AAL07382;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 10070.
DE
DE DE
DE DE
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
KW

Query Match 3.6%; Score 85.2; DB 1; Length 98;
Best Local Similarity 91.8%; Pred. No. 2.1;
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Matches 90; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2268 GAGACAGGGTTTACCCGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCGGCC 2327
DB 1 GAGATGGGATTTACCCGAGTTAGCCAGGATGGTCTCGATCTCTGACCTTGATCGGCC 60
QY 2328 CACCTCGGCCCTCCCAAGTGTGGGATTACAGGCATGA 2365
DB 61 CACCTCGGCCCTCCCAAGTGTGAGATTACAGGCGTGA 98

RESULT 7
ID AAL07385 standard; DNA; 98 BP.
XX
AC AAL07385;
XX
DT 21-NOV-2001 (first entry)
DE Human reproductive system related antigen DNA SEQ ID NO: 10073.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.

Query Match 3.6%; Score 85.2; DB 1; Length 98;
Best Local Similarity 91.8%; Pred. No. 2.1;
Matches 90; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2268 GAGACAGGGTTTACCCGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCGGCC 2327
DB 1 GAGATGGGATTTACCCGAGTTAGCCAGGATGGTCTCGATCTCTGACCTTGATCGGCC 60
QY 2328 CACCTCGGCCCTCCCAAGTGTGGGATTACAGGCATGA 2365
DB 61 CACCTCGGCCCTCCCAAGTGTGAGATTACAGGCGTGA 98

RESULT 8
ID ABL98854 standard; DNA; 98 BP.
XX
AC ABL98854;
XX
DT 21-JUN-2002 (first entry)
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3506.
XX
KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;

Query Match 3.6%; Score 85.2; DB 1; Length 98;
Best Local Similarity 91.8%; Pred. No. 2.1;
Matches 90; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2268 GAGACAGGGTTTACCCGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCGGCC 2327
DB 1 GAGATGGGATTTACCCGAGTTAGCCAGGATGGTCTCGATCTCTGACCTTGATCGGCC 60
QY 2328 CACCTCGGCCCTCCCAAGTGTGGGATTACAGGCATGA 2365
DB 61 CACCTCGGCCCTCCCAAGTGTGAGATTACAGGCGTGA 98

RESULT 9
ID ABL98851 standard; DNA; 98 BP.
XX
AC ABL98851;
XX
DT 21-JUN-2002 (first entry)
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3503.
XX
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KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;

Query Match 3.6%; Score 85.2; DB 1; Length 98;
Best Local Similarity 91.8%; Pred. No. 2.1;
Matches 90; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2268 GAGACAGGGTTTACCCGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCGGCC 2327
DB 1 GAGATGGGATTTACCCGAGTTAGCCAGGATGGTCTCGATCTCTGACCTTGATCGGCC 60
QY 2328 CACCTCGGCCCTCCCAAGTGTGGGATTACAGGCATGA 2365
DB 61 CACCTCGGCCCTCCCAAGTGTGAGATTACAGGCGTGA 98

RESULT 10
ID AAS3440/c
XX
ID AAS34440 standard; DNA; 99 BP.
XX
AC AAS34440;
XX
DT 17-DEC-2001 (first entry)
DE Human DNA for a novel foetal antigen, SEQ ID No 1864.
XX
KW Human; foetal tissue antigen; ds; antiinflammatory; neuroprotective;
KW immunomodulator; cardiovascular; cytostatic; nephrothropic;

Query Match 3.5%; Score 83.6; DB 1; Length 99;
Best Local Similarity 90.8%; Pred. No. 2.6;
Matches 89; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2250 TTTTGTACTTTTAGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTC 2309
DB 98 TTTTGTATTTTAGTAGAGATGGGATTTACCGTGTAGCCAGGATGGTCTCGCTCTC 39
QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCCTCCCAAGTG 2347
DB 38 CTGACCTCGTGATCTGCCGCCCTTGGCCTCCCAAAATG 1

RESULT 11
ID AAS28286 standard; DNA; 100 BP.
XX
AC AAS28286;
XX
DT 07-NOV-2001 (first entry)
DE Genomic sequence #126 encoding for novel human respiratory antigen.
XX
KW Human; respiratory antigen; respiratory disorder; throat disorder;
KW lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;

Query Match 3.5%; Score 82.6; DB 1; Length 100;
Best Local Similarity 90.7%; Pred. No. 2.9;
Matches 88; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2264 AGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
DB 1 AGTAGAGATGGGGTTTACCGTGTGGTACAGGATGGTCTCGATCTCTGACCTTGATC 60
QY 2324 CGCCCACTCGGCCCTCCCAAGTGTGGGATTACAGG 2360
DB 61 CTCCCGCCTCGGCCCTCCAAAGGTGCTGGGATTACAGG 97

RESULT 12
ID ADG41482 standard; DNA; 100 BP.
XX
AC ADG41482;
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XX 26-FEB-2004 (first entry)
XX Human respiratory system associated genomic DNA seq id 720.
XX antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
XX respiratory system antigen;
KW

Query Match 3.4%; Score 82.6; DB 1; Length 100;
Best Local Similarity 90.7%; Pred. No. 2.9;
Matches 88; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2264 AGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
DB 1 AGTAGAGATGGGTTTACCGTGTGGTCCAGGATGGTCTCGATCTCTGACCTGTGATC 60
QY 2324 CGCCACCTCGGCTCCCAAGTCTGGGATTACAGG 2360
DB 61 CTCGCCCTCGGCTCCAAAGGTGCTGGGATTACAGG 97

RESULT 13
AAK85166
ID AAK85166 standard; DNA; 96 BP.
XX
AC AAK85166;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39978.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 3.4%; Score 81.6; DB 1; Length 96;
Best Local Similarity 90.6%; Pred. No. 3.2;
Matches 87; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTGACTTTTAGTAGACAGAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
DB 1 TTTTGTGATTTTAGTAGACAGAGGGTTTACCATCTTGGCCAGGATGGTCTCGACTCC 60
QY 2311 TGACCTCGTATCCACCTGCTCGGCTCCCAAGT 2346
DB 61 TGACCTCGTATCCACCTGCTCGGCTCCCAAGT 96

RESULT 14
AAK90852/c
ID AAK90852 standard; DNA; 100 BP.
XX
AC AAK90852;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4428.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 3.4%; Score 81.5; DB 1; Length 100;
Best Local Similarity 94.1%; Pred. No. 3.3;
Matches 95; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2254 TTGTACTTTTAGTAGACAGAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGA 2313
DB 100 TTGTATTTTAGTAGACAGGGTTTCA-CGTGTAGCCAGGATGGTCTCGATCTCTGA 42
QY 2314 CCTCGTATCGGCCACCTCGGCTCCCAAGTCTGGAT 2354
DB 41 CCTCATGCTCGGCTCGGCTCCCAAGTCTGGAT 1
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RESULT 15
AAK72850/c
ID AAK72850 standard; DNA; 99 BP.
XX
AC AAK72850;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27662.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 3.4%; Score 81.4; DB 1; Length 99;
Best Local Similarity 88.9%; Pred. No. 3.3;
Matches 88; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2265 GTAGACAGAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2324
DB 99 GTAGACAGAGGGTTTACCATGTGGCCAGGTTGTTGAACCTCTGAACCTCGTGATC 40
QY 2325 GCCACCTCGGCTCCCAAGTCTGGGATTACAGGCAT 2363
DB 39 GCCCGCTTGGCTCCCAAGTCTGGGATTACAGGCGT 1

RESULT 16
AAK23951
ID AAK23951 standard; cDNA; 94 BP.
XX
AC AAK23951;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 28026.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.4%; Score 81.2; DB 1; Length 94;
Best Local Similarity 91.5%; Pred. No. 3.3;
Matches 86; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2263 TAGTAGACAGAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322
DB 1 TAGTAGACAGAGGGTTTACCGAATTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 60
QY 2323 CGGCCACCTCGGCTCCCAAGTCTGGGATTA 2356
DB 61 CTGCCGCTTGGCTCCCAAGTCTGGGATTA 94

RESULT 17
AAK28711
ID AAK28711 standard; cDNA; 95 BP.
XX
AC AAK28711;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 32786.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.4%; Score 80.6; DB 1; Length 95;
Best Local Similarity 90.5%; Pred. No. 3.6;
Matches 86; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2264 AGTAGACAGAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
DB 1 AGTAGACAGAGGGTTTACCGCTGTAGCCAGGATGGTCTCGATCTCTGATCTTGTGATC 60
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QY 2324 CGCCACCTCGCCTCCCAAGTCTGGGATTACA 2358
|||||
Db 61 CGCCTGCTTATCTCTCTGAAGTCTGGGATTACA 95

RESULT 18
AAC11043/c
ID AAC11043 standard; cDNA; 100 BP.
XX AAC11043;
XX
DT 06-OCT-2000 (first entry)
DE Human secreted protein 5' EST, SEQ ID NO: 15118.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.4%; Score 80; DB 1; Length 100;
Best Local Similarity 89.6%; Pred. No. 3.9;
Matches 86; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2250 TTTTGTACTTTTAGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTC 2309
|||||
Db 96 TTTTGTACTTTTAGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTC 37

QY 2310 CTGACCTCGTATCGGCCACCTCGGCTCCCAAG 2345
|||||
Db 36 CTGACCTGTGATCCATCCACCTCGGCTCCCAAG 1

RESULT 19
ADJ12759
ID ADJ12759 standard; DNA; 88 BP.
XX ADJ12759;
XX
DT 20-MAY-2004 (first entry)
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq613.
XX
XX human; secreted; cancer; haematopoietic disease; anaemia;
KW multiple myeloma; reproductive system disorder; prostatitis;

Query Match 3.3%; Score 78.4; DB 1; Length 88;
Best Local Similarity 93.2%; Pred. No. 4.5;
Matches 82; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTAGCCAGGATGGTCTCGATCTCCCTGACCTCGTATCGGCCACCTCGGCC 2337
1 TTCACCATGTTGGCCAGGATGGTCTCGATCTCCCTGACCCCGTATCGGCCCGCTCGGCC 60

QY 2338 TCCCAAGTCTGGGATTACAGGCATGA 2365
|||||
Db 61 TCTCAAGTCTGGGATTACAGGCGTGA 88

RESULT 20
AAC23570/c
ID AAC23570 standard; cDNA; 90 BP.
XX AAC23570;
XX
DT 06-OCT-2000 (first entry)
DE Human secreted protein 5' EST, SEQ ID NO: 27645.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.3%; Score 78.4; DB 1; Length 90;
Best Local Similarity 91.1%; Pred. No. 4.5;
Matches 82; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
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QY 2250 TTTTGTACTTTTAGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTC 2309
|||||
Db 90 TTTTGTACTTTTAGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTC 31

QY 2310 CTGACCTCGTATCGGCCACCTCGGCTC 2339
|||||
Db 30 CTGACCTCGTATCCACCCAAKGGGCTC 1

RESULT 21
AAC14994/c
ID AAC14994 standard; cDNA; 86 BP.
XX AAC14994;
XX
DT 06-OCT-2000 (first entry)
DE Human secreted protein 5' EST, SEQ ID NO: 19069.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.3%; Score 78; DB 1; Length 86;
Best Local Similarity 94.2%; Pred. No. 4.6;
Matches 81; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2260 TTTTGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGT 2319
|||||
Db 86 TTTTGTAGACAGAGGTTTAACTGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGT 27

QY 2320 GATCCGCCACCTCGGCTCCCAAG 2345
|||||
Db 26 GATCCTCCACCTCGGCTCCCAAG 1

RESULT 22
AAL37410/c
ID AAL37410 standard; DNA; 87 BP.
XX AAL37410;
XX
DT 08-JAN-2002 (first entry)
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3775.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;

Query Match 3.2%; Score 75.8; DB 1; Length 87;
Best Local Similarity 92.0%; Pred. No. 6;
Matches 80; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCGGCCACCTCGGCCCTC 2339
|||||
Db 87 CACCATGTTGGCCAGGCTGGTCTCGAACTCTGACCTCATGATCCGCCACCTCGGCCCTC 28

QY 2340 CCAAGTCTGGGATTACAGGCATGAG 2366
|||||
Db 27 CCAAGTCTGGGATTACAGGTGTGAG 1

RESULT 23
ABX60398/c
ID ABX60398 standard; cDNA; 87 BP.
XX ABX60398;
XX
DT 26-FEB-2003 (first entry)
DE cDNA encoding novel human musculoskeletal system antigen #2742.
XX
XX Gene; ss; musculoskeletal system antigen; cancer; metastasis;
```

KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;  
Query Match 3.2%; Score 75.8; DB 1; Length 87;  
Best Local Similarity 92.0%; Pred. No. 6;  
Matches 80; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTC 2339  
DB 87 CACCATGTTGGCCAGGCTGTCTCGAACTCTGACCTCATGATCCGCCACCTCGGCCTC 28  
QY 2340 CCAAAGTGCTGGGATTACAGGCATGAG 2366  
DB 27 CCAAAGTGCTGGGATTACAGGTGTAG 1  
RESULT 24  
ADJ31148/c  
ID ADJ31148 standard; DNA; 87 BP.  
XX AC ADJ31148;  
XX DT 20-MAY-2004 (first entry)  
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3775.  
XX DE musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;  
KW gene therapy; vaccine; human; ds.  
Query Match 3.2%; Score 75.8; DB 1; Length 87;  
Best Local Similarity 92.0%; Pred. No. 6;  
Matches 80; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTC 2339  
DB 87 CACCATGTTGGCCAGGCTGTCTCGAACTCTGACCTCATGATCCGCCACCTCGGCCTC 28  
QY 2340 CCAAAGTGCTGGGATTACAGGCATGAG 2366  
DB 27 CCAAAGTGCTGGGATTACAGGTGTAG 1  
RESULT 25  
AAK79823/c  
ID AAK79823 standard; DNA; 87 BP.  
XX AC AAK79823;  
XX DT 07-NOV-2001 (first entry)  
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34635.  
XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; db.  
Query Match 3.1%; Score 74.2; DB 1; Length 87;  
Best Local Similarity 90.8%; Pred. No. 7.2;  
Matches 79; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTC 2339  
DB 87 CACCATGTTGGCCAGGCTGTCTCGAACTCTGACCTCATGATCCGCCACCTCGGCCTC 28  
QY 2340 CCAAAGTGCTGGGATTACAGGCATGAG 2366  
DB 27 CCAAAGTGCTGGGATTACAGGTGTAG 1  
RESULT 26  
AAK35141/c  
ID AAK35141 standard; DNA; 73 BP.  
XX AC AAK35141;  
XX XX

DT 01-JUL-1999 (first entry)  
XX DE Nucleotide sequence SEQ ID 49.  
XX KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;  
KW inhibition; tumour growth; DNA-damaging agent; camptothecin;  
Query Match 3.1%; Score 73; DB 1; Length 73;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 665 AGGTACATCTGTGAGTGAGAACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGACCT 724  
DB 73 AGGTACATCTGTGAGTGAGAACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGACCT 14  
QY 725 TGTACAAGAGCTT 737  
DB 13 TGTACAAGAGCTT 1  
RESULT 27  
AAD65023/c  
ID AAD65023 standard; DNA; 73 BP.  
XX AC AAD65023;  
XX DT 11-MAR-2004 (first entry)  
XX DE Human mouse double minute (MDM2) non-coding antisense oligonucleotide.  
XX KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;  
KW therapeutic; antisense therapy; human; antisense; ss.  
Query Match 3.1%; Score 73; DB 1; Length 73;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 665 AGGTACATCTGTGAGTGAGAACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGACCT 724  
DB 73 AGGTACATCTGTGAGTGAGAACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGACCT 14  
QY 725 TGTACAAGAGCTT 737  
DB 13 TGTACAAGAGCTT 1  
RESULT 28  
AAC13689/c  
ID AAC13689 standard; cDNA; 76 BP.  
XX AC AAC13689;  
XX DT 06-OCT-2000 (first entry)  
XX DE Human secreted protein 5' EST, SEQ ID NO: 17764.  
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping; ss.  
Query Match 3.1%; Score 72.8; DB 1; Length 76;  
Best Local Similarity 97.4%; Pred. No. 8;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2285 TGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTCCCAA 2344  
DB 76 TGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCGGCCCTCTCAGCCTCCCAA 17  
QY 2345 GTGCTGGGATTACAGG 2360  
DB 16 GTGCTGGGATTACAGG 1  
RESULT 29



QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 Db 87 CACCATGTGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGGCTGCTGGCCTC 28  
 QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 35  
 AAS28528  
 ID AAS28528 standard; DNA; 87 BP.  
 XX AAS28528;

XX 07-NOV-2001 (first entry)  
 XX Genomic sequence #368 encoding for novel human respiratory antigen.  
 DE Human; respiratory antigen; respiratory disorder; throat disorder;  
 XX lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;  
 KW gene therapy; cytostatic;

Query Match 3.1%; Score 72.6; DB 1; Length 87;  
 Best Local Similarity 89.7%; Pred. No. 8.7;  
 Matches 78; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 Db 1 CACCATGTGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGGCTGCTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 36  
 ADG41724  
 ID ADG41724 standard; DNA; 87 BP.  
 XX ADG41724;  
 AC ADG41724;  
 DT 26-FEB-2004 (first entry)  
 XX Human respiratory system associated genomic DNA seq id 962.  
 DE antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;  
 KW respiratory system antigen;

Query Match 3.1%; Score 72.6; DB 1; Length 87;  
 Best Local Similarity 89.7%; Pred. No. 8.7;  
 Matches 78; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 Db 1 CACCATGTGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGGCTGCTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 37  
 AAC12517  
 ID AAC12517 standard; cDNA; 84 BP.  
 XX AAC12517;  
 AC AAC12517;  
 XX 06-OCT-2000 (first entry)  
 XX Human secreted protein 5' EST, SEQ ID NO: 16592.  
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.

Query Match 3.0%; Score 71.4; DB 1; Length 84;  
 Best Local Similarity 92.6%; Pred. No. 9.8;  
 Matches 75; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 2248 AATTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 2307  
 Db 2 AATTTTGTATTTTAGTAGAGATGGGGTTTCACCATGTGTAGCCAGGATGGTCTCGATC 61

QY 2308 TCCTGACCTCGTGATCCGCC 2328  
 Db 62 TCCTGACCTCGTGATCCACCC 82

RESULT 38  
 AAC24033  
 ID AAC24033 standard; cDNA; 79 BP.  
 XX AAC24033;

XX 06-OCT-2000 (first entry)  
 XX Human secreted protein 5' EST, SEQ ID NO: 28108.  
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.

Query Match 3.0%; Score 71; DB 1; Length 79;  
 Best Local Similarity 93.7%; Pred. No. 10;  
 Matches 74; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 2252 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCT 2311  
 Db 1 TTTTGTATTTTAGTAGAGACCGGGTTTCACCATGTTAACAGGATGGTCTCGATCTCCT 60

QY 2312 GACCTCGTATCCGCCAC 2330  
 Db 61 GACCTCGTATCCGCCCGC 79

RESULT 39  
 AAI99210  
 ID AAI99210 standard; DNA; 87 BP.  
 XX AAI99210;

XX 07-JAN-2002 (first entry)  
 XX Human excretory related polynucleotide SEQ ID NO 974.  
 DE Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;  
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match 3.0%; Score 71; DB 1; Length 87;  
 Best Local Similarity 88.5%; Pred. No. 10;  
 Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 Db 1 CACCATGTGGTCCAGGCTGGTCTCAAACTCTGACTTCGTGATCTGCCACCTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 40  
 AAI99208  
 ID AAI99208 standard; DNA; 87 BP.  
 XX AAI99208;

XX 07-JAN-2002 (first entry)

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XX Human excretory related polynucleotide SEQ ID NO 972.
DE
XX
KW Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
  immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTCAGGCTGGTCTCAAACTCTGACTTCTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 41
AAK87263/c
ID AAK199211 standard; DNA; 87 BP.
XX
AC AAK199211;
DT 07-JAN-2002 (first entry)
XX
DE Human excretory related polynucleotide SEQ ID NO 975.
KW Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
  immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTCAGGCTGGTCTCAAACTCTGACTTCTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 42
AAK87263/c
ID AAK87263 standard; DNA; 87 BP.
XX
AC AAK87263;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42075.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGTCAGGCTGGTCTCAAACTCTGACTTCTGATCTGCCACCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 43
AAK84994
ID AAK84994 standard; DNA; 87 BP.
XX
AC AAK84994;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39806.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTCAGGCTGGTCTCAAACTCTGACTTCTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 44
AAK87262/c
ID AAK87262 standard; DNA; 87 BP.
XX
AC AAK87262;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42074.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGTCAGGCTGGTCTCAAACTCTGACTTCTGATCTGCCACCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 45
AAK78040
ID AAK78040 standard; DNA; 87 BP.
XX
AC AAK78040;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32852.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTCAGGCTGGTCTCGAACTCTGACTTCTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
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XX AAK84994 standard; DNA; 87 BP.
XX
AC AAK84994;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39806.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTCAGGCTGGTCTCAAACTCTGACTTCTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 44
AAK87262/c
ID AAK87262 standard; DNA; 87 BP.
XX
AC AAK87262;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42074.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGTCAGGCTGGTCTCAAACTCTGACTTCTGATCTGCCACCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 45
AAK78040
ID AAK78040 standard; DNA; 87 BP.
XX
AC AAK78040;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32852.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTCAGGCTGGTCTCGAACTCTGACTTCTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
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Db      61 CCAAAGTGTGGGATTACAGGTGTGAG 87
RESULT 46
AAK84995
ID      AAK84995 standard; DNA; 87 BP.
XX
XX      AAK84995;
AC
XX      07-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39807.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
KW      Query Match      3.0%; Score 71; DB 1; Length 87;
      Best Local Similarity 88.5%; Pred. No. 10;
      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
      1 CACCATGTTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
Db
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
      61 CCAAAGTGTGGGATTACAGGCATGAG 87
Db
RESULT 47
AAK68262
ID      AAK68262 standard; DNA; 87 BP.
XX
XX      AAK68262;
AC
XX      06-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23074.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
KW      Query Match      3.0%; Score 71; DB 1; Length 87;
      Best Local Similarity 88.5%; Pred. No. 10;
      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
      1 CACCATGTTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
Db
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
      61 CCAAAGTGTGGGATTACAGGCATGAG 87
Db
RESULT 48
AAK84992
ID      AAK84992 standard; DNA; 87 BP.
XX
XX      AAK84992;
AC
XX      07-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39804.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
KW      Query Match      3.0%; Score 71; DB 1; Length 87;
      Best Local Similarity 88.5%; Pred. No. 10;
      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
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Db      1 CACCATGTTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
      61 CCAAAGTGTGGGATTACAGGCATGAG 87
Db
RESULT 49
AAK68855
ID      AAK68855 standard; DNA; 87 BP.
XX
XX      AAK68855;
AC
XX      06-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23667.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
KW      Query Match      3.0%; Score 71; DB 1; Length 87;
      Best Local Similarity 88.5%; Pred. No. 10;
      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
      1 CACCATGTTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
Db
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
      61 CCAAAGTGTGGGATTACAGGCATGAG 87
Db
RESULT 50
AAK68854
ID      AAK68854 standard; DNA; 87 BP.
XX
XX      AAK68854;
AC
XX      06-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23666.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
KW      Query Match      3.0%; Score 71; DB 1; Length 87;
      Best Local Similarity 88.5%; Pred. No. 10;
      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
      1 CACCATGTTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
Db
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
      61 CCAAAGTGTGGGATTACAGGCATGAG 87
Db
RESULT 51
AAS28332
ID      AAS28332 standard; DNA; 87 BP.
XX
XX      AAS28332;
AC
XX      07-NOV-2001 (first entry)
DT
XX      Genomic sequence #172 encoding for novel human respiratory antigen.
DE
XX      Human; respiratory antigen; respiratory disorder; throat disorder;
XX      lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
KW
```

Query Match 3.0%; Score 71; DB 1; Length 87;  
 Best Local Similarity 88.5%; Pred. No. 10;  
 Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 |||||  
 Db 1 CACCATGTGTGGTCAGGCTGGTCTCAAACTCTGACCTCTTGATCGGCCCTCAGCCTC 60  
 |||||

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 |||||  
 Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87  
 |||||

RESULT 52  
 AA163561  
 ID AA163561 standard; DNA; 87 BP.  
 AC AA163561;  
 XX  
 XX 22-OCT-2001 (first entry)  
 DT  
 DE Human kidney related polynucleotide SEQ ID NO 876.  
 DE  
 XX Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;

Query Match 3.0%; Score 71; DB 1; Length 87;  
 Best Local Similarity 88.5%; Pred. No. 10;  
 Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 |||||  
 Db 1 CACCATGTGTGGTCAGGCTGGTCTCAAACTCTGACCTCTTGATCGGCCCTCAGCCTC 60  
 |||||

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 |||||  
 Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87  
 |||||

RESULT 53  
 AA163558  
 ID AA163558 standard; DNA; 87 BP.  
 AC AA163558;  
 XX  
 XX 22-OCT-2001 (first entry)  
 DT  
 DE Human kidney related polynucleotide SEQ ID NO 873.  
 DE  
 XX Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;

Query Match 3.0%; Score 71; DB 1; Length 87;  
 Best Local Similarity 88.5%; Pred. No. 10;  
 Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 |||||  
 Db 1 CACCATGTGTGGTCAGGCTGGTCTCAAACTCTGACCTCTTGATCGGCCCTCAGCCTC 60  
 |||||

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 |||||  
 Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87  
 |||||

RESULT 54  
 AA163560  
 ID AA163560 standard; DNA; 87 BP.  
 AC AA163560;  
 XX  
 XX 22-OCT-2001 (first entry)  
 DT  
 DE Human kidney related polynucleotide SEQ ID NO 875.

DE Human kidney related polynucleotide SEQ ID NO 875.  
 XX Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;

Query Match 3.0%; Score 71; DB 1; Length 87;  
 Best Local Similarity 88.5%; Pred. No. 10;  
 Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 |||||  
 Db 1 CACCATGTGTGGTCAGGCTGGTCTCAAACTCTGACCTCTTGATCGGCCCTCAGCCTC 60  
 |||||

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 |||||  
 Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87  
 |||||

RESULT 55  
 ABZ74272/c  
 ID ABZ74272 standard; DNA; 87 BP.  
 AC ABZ74272;  
 XX  
 XX 12-MAY-2003 (first entry)  
 DT  
 DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1419.  
 DE  
 XX Human; secreted protein; cancer; tumour; hyperproliferative disorder;  
 KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;

Query Match 3.0%; Score 71; DB 1; Length 87;  
 Best Local Similarity 88.5%; Pred. No. 10;  
 Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 |||||  
 Db 87 CACCATGTGTGGTCAGGCTGGTCTCAAACTCTGACCTCTTGATCGGCCCTCAGCCTC 28  
 |||||

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 |||||  
 Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1  
 |||||

RESULT 56  
 ADA9801/c  
 ID ADA9801 standard; DNA; 87 BP.  
 AC ADA9801;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 DE Human secreted protein-related DNA sequence #394.  
 DE  
 XX human; secreted protein; cardiovascular disorder; arrhythmia;  
 KW atherosclerosis; stroke; endocarditis; congestive heart failure;

Query Match 3.0%; Score 71; DB 1; Length 87;  
 Best Local Similarity 88.5%; Pred. No. 10;  
 Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
 |||||  
 Db 87 CACCATGTGTGGTCAGGCTGGTCTCAAACTCTGACCTCTTGATCGGCCCTCAGCCTC 28  
 |||||

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
 |||||  
 Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1  
 |||||

RESULT 57  
 ADG41528  
 ID ADG41528 standard; DNA; 87 BP.



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XX ADG41528;
XX AC
XX DT
XX 26-FEB-2004 (first entry)
XX Human respiratory system associated genomic DNA seq id 766.
XX
XX antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
XX respiratory system antigen;
KW

Query Match 3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCAATGTTGGTCAGGTGCTCTCAAACTCTGATCTTGATCCGCCCTCAGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87

RESULT 58
ABZ67838/c
ID ABZ67838 standard; DNA; 87 BP.
XX
AC ABZ67838;
XX
DT 26-MAR-2003 (first entry)
XX
DE Human secreted protein encoding genomic DNA SEQ ID NO 1361.
XX
KW Human; secreted protein; neurotropic; neuroprotective; cytostatic;
KW virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV;
KW

Query Match 3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCAATGTTGGTCAGGTGCTCTCAAACTCTGATCTTGATCCGCCCTCAGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1

RESULT 59
ABK45727
ID ABK45727 standard; cDNA; 84 BP.
XX
AC ABK45727;
XX
DT 05-JUN-2002 (first entry)
XX
DE cDNA encoding colon tumour protein, SEQ ID NO 1278.
XX
KW Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
KW gene; ss.

Query Match 3.0%; Score 70.8; DB 1; Length 84;
Best Local Similarity 91.5%; Pred. No. 11;
Matches 75; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2291 CCAGGATGGTCTCGATCTCTGACCTCGTATCCGCCACCTCGGCCTCCCAAAGTGCTG 2350
Db 1 CCAGATGGTCTGATCTCTGACCTCGTATCTGCCGCTCGGCCTCCCAAAGTGCTG 60

QY 2351 GGATTACAGGCATGAGCCACG 2372
Db 61 GGATTACCGGTGTGAGCCACCG 82
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RESULT 60
AAC11340
ID AAC11340 standard; cDNA; 92 BP.
XX
AC AAC11340;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 15415.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.0%; Score 70.2; DB 1; Length 92;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 78; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
Db 1 TTTTGTATTTTAGTAGAGACGGGTTTTCACCATGTGTCTGTCAGGCTGGTCTTGAACCTCC 60

QY 2311 TGACCTCGTGATCCGCCACCTCGGCCTCCC 2341
Db 61 TGACCTTGTGATCCACCTCGCTTGGCCTCCC 91

RESULT 61
AAS36366
ID AAS36366 standard; DNA; 87 BP.
XX
AC AAS36366;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1866.
XX
KW Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;
KW

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGGTCAGGCTGATCTCGAACTCTGACCTCGTGATCCGCCCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGATGAG 87

RESULT 62
AAK91304
ID AAK91304 standard; DNA; 87 BP.
XX
AC AAK91304;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4880.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGGTCAGGCTGATCTCGAACTCTGACCTCGTGATCCGCCCTTGGCCTC 60
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Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGTATCCGCCGCTTGGCCTC 60
QY 2340 CCAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAAGTCTGAGATTACCGCGTGAG 87

RESULT 63
AAK91305
ID AAK91305 standard; DNA; 87 BP.
XX
AC AAK91305;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4881.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGTATCCGCCGCTTGGCCTC 60

QY 2340 CCAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAAGTCTGAGATTACCGCGTGAG 87

RESULT 64
AAK91307
ID AAK91307 standard; DNA; 87 BP.
XX
AC AAK91307;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4883.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGTATCCGCCGCTTGGCCTC 60

QY 2340 CCAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAAGTCTGAGATTACCGCGTGAG 87

RESULT 65
AAK86755
ID AAK86755 standard; DNA; 87 BP.
XX
AC AAK86755;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41567.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
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Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCGAACTCCTGACCTTGTGTATCCACCTGCTTGGCCTC 60

QY 2340 CCAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAAGTCTGGGATTACAGGTGTGAG 87

RESULT 66
AAK75934/c
ID AAK75934 standard; DNA; 87 BP.
XX
AC AAK75934;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30746.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATCTTGGTCCAGGCTGGTCTCCAACCTCCTGACCTCGTGATCCACCGCCTCGGCCTC 28

QY 2340 CCAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAAGTCTGGGATTATAGGTGTGAG 1

RESULT 67
AAK81974/c
ID AAK81974 standard; DNA; 87 BP.
XX
AC AAK81974;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36786.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATCTTGGTCCAGGCTGGTCTCGAACTCCTGACCTTGTGTATCCGCCGCTTGGCCTC 28

QY 2340 CCAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 68
AAK81975/c
ID AAK81975 standard; DNA; 87 BP.
XX
AC AAK81975;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36787.
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XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCTGATCCGCCACCTCGGCCTC 2339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 87 CACCATGTGTGTCAGGCTGGTCTCGAACTCTGACCTTGTGATCCGCTGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
    ||||| ||||| ||||| ||||| |||||
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 69
AAK75935/c
ID AAK75935 standard; DNA; 87 BP.
XX
AC AAK75935;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30747.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCTGATCCGCCACCTCGGCCTC 2339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 87 CACCATGTGTGTCAGGCTGGTCTCGAACTCTGACCTTGTGATCCGCTGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
    ||||| ||||| ||||| ||||| |||||
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 70
AAK81973/c
ID AAK81973 standard; DNA; 87 BP.
XX
AC AAK81973;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36785.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCTGATCCGCCACCTCGGCCTC 2339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 87 CACCATGTGTGTCAGGCTGGTCTCGAACTCTGACCTTGTGATCCGCTGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
    ||||| ||||| ||||| ||||| |||||
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 71
AAK83799/c
ID AAK83799 standard; DNA; 87 BP.
XX
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AC AAK83799;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38611.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCTGATCCGCCACCTCGGCCTC 2339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 87 CACCATGTGTGTCAGGCTGGTCTCGAACTCTGACCTTGTGATCTGCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
    ||||| ||||| ||||| ||||| |||||
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 72
AAK86753
ID AAK86753 standard; DNA; 87 BP.
XX
AC AAK86753;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41565.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCTGATCCGCCACCTCGGCCTC 2339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CACCATGTGTGTCAGGCTGGTCTCGAACTCTGACCTTGTGATCTGCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
    ||||| ||||| ||||| ||||| |||||
Db 61 CCAAAGTCTGGGATTACAGGTGTGAG 87

RESULT 73
AAL36467/c
ID AAL36467 standard; DNA; 87 BP.
XX
AC AAL36467;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2832.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;

Query Match      2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCTGATCCGCCACCTCGGCCTC 2339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 87 CACCATGTGTGTCAGGCTGGTCTAGAACTCTGACCTCTGATCCGCCACCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
    ||||| ||||| ||||| ||||| |||||
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1
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RESULT 74  
AAL36466/c  
ID AAL36466 standard; DNA; 87 BP.  
XX  
AC AAL36466;  
XX  
DT 08-JAN-2002 (first entry)  
XX  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2831.  
XX  
DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
KW  
Query Match 2.9%; Score 69.4; DB 1; Length 87;  
Best Local Similarity 87.4%; Pred. No. 13;  
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
Db 87 CACCATGTGGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28  
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1  
RESULT 75  
AAL36464/c  
ID AAL36464 standard; DNA; 87 BP.  
XX  
AC AAL36464;  
XX  
DT 08-JAN-2002 (first entry)  
XX  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2829.  
XX  
DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
KW  
Query Match 2.9%; Score 69.4; DB 1; Length 87;  
Best Local Similarity 87.4%; Pred. No. 13;  
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
Db 87 CACCATGTGGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28  
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1  
RESULT 76  
AAL02848  
ID AAL02848 standard; DNA; 87 BP.  
XX  
AC AAL02848;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human reproductive system related antigen DNA SEQ ID NO: 5536.  
XX  
DE Human; reproductive system related antigen; reproductive system disorder;  
KW cancer; gene therapy; ds.  
Query Match 2.9%; Score 69.4; DB 1; Length 87;  
Best Local Similarity 87.4%; Pred. No. 13;  
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
Db 1 CACCATGTGGCCAGGCTTGTCTCAAACTCTGACCTCGTGATCCGCCACTTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
Db 61 CCAAAGTCTGGGATTACAGCGTAAG 87  
RESULT 77  
AAL02849  
ID AAL02849 standard; DNA; 87 BP.  
XX  
AC AAL02849;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human reproductive system related antigen DNA SEQ ID NO: 5537.  
XX  
DE Human; reproductive system related antigen; reproductive system disorder;  
KW cancer; gene therapy; ds.  
Query Match 2.9%; Score 69.4; DB 1; Length 87;  
Best Local Similarity 87.4%; Pred. No. 13;  
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
Db 1 CACCATGTGGCCAGGCTTGTCTCAAACTCTGACCTCGTGATCCGCCACTTTGGCCTC 60  
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
Db 61 CCAAAGTCTGGGATTACAGCGTAAG 87  
RESULT 78  
AAL07338/c  
ID AAL07338 standard; DNA; 87 BP.  
XX  
AC AAL07338;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human reproductive system related antigen DNA SEQ ID NO: 10026.  
XX  
DE Human; reproductive system related antigen; reproductive system disorder;  
KW cancer; gene therapy; ds.  
Query Match 2.9%; Score 69.4; DB 1; Length 87;  
Best Local Similarity 87.4%; Pred. No. 13;  
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
Db 87 CACCATGTGGCCAGGCTTGTCTCGAACTCTGACCTCGTGATCCGCCACTTTGGCCTC 28  
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
Db 27 CCAAAGTCTGGGATTACAGATGTGAG 1  
RESULT 79  
AAS32132  
ID AAS32132 standard; DNA; 87 BP.  
XX  
AC AAS32132;  
XX  
DT 04-DEC-2001 (first entry)  
XX  
DE Human liver associated genomic DNA #306.  
XX  
DE Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;  
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;  
KW  
Query Match 2.9%; Score 69.4; DB 1; Length 87;  
Best Local Similarity 87.4%; Pred. No. 13;

```
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGCTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGCTGAGATTACCGGCGTGAG 87

RESULT 80
AAS32134
ID AAS32134 standard; DNA; 87 BP.
XX
AC AAS32134;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #308.
XX
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGCTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGCTGAGATTACCGGCGTGAG 87

RESULT 81
AAS32131
ID AAS32131 standard; DNA; 87 BP.
XX
AC AAS32131;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #305.
XX
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGCTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGCTGAGATTACCGGCGTGAG 87

RESULT 82
AEN90487
ID AEN90487 standard; DNA; 87 BP.
XX
AC AEN90487;
XX
DT 24-JUL-2002 (first entry)
XX
DE Human liver antigen HFVID08 genomic sequence, SEQ ID NO:608.
XX
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KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGCTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGCTGAGATTACCGGCGTGAG 87

RESULT 83
AEN90489
ID AEN90489 standard; DNA; 87 BP.
XX
AC AEN90489;
XX
DT 24-JUL-2002 (first entry)
XX
DE Human liver antigen HFVID08 genomic sequence, SEQ ID NO:610.
XX
KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGCTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGCTGAGATTACCGGCGTGAG 87

RESULT 84
AEN90486
ID AEN90486 standard; DNA; 87 BP.
XX
AC AEN90486;
XX
DT 24-JUL-2002 (first entry)
XX
DE Human liver antigen HFVID08 genomic sequence, SEQ ID NO:607.
XX
KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGCTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGCTGAGATTACCGGCGTGAG 87

RESULT 85
ABX59454/c
ID ABX59454 standard; cDNA; 87 BP.
XX
AC ABX59454;
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XX 26-FEB-2003 (first entry)
DT
DE cDNA encoding novel human musculoskeletal system antigen #1798.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGGCCAGGCTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTAG 1

RESULT 86
ABX59455/c
ID ABX59455 standard; cDNA; 87 BP.
XX
AC ABX59455;
XX
DT 26-FEB-2003 (first entry)
DE cDNA encoding novel human musculoskeletal system antigen #1799.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGGCCAGGCTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTAG 1

RESULT 87
ABX59452/c
ID ABX59452 standard; cDNA; 87 BP.
XX
AC ABX59452;
XX
DT 26-FEB-2003 (first entry)
DE cDNA encoding novel human musculoskeletal system antigen #1796.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGGCCAGGCTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTAG 1

RESULT 88
ADE47060
ID ADE47060 standard; DNA; 87 BP.
XX
AC ADE47060;
XX
DT 29-JAN-2004 (first entry)
DE Human cardiovascular system related genomic DNA #626.
XX
KW Human; cardiovascular system related polypeptide; cancer;
proliferative disorder; foetal abnormality; developmental abnormality;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGGTCCAGGCTGTCTGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGAGTGAG 87

RESULT 89
ADJ15402
ID ADJ15402 standard; DNA; 87 BP.
XX
AC ADJ15402;
XX
DT 20-MAY-2004 (first entry)
DE Human liver-related genomic DNA - SEQ ID 610.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGAGATTACCGGCGTGAG 87

RESULT 90
ADJ15399
ID ADJ15399 standard; DNA; 87 BP.
XX
AC ADJ15399;
XX
DT 20-MAY-2004 (first entry)
DE Human liver-related genomic DNA - SEQ ID 607.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGAGATTACCGGCGTGAG 87
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XX 26-FEB-2003 (first entry)
DT
DE cDNA encoding novel human musculoskeletal system antigen #1798.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGGCCAGGCTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTAG 1

RESULT 86
ABX59455/c
ID ABX59455 standard; cDNA; 87 BP.
XX
AC ABX59455;
XX
DT 26-FEB-2003 (first entry)
DE cDNA encoding novel human musculoskeletal system antigen #1799.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGGCCAGGCTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTAG 1

RESULT 87
ABX59452/c
ID ABX59452 standard; cDNA; 87 BP.
XX
AC ABX59452;
XX
DT 26-FEB-2003 (first entry)
DE cDNA encoding novel human musculoskeletal system antigen #1796.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGGCCAGGCTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTAG 1

RESULT 88
ADE47060
ID ADE47060 standard; DNA; 87 BP.
XX
AC ADE47060;
XX
DT 29-JAN-2004 (first entry)
DE Human cardiovascular system related genomic DNA #626.
XX
KW Human; cardiovascular system related polypeptide; cancer;
proliferative disorder; foetal abnormality; developmental abnormality;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGGTCCAGGCTGTCTGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGAGTGAG 87

RESULT 89
ADJ15402
ID ADJ15402 standard; DNA; 87 BP.
XX
AC ADJ15402;
XX
DT 20-MAY-2004 (first entry)
DE Human liver-related genomic DNA - SEQ ID 610.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGAGATTACCGGCGTGAG 87

RESULT 90
ADJ15399
ID ADJ15399 standard; DNA; 87 BP.
XX
AC ADJ15399;
XX
DT 20-MAY-2004 (first entry)
DE Human liver-related genomic DNA - SEQ ID 607.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGAGATTACCGGCGTGAG 87
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QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87

RESULT 91
ADJ30205/c
ID ADJ30205 standard; DNA; 87 BP.
XX AC ADJ30205;
XX DT 20-MAY-2004 (first entry)
XX DE Human liver-related genomic DNA - SEQ ID 608.
XX DE liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
KW antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;
KW

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87

RESULT 92
ADJ30205/c
ID ADJ30205 standard; DNA; 87 BP.
XX AC ADJ30205;
XX DT 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2832.
XX DE musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
KW gene therapy; vaccine; human; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1

RESULT 93
ADJ30202/c
ID ADJ30202 standard; DNA; 87 BP.
XX AC ADJ30202;
XX DT 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2829.
XX DE musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
KW gene therapy; vaccine; human; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY 2280 CACCGTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1

RESULT 94
ADJ30204/c
ID ADJ30204 standard; DNA; 87 BP.
XX AC ADJ30204;
XX DT 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2831.
XX DE musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
KW gene therapy; vaccine; human; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1

RESULT 95
AAK83861
ID AAK83861 standard; DNA; 90 BP.
XX AC AAK83861;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38673.
XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 68.3; DB 1; Length 90;
Best Local Similarity 91.2%; Pred. No. 14;
Matches 83; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 2233 CCACCACACCTGGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTCCCGTGTAGCC 2292
Db 1 CCACCACACCTGGCTAA-TTTTGTATTTTGTAGTAGACAGGGTTTCCACCATGTTGGCC 59

QY 2293 AGGATGCTCGATCTCTGACCTCGTGATC 2323
Db 60 AGGCTGCTCTCGAACTCTCTGACCTCGTGATC 90

RESULT 96
AAK85686/c
ID AAK85686 standard; DNA; 90 BP.
XX AC AAK85686;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40498.
XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 68.3; DB 1; Length 90;  
Best Local Similarity 91.2%; Pred. No. 14;  
Matches 83; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 2233 CCACCACACCTGGCTAAATTTTGTGACCTTTAGTAGACAGGGCTTTCCACGGTGTAGCC 2292  
DB 90 CCACCACACCTGGCTAA-TTTTGTGATTTTGTGGAGCGGGTTTCACCATGTTGGCC 32

QY 2283 AGGATGGTCTCGATCTCCTGACCTCGTGATC 2323  
DB 31 AGGCTGGTCTCGAACTCTCGACCTCGTGATC 1

RESULT 97  
AAK90874  
ID AAK90874 standard; DNA; 87 BP.  
XX AAK90874;  
XX  
DT 05-NOV-2001 (first entry)  
DE Human digestive system antigen genomic sequence SEQ ID NO: 4450.  
XX  
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;  
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 2.9%; Score 67.8; DB 1; Length 87;  
Best Local Similarity 86.2%; Pred. No. 15;  
Matches 75; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
DB 1 CACCATGTTGGCTAGCGCTGCTTGAACCTCGTACCTCGTGATCCGCCCGCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
DB 61 CTGAAGTCTGGGATTACAGGTGTGAG 87

RESULT 98  
ABA15851/c  
ID ABA15851 standard; DNA; 87 BP.  
XX ABA15851;  
XX  
DT 23-JAN-2002 (first entry)  
DE Human nervous system related polynucleotide SEQ ID NO 8182.  
XX  
KW Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match 2.9%; Score 67.8; DB 1; Length 87;  
Best Local Similarity 86.2%; Pred. No. 15;  
Matches 75; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
DB 87 CACCATATTGGCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
DB 27 CCAAAGTCTGGGATTACATGATGAG 1

RESULT 99  
ABA15852/c  
ID ABA15852 standard; DNA; 87 BP.  
XX ABA15852;  
XX

DT 23-JAN-2002 (first entry)  
DE Human nervous system related polynucleotide SEQ ID NO 8183.  
XX  
KW Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match 2.9%; Score 67.8; DB 1; Length 87;  
Best Local Similarity 86.2%; Pred. No. 15;  
Matches 75; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
DB 87 CACCATATTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
DB 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 102

DT 23-JAN-2002 (first entry)  
DE Human nervous system related polynucleotide SEQ ID NO 8183.  
XX  
KW Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match 2.9%; Score 67.8; DB 1; Length 87;  
Best Local Similarity 86.2%; Pred. No. 15;  
Matches 75; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
DB 87 CACCATATTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
DB 27 CCAAAGTCTGGGATTACATGATGAG 1

RESULT 100  
AAK65876/c  
ID AAK65876 standard; DNA; 87 BP.  
XX AAK65876;  
XX  
DT 06-NOV-2001 (first entry)  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20688.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.8%; Score 66.2; DB 1; Length 87;  
Best Local Similarity 85.1%; Pred. No. 18;  
Matches 74; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
DB 87 CACCATGTTGGCCAGGCTGGTCTCAAACTCTGACCTCATATAATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
DB 27 CCAAATGCTGGGATTACAGGTGTGAG 1

RESULT 101  
AAK65878/c  
ID AAK65878 standard; DNA; 87 BP.  
XX AAK65878;  
XX  
DT 06-NOV-2001 (first entry)  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20690.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.8%; Score 66.2; DB 1; Length 87;  
Best Local Similarity 85.1%; Pred. No. 18;  
Matches 74; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
DB 87 CACCATGTTGGCCAGGCTGGTCTCAAACTCTGACCTCATATAATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366  
DB 27 CCAAATGCTGGGATTACAGGTGTGAG 1

RESULT 102



AAK76883  
ID AAK76883 standard; DNA; 82 BP.  
XX  
AC AAK76883;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31695.  
XX  
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
KW  
Query Match 2.8%; Score 66; DB 1; Length 82;  
Best Local Similarity 87.8%; Pred. No. 18;  
Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 2263 TAGTAGAGACAGGGTTTACCGTCTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTAT 2322  
Db 1 TAATAGACACAGGGTTTACCATGTTGGCCAGGATGGTCTTGATCTCTTGACCTTGTAT 60  
QY 2323 CCGCCCACTTCGGCTCCCAA 2344  
Db 61 CTGCCCGCTTGGCTCCCAA 82  
RESULT 103  
AD112544/c  
ID AD112544 standard; DNA; 80 BP.  
XX  
AC AD112544;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mutant human BRCA1 genomic DNA resulting from deletion 3 SeqID 27.  
KW db; cancer; human; tumour suppressor;  
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;  
Query Match 2.7%; Score 64.4; DB 1; Length 80;  
Best Local Similarity 91.9%; Pred. No. 21;  
Matches 68; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2298 GGTCTCGATCTCTGACCTCGTATCGCCACCTCGGCCCTCCCAAAGTCTGGATTAC 2357  
Db 80 GGTCTCGAATCTCTGACCTGTGATCGCCGCTCGGCCCTCCCAAAGTCTGGATTAC 21  
QY 2358 AGGCATGAGCCACC 2371  
Db 20 AGGCGTAAGCCACC 7  
RESULT 104  
AAC11941  
ID AAC11941 standard; cDNA; 81 BP.  
XX  
AC AAC11941;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein 5' EST, SEQ ID NO: 16016.  
XX  
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping; ss.  
Query Match 2.6%; Score 62.2; DB 1; Length 81;  
Best Local Similarity 84.8%; Pred. No. 28;  
Matches 67; Conservative 1; Mismatches 11; Indels 0; Gaps 0;  
QY 2253 TTGTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312  
Db 2 TATTNNNTTAAAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTG 61  
QY 2313 ACCTCGTGTATCCGCCACC 2331

Db 62 ACCTCGTGATCTGCCGCC 80  
RESULT 105  
ABN39842  
ID ABN39842 standard; DNA; 60 BP.  
XX  
AC ABN39842;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:12590.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
Query Match 2.5%; Score 60; DB 1; Length 60;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 98 TGACCGAGATCTCTGCTTTCGACGCCAGGACCGTCCCTCCCGGATTAGTCGTA 157  
Db 1 TGACCGAGATCTCTGCTTTCGACGCCAGGACCGTCCCTCCCGGATTAGTCGTA 60  
RESULT 106  
ABZ09613/c  
ID ABZ09613 standard; DNA; 68 BP.  
XX  
AC ABZ09613;  
XX  
DT 16-JAN-2003 (first entry)  
XX  
DE Human oligonucleotide SEQ ID 773.  
KW Human; tumour suppressor; virucide; cytostatic; neurotropic;  
KW neuroprotective; neuroleptic; gene therapy; tumour suppression;  
Query Match 2.5%; Score 60; DB 1; Length 68;  
Best Local Similarity 92.6%; Pred. No. 33;  
Matches 63; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2256 GTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315  
Db 68 GTATTTTAGTAGACAGGGTTTACCATGTTAGTAGATGGTCTCGATTTCTCTGACC 9  
QY 2316 TCGTGATC 2323  
Db 8 TCGTGATC 1  
RESULT 107  
ABZ79066/c  
ID ABZ79066 standard; DNA; 68 BP.  
XX  
AC ABZ79066;  
XX  
DT 24-APR-2003 (first entry)  
XX  
DE Tumour suppression-related sequence, SEQ ID 773.  
KW Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;  
KW tumour reversion; apoptosis; virus resistance; viral infection; tumour;  
Query Match 2.5%; Score 60; DB 1; Length 68;  
Best Local Similarity 92.6%; Pred. No. 33;  
Matches 63; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2256 GTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315  
Db 68 GTATTTTAGTAGACAGGGTTTACCATGTTAGTAGATGGTCTCGATTTCTCTGACC 9

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QY 2316 TCGTGATC 2323
|||
Db 8 TCGTGATC 1

RESULT 108
ID ABZ09678/c
XX ABZ09678 standard; DNA; 68 BP.
XX ABZ09678;
XX 16-JAN-2003 (first entry)
XX Human oligonucleotide SEQ ID 838.
DE Human; tumour suppressor; virucide; cytostatic; neutropic;
XX neuroprotective; neuroleptic; gene therapy; tumour suppression;
KW Human; tumour suppressor; virucide; cytostatic; neutropic;
XX neuroprotective; neuroleptic; gene therapy; tumour suppression;
KW

Query Match 2.5%; Score 58.4; DB 1; Length 68;
Best Local Similarity 91.2%; Pred. No. 40;
Matches 62; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGACAGGGTTTCACCGTTAGCCAGGATGCTCTCGATCTCCTGACC 2315
|||
Db 68 GTATTTTATAGAGAGTGGGTTTCACCATGTTAGCCAGGATGCTCTCAATCTCCTGACC 9

QY 2316 TCGTGATC 2323
|||
Db 8 TCGTGATC 1

RESULT 109
ID ABZ79131/c
XX ABZ79131 standard; DNA; 68 BP.
XX ABZ79131;
XX 24-APR-2003 (first entry)
XX Tumour suppression-related sequence, SEQ ID 838.
DE Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
XX tumour reversion; apoptosis; virus resistance; viral infection; tumour;
KW

Query Match 2.5%; Score 58.4; DB 1; Length 68;
Best Local Similarity 91.2%; Pred. No. 40;
Matches 62; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGACAGGGTTTCACCGTTAGCCAGGATGCTCTCGATCTCCTGACC 2315
|||
Db 68 GTATTTTATAGAGAGTGGGTTTCACCATGTTAGCCAGGATGCTCTCAATCTCCTGACC 9

QY 2316 TCGTGATC 2323
|||
Db 8 TCGTGATC 1

RESULT 110
ID ABZ09289
XX ABZ09289 standard; DNA; 68 BP.
XX ABZ09289;
XX 16-JAN-2003 (first entry)
XX Human oligonucleotide SEQ ID 449.
DE Human; tumour suppressor; virucide; cytostatic; neutropic;
XX neuroprotective; neuroleptic; gene therapy; tumour suppression;
KW

Query Match 2.4%; Score 56.8; DB 1; Length 68;
Best Local Similarity 85.3%; Pred. No. 48;
Matches 58; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2316 TCGTGATC 2323
|||
Db 61 TYGTGATC 68

RESULT 111
ID ABZ78742
XX ABZ78742 standard; DNA; 68 BP.
XX ABZ78742;
XX 24-APR-2003 (first entry)
XX Tumour suppression-related sequence, SEQ ID 449.
DE Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
XX tumour reversion; apoptosis; virus resistance; viral infection; tumour;
KW

Query Match 2.4%; Score 56.8; DB 1; Length 68;
Best Local Similarity 85.3%; Pred. No. 48;
Matches 58; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGACAGGGTTTCACCGTTAGCCAGGATGCTCTCGATCTCCTGACC 2315
|||
Db 1 GTATTTTATAGAGAGTGGGTTTCACCRGTGGTCAGGCTGGTCTCGAACTCTGACC 60

QY 2316 TCGTGATC 2323
|||
Db 61 TYGTGATC 68

RESULT 112
ID AAS57672
XX AAS57672 standard; cDNA; 69 BP.
XX AAS57672;
XX 13-FEB-2002 (first entry)
XX cDNA #348 encoding portion of a human colon tumour protein.
DE Human; colon tumour protein; colon cancer; gene therapy; cytostatic; ss.
KW

Query Match 2.4%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 52;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2291 CCAGGATGCTCGATCTCTGACCTCGATCGCCACCTCGGCTCCCAAGTCTG 2350
|||
Db 1 CCAGGCCGGTCTCGAACTCCAGACCTCATGATCCCGGCTTGGCTCCCAAGTCTG 60

QY 2351 GGATTACAG 2359
|||
Db 61 GGATTACAG 69

RESULT 113
ID AAC12925
XX AAC12925 standard; cDNA; 65 BP.
XX AAC12925;
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 17000.
DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW
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KW gene therapy; chromosome mapping; ss.
Query Match 2.3%; Score 54.4; DB 1; Length 65;
Best Local Similarity 90.6%; Pred. No. 62;
Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2270 GACAGGGTTTCACCGTGTAGCCAGGATGTCGATCTCCTGACCTCGTGATCCGCCCA 2329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GACGGGGTTTCCTCGTGTAGCCAGGATGTCGATCTCCTGACCTTGTAAATCCGCCCA 60

QY 2330 CCTC 2333
    ||| |||
Db 61 CCGC 64

RESULT 114
ABZ09729/c
ID ABZ09729 standard; DNA; 60 BP.
XX AC ABZ09729;
XX 16-JAN-2003 (first entry)
XX DE Human oligonucleotide SEQ ID 889.
XX KW Human; tumour suppressor; virucide; cytostatic; nootropic;
KW neuroprotective; neuroleptic; gene therapy; tumour suppression;
Query Match 2.2%; Score 52; DB 1; Length 60;
Best Local Similarity 91.7%; Pred. No. 79;
Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGTCGATCTCCTGACCTCGTGATC 2323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 AGTAGAGATGGGGTTTCACCTGTGTAGCCAGGATGTCCTCACTCTCCTGACCTCGTGATC 1

RESULT 115
ABZ79182/c
ID ABZ79182 standard; DNA; 60 BP.
XX AC ABZ79182;
XX 24-APR-2003 (first entry)
XX DE Tumour suppression-related sequence, SEQ ID 889.
XX KW Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
KW tumour reversion; apoptosis; virus resistance; viral infection; tumour;
Query Match 2.2%; Score 52; DB 1; Length 60;
Best Local Similarity 91.7%; Pred. No. 79;
Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGTCGATCTCCTGACCTCGTGATC 2323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 AGTAGAGATGGGGTTTCACCTGTGTAGCCAGGATGTCCTCACTCTCCTGACCTCGTGATC 1

RESULT 116
ADI12543/c
ID ADI12543 standard; DNA; 60 BP.
XX AC ADI12543;
XX 22-APR-2004 (first entry)
XX DE Mutant human BRCA1 genomic DNA resulting from deletion 3 SeqID 26.
XX KW de; cancer; human; tumour suppressor;
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
Query Match 2.2%; Score 52; DB 1; Length 60;

Best Local Similarity 91.7%; Pred. No. 79;
Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2308 TCTGTACCTCGTGATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGC 2367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 TCTGTACCTTGTGATCTGCCCGCTCGGCTCCCAAAGTCTGGGATTACAGGCGTAAGC 1

RESULT 117
AAK91064
ID AAK91064 standard; DNA; 66 BP.
XX AC AAK91064;
XX 05-NOV-2001 (first entry)
XX DE Human digestive system antigen genomic sequence SEQ ID NO: 4640.
XX KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
Query Match 2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 86.4%; Pred. No. 86;
Matches 57; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 TTTTGTATTTTAGTAGAGACGGGGTTTCACCATATTGACCAGGCTGGTCTCAAACTCC 60

QY 2311 TGACCT 2316
    ||| ||| ||| |||
Db 61 TGACCT 66

RESULT 118
AAS32099
ID AAS32099 standard; DNA; 66 BP.
XX AC AAS32099;
XX 04-DEC-2001 (first entry)
XX DE Human liver associated genomic DNA #273.
XX KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
Query Match 2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 86.4%; Pred. No. 86;
Matches 57; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 TTTTGTATTTTAGTAGAGACGGGGTTTCACCATATTGACCAGGCTGGTCTCAAACTCC 60

QY 2311 TGACCT 2316
    ||| ||| ||| |||
Db 61 TGACCT 66

RESULT 119
ABN90454
ID ABN90454 standard; DNA; 66 BP.
XX AC ABN90454;
XX 24-JUL-2002 (first entry)
XX DE Human liver antigen HLD4V38 genomic sequence, SEQ ID NO:575.
XX KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;
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Query Match      2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 86.4%; Pred. No. 86;
Matches 57; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
      |||||
Db 1 TTTTGTATTTTAGTAGAGACAGGGTTTCACCATATTGACCAGGCTGGTCTCAAACTCC 60

QY 2311 TGACCT 2316
      |||||
Db 61 TGACCT 66

RESULT 120
ADJ15367
ID ADJ15367 standard; DNA; 66 BP.
XX
XX ADJ15367;
DT
XX 20-MAY-2004 (first entry)
XX
DE Human liver-related genomic DNA - SEQ ID 575.
XX
XX liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
KW antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match      2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 86.4%; Pred. No. 86;
Matches 57; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
      |||||
Db 1 TTTTGTATTTTAGTAGAGACAGGGTTTCACCATATTGACCAGGCTGGTCTCAAACTCC 60

QY 2311 TGACCT 2316
      |||||
Db 61 TGACCT 66

RESULT 121
AAC11032/c
ID AAC11032 standard; cDNA; 68 BP.
XX
XX AAC11032;
DT
XX 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 15107.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match      2.2%; Score 51; DB 1; Length 68;
Best Local Similarity 85.1%; Pred. No. 93;
Matches 57; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
      |||||
Db 67 TTTTGTATTTTAGTAGAGACAGGGTTTCACCATATTGTCAGGCTGGTCTCGAACTCC 8

QY 2311 TGACCTC 2317
      |||||
Db 7 TGACCTC 1

RESULT 122
AAC15723
ID AAC15723 standard; cDNA; 64 BP.
XX
XX AAC15723;
DT
XX 06-OCT-2000 (first entry)
XX
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DE Human secreted protein 5' EST, SEQ ID NO: 19798.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match      2.1%; Score 50.2; DB 1; Length 64;
Best Local Similarity 87.3%; Pred. No. 99;
Matches 55; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2255 TGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTCGAC 2314
      |||||
Db 2 TGTATTTTAGTAGAGACAGGGTTTCGCCATGTTGTCGGGCTGGTCTCGAACTCTCTCGAC 61

QY 2315 CTC 2317
      |||
Db 62 CTC 64

RESULT 123
ABZ04758
ID ABZ04758 standard; DNA; 50 BP.
XX
XX ABZ04758;
DT
XX 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 4749.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;

Query Match      2.1%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1747 GACAACCAATTCAAATGATTGTGCTAACTTATTTCCCTAGTTGACCTGT 1796
      |||||
Db 1 GACAACCAATTCAAATGATTGTGCTAACTTATTTCCCTAGTTGACCTGT 50

RESULT 124
ADP10274
ID ADP10274 standard; DNA; 50 BP.
XX
XX ADP10274;
DT
XX 12-AUG-2004 (first entry)
XX
DE 50-mer oligonucleotide marker probe of the invention #283.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.

Query Match      2.1%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1747 GACAACCAATTCAAATGATTGTGCTAACTTATTTCCCTAGTTGACCTGT 1796
      |||||
Db 1 GACAACCAATTCAAATGATTGTGCTAACTTATTTCCCTAGTTGACCTGT 50

RESULT 125
AAI69056
ID AAI69056 standard; DNA; 63 BP.
XX
XX AAI69056;
DT
XX 29-JAN-2002 (first entry)
XX
XX Activated T-cell derived DNA fragment #192.
XX
XX Activated T-cell; immunosuppressive; immunostimulant; antiinflammatory;
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KW cytotostatic; gene therapy; vaccine; allergen; transplamt rejection;  
Query Match 2.1%; Score 50; DB 1; Length 63;  
Best Local Similarity 91.4%; Pred. No. 1e+02;  
Matches 53; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2250 TTTTTCGATCTTTAGTAGAGACAGGTTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307  
DB 6 TTTTTCGAATTTTAGTAGATACGGGTTTTCACCGTGTAGCCCTGGATGCTCTCGATC 63  
RESULT 126  
AAI32116/c  
ID AAL32116 standard; DNA; 51 BP.  
XX  
AC AAL32116;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #5324.  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytotostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
Query Match 2.1%; Score 49.4; DB 1; Length 51;  
Best Local Similarity 98.0%; Pred. No. 99;  
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2292 CAGGATGGTCTCGATCTCTGACCTCGTGTATCGCCACCTCGGCCTCCCA 2342  
DB 51 CAGGATGGTCTCGATCTCTGACCTCGTGTATCGCCACCTCGGCCTCCCA 1  
RESULT 127  
AAA77488  
ID AAA77488 standard; cDNA; 51 BP.  
XX  
AC AAA77488;  
XX  
DT 16-NOV-2000 (first entry)  
XX  
DE Human Alu subfamily SB gene polymorphic site, SEQ ID NO:1171.  
KW Human; single nucleotide polymorphism; SNP; detection; identification;  
KW gene therapy; ss.  
Query Match 2.0%; Score 48.4; DB 1; Length 51;  
Best Local Similarity 98.0%; Pred. No. 1.1e+02;  
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2301 CTCGATCTCTGACCTCGTGTATCGCCACCTCGGCCTCCCAAGTCTG 2350  
DB 2 CTCGATCTCTGACCTCGTGTATCGCCACCTTGGCTCTCCAAAGTCTG 51  
RESULT 128  
AAI77877  
ID AAI77877 standard; DNA; 51 BP.  
XX  
AC AAI77877;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:4818.  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
Query Match 2.0%; Score 47.8; DB 1; Length 51;  
Best Local Similarity 96.1%; Pred. No. 1.2e+02;  
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2292 CAGGATGGTCTCGATCTCTGACCTCGTGTATCGCCACCTCGGCCTCCCA 2342

DB 1 CAGGATGGTCTCGATCTCTGACCTCGTGTATCGCCACCTCGGCCTCCCA 51  
RESULT 129  
AAI79838/c  
ID AAI79838 standard; DNA; 51 BP.  
XX  
AC AAI79838;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6779.  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
Query Match 2.0%; Score 47.8; DB 1; Length 51;  
Best Local Similarity 96.1%; Pred. No. 1.2e+02;  
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2318 GTGATCGGCCACCTCGGCCTCCCAAGTCTGGGATTACAGGCATGAGCC 2368  
DB 51 GTGATCGGCCATCTCGGCCTCCCAAAATGCTGGGATTACAGGCATGAGCC 1  
RESULT 130  
AAI79700/c  
ID AAI79700 standard; DNA; 51 BP.  
XX  
AC AAI79700;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human conservative amino acid changing SNP nucleic acid SEQ:6641.  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
Query Match 2.0%; Score 47.8; DB 1; Length 51;  
Best Local Similarity 96.1%; Pred. No. 1.2e+02;  
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2319 TGATCGGCCACCTCGGCCTCCCAAGTCTGGGATTACAGGCATGAGCC 2369  
DB 51 TGATCGGCCATCTCGGCCTCCCAAAATGCTGGGATTACAGGCATGAGCC 1  
RESULT 131  
AAH89466/c  
ID AAH89466 standard; DNA; 51 BP.  
XX  
AC AAH89466;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 247.  
KW Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression; ds.  
Query Match 2.0%; Score 47.8; DB 1; Length 51;  
Best Local Similarity 96.1%; Pred. No. 1.2e+02;  
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2300 TCTCGATCTCTGACCTCGTGTATCGCCACCTCGGCCTCCCAAGTCTG 2350  
DB 51 TCTTGATCTCTGACCTCGTGTATCGCCACCTCGGCCTCCCAAGTCTG 1  
RESULT 132  
AAK86585  
ID AAK86585 standard; DNA; 63 BP.

```
XX AAK86585;
AC
XX
XX
XX 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41397.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
KW

Query Match 2.0%; Score 47.6; DB 1; Length 63;
Best Local Similarity 85.5%; Pred. No. 1.3e+02;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
Db 1 GTAATTTTAGTAGAGATGGTGTTCACCCCTGTGGTCAGGCTGGTCTCGAATCTCCTGACC 60
QY 2316 TC 2317
Db 61 TC 62

RESULT 133
AAK85681/c
ID AAK85681 standard; DNA; 63 BP.
XX
XX AAK85681;
AC
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40493.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
KW

Query Match 2.0%; Score 47.6; DB 1; Length 63;
Best Local Similarity 85.5%; Pred. No. 1.3e+02;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
Db 63 GTAATTTTAGTAGAGATGGTGTTCACCCCTGTGGTCAGGCTGGTCTCGAATCTCCTGACC 4
QY 2316 TC 2317
Db 3 TC 2

RESULT 134
ABZ09432
ID ABZ09432 standard; DNA; 52 BP.
XX
XX ABZ09432;
AC
XX
XX 16-JAN-2003 (first entry)
XX
XX Human oligonucleotide SEQ ID 592.
XX
XX Human; tumour suppressor; virucide; cytostatic; neutropic;
XX neuroprotective; neuroleptic; gene therapy; tumour suppression;
KW

Query Match 2.0%; Score 47.2; DB 1; Length 52;
Best Local Similarity 94.2%; Pred. No. 1.3e+02;
Matches 49; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 2307
Db 1 GCATTTTAGTAGACAGAGGGTTTCACCATGTTAGCCAGGATGGTCTCGATC 52

RESULT 135
ABZ78885
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ID ABZ78885 standard; DNA; 52 BP.
XX
XX ABZ78885;
AC
XX
XX 24-APR-2003 (first entry)
XX
XX Tumour suppression-related sequence, SEQ ID 592.
XX
XX Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
XX tumour reversion; apoptosis; virus resistance; viral infection; tumour;
KW

Query Match 2.0%; Score 47.2; DB 1; Length 52;
Best Local Similarity 94.2%; Pred. No. 1.3e+02;
Matches 49; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 2307
Db 1 GCATTTTAGTAGACAGAGGGTTTCACCATGTTAGCCAGGATGGTCTCGATC 52

RESULT 136
AAZ69526
ID AAZ69526 standard; DNA; 47 BP.
XX
XX AAZ69526;
AC
XX
XX 10-SEP-2001 (first entry)
XX
XX Human map-related biallelic marker SEQ ID NO:3882.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW

Query Match 2.0%; Score 47; DB 1; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTC 2317
Db 1 ACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTC 47

RESULT 137
AAA77489
ID AAA77489 standard; cDNA; 51 BP.
XX
XX AAA77489;
AC
XX
XX 16-NOV-2000 (first entry)
XX
XX Human Alu subfamily SB gene polymorphic site, SEQ ID NO:1172.
XX
XX Human; single nucleotide polymorphism; SNP; detection; identification;
XX gene therapy; ss.

Query Match 2.0%; Score 46.8; DB 1; Length 51;
Best Local Similarity 96.0%; Pred. No. 1.3e+02;
Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTGATCCGCCACCTCGCGCTCCCAAGTCTG 2350
Db 2 CTCGATCTCTGACCTCGTGATCCACCACCTTGGCTCCCAAGTCTG 51

RESULT 138
ABK45620/c
ID ABK45620 standard; cDNA; 59 BP.
XX
XX ABK45620;
AC
XX
XX 05-JUN-2002 (first entry)
XX
XX cDNA encoding colon tumour protein, SEQ ID NO 1171.
DE
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XX Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
KW gene; ss.

Query Match      2.0%; Score 46.8; DB 1; Length 59;
Best Local Similarity 87.9%; Pred. No. 1.4e+02;
Matches 51; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2233 CCACCACCTGGCTAAATTTTGTACTTTTAGTAGACACAGGGTTTCACCGTGTAG 2290
DB 58 CCACCACACCGAGCTAATTTTGTATCTTAGTAGACAGGGGTTTCACCATGTTGG 1

RESULT 139
ABK41287
ID ABK41287 standard; DNA; 47 BP.
XX
AC ABK41287;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human USP2 gene biallelic marker.
XX
DE Human; obesity associated-biallelic marker; db; LSR; USP2; drug response;
KW hyperuricaemia; digestive pathology; hypertension; cancer;
KW

Query Match      2.0%; Score 46.6; DB 1; Length 47;
Best Local Similarity 97.9%; Pred. No. 1.3e+02;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
DB 1 ACAGGGTTTCACCGTGTAGCCAKGATGGTCTCGATCTCTGACCTC 47

RESULT 140
AAI68926
ID AAI68926 standard; DNA; 54 BP.
XX
AC AAI68926;
XX
DT 29-JAN-2002 (first entry)
XX
DE Activated T-cell derived DNA fragment #62.
XX
DE Activated T-cell; immunosuppressive; immunostimulant; antiinflammatory;
KW cytostatic; gene therapy; vaccine; allergen; transplant rejection;
KW

Query Match      2.0%; Score 46.4; DB 1; Length 54;
Best Local Similarity 97.9%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 2307
DB 7 TTTTAGTAGACACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 54

RESULT 141
AAI77876
ID AAI77876 standard; DNA; 51 BP.
XX
AC AAI77876;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4817.
XX
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW

Query Match      1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
KW gene; ss.

Query Match      2.0%; Score 46.8; DB 1; Length 59;
Best Local Similarity 87.9%; Pred. No. 1.4e+02;
Matches 51; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2233 CCACCACCTGGCTAAATTTTGTACTTTTAGTAGACACAGGGTTTCACCGTGTAG 2290
DB 58 CCACCACACCGAGCTAATTTTGTATCTTAGTAGACAGGGGTTTCACCATGTTGG 1

RESULT 139
ABK41287
ID ABK41287 standard; DNA; 47 BP.
XX
AC ABK41287;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human USP2 gene biallelic marker.
XX
DE Human; obesity associated-biallelic marker; db; LSR; USP2; drug response;
KW hyperuricaemia; digestive pathology; hypertension; cancer;
KW

Query Match      2.0%; Score 46.6; DB 1; Length 47;
Best Local Similarity 97.9%; Pred. No. 1.3e+02;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
DB 1 ACAGGGTTTCACCGTGTAGCCAKGATGGTCTCGATCTCTGACCTC 47

RESULT 140
AAI68926
ID AAI68926 standard; DNA; 54 BP.
XX
AC AAI68926;
XX
DT 29-JAN-2002 (first entry)
XX
DE Activated T-cell derived DNA fragment #62.
XX
DE Activated T-cell; immunosuppressive; immunostimulant; antiinflammatory;
KW cytostatic; gene therapy; vaccine; allergen; transplant rejection;
KW

Query Match      2.0%; Score 46.4; DB 1; Length 54;
Best Local Similarity 97.9%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 2307
DB 7 TTTTAGTAGACACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 54

RESULT 141
AAI77876
ID AAI77876 standard; DNA; 51 BP.
XX
AC AAI77876;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4817.
XX
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW

Query Match      1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2292 CAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCA 2342
DB 1 CAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCA 51

RESULT 142
AAI79701/c
ID AAI79701 standard; DNA; 51 BP.
XX
AC AAI79701;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human conservative amino acid changing SNP nucleic acid SEQ:6642.
XX
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW

Query Match      1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 2369
DB 51 TGATCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 1

RESULT 143
AAI79839/c
ID AAI79839 standard; DNA; 51 BP.
XX
AC AAI79839;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6780.
XX
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW

Query Match      1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCC 2368
DB 51 GTGATCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCC 1

RESULT 144
AAH89467/c
ID AAH89467 standard; DNA; 51 BP.
XX
AC AAH89467;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 248.
XX
DE Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match      1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGCTG 2350
DB 51 TCTCGATCTCTGACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGCTG 1

RESULT 145

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AAH40328/c
ID AAH40328 standard; DNA; 51 BP.
XX
AC AAH40328;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 3124.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPs; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2304 GATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGTGGGAT 2354
DB 51 GATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGTGGGAT 1

RESULT 146
ABL00161
ID ABL00161 standard; DNA; 51 BP.
XX
AC ABL00161;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:152.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antinflammatory; neuroprotective; antimicrobial;

Query Match 1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2258 ACTTTAGTAGACAGGGTTTACCGTGTAGCCAGATGCTCGATCT 2308
DB 1 ATTTTAGTAGACAGGGTTTACCGTGTAGCCAGATGCTCGATCT 51

RESULT 147
AAH38992
ID AAH38992 standard; DNA; 51 BP.
XX
AC AAH38992;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 1788.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPs; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.9%; Score 45.8; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.5e+02;
Matches 47; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2300 TCTGATCTCTGACCTGTCATCCGCCACCTCGGCTCCCAAAGTGCTG 2350
DB 1 TCTGATCTCTGACCTGTCATCCGCCACCTCGGCTCCCAAAGTGCTG 51

RESULT 148
AAC29627/c
ID AAC29627 standard; cDNA; 57 BP.
XX
AC AAC29627;
XX
DT 06-OCT-2000 (first entry)
XX

DE Human secreted protein 5' EST, SEQ ID NO: 33702.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 1.9%; Score 45.8; DB 1; Length 57;
Best Local Similarity 87.7%; Pred. No. 1.6e+02;
Matches 50; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGATGCTCGATCT 2308
DB 57 TTTTGTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGATGCTCGATCT 1

RESULT 149
AAK83961/c
ID AAK83961 standard; DNA; 57 BP.
XX
AC AAK83961;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38773.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 1.9%; Score 45.6; DB 1; Length 57;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 48; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2320 GATCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACC 2371
DB 57 GATCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACC 6

RESULT 150
AAI77324
ID AAI77324 standard; DNA; 51 BP.
XX
AC AAI77324;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4265.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.9%; Score 45.2; DB 1; Length 51;
Best Local Similarity 94.0%; Pred. No. 1.6e+02;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2323 CCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACC 2372
DB 1 CCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACC 50

RESULT 151
AAI79589
ID AAI79589 standard; DNA; 51 BP.
XX
AC AAI79589;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6530.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.9%; Score 45.2; DB 1; Length 51;
Best Local Similarity 94.0%; Pred. No. 1.6e+02;

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Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2323 CCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 2372
    |||
    |||
    |||
Db 1 CCACCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 50

RESULT 152
AAH89302
ID AAH89302 standard; DNA; 51 BP.
XX
AC AAH89302;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 83.
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; db.
Query Match 1.9%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.7e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2252 TTTTGTACTTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGATGGTCT 2302
    |||
    |||
    |||
Db 1 TTTTGTATTTTAGTAGAGAGCGGGTTTCTCCGTGTATCCAGATGGTCT 51

RESULT 153
AAH40072/c
ID AAH40072 standard; DNA; 51 BP.
XX
AC AAH40072;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 2869.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
Query Match 1.9%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.7e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2306 TCTCCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGTGGGATTA 2356
    |||
    |||
    |||
Db 51 TCTCCTGACCTCGTGATCCACCACCCCGGCTCCCAAAGGGGTGGGATTA 1

RESULT 154
AD112542/c
ID AD112542 standard; DNA; 49 BP.
XX
AC AD112542;
XX
DT 22-APR-2004 (first entry)
XX
DE Mutant human BRCA1 genomic DNA resulting from deletion 3 SeqID 25.
KW db; cancer; human; tumour suppressor;
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
Query Match 1.9%; Score 44.2; DB 1; Length 49;
Best Local Similarity 93.9%; Pred. No. 1.8e+02;
Matches 46; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2313 ACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGC 2361
    |||
    |||
    |||
Db 49 ACCTTGATGTCGCCGCTCGGCTCCCAAAGTGTGGGATTACAGGC 1
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RESULT 155
AAI79588
ID AAI79588 standard; DNA; 51 BP.
XX
AC AAI79588;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6529.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.8%; Score 43.6; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.9e+02;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2323 CGCCCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 2372
    |||
    |||
    |||
Db 1 CCACCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 50

RESULT 156
AAI77325
ID AAI77325 standard; DNA; 51 BP.
XX
AC AAI77325;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4266.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.8%; Score 43.6; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.9e+02;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2323 CGCCCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 2372
    |||
    |||
    |||
Db 1 CCTCCGCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 50

RESULT 157
AAI73532/c
ID AAI73532 standard; DNA; 51 BP.
XX
AC AAI73532;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:473.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.8%; Score 43.2; DB 1; Length 51;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2324 CGCCCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 2371
    |||
    |||
    |||
Db 51 CGCCCGCTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGTCACCG 4

RESULT 158
AAA77442
ID AAA77442 standard; cDNA; 51 BP.
XX
AC AAA77442;
XX
DT 16-NOV-2000 (first entry)
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XX Human Alueubfamily SQ gene polymorphic site, SEQ ID NO:1125.
DE
XX
XX Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2302
Db 1 TTTTGTATTTTAGTAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCT 51

RESULT 159
AAI76988/c
ID AAI76988 standard; cDNA; 51 BP.
XX
AC AAI76988;
XX
DT 16-NOV-2000 (first entry)
DE Human clone cg42924993 polymorphic site, SEQ ID NO:671.
XX
KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2302
Db 51 TTTTGTATTTTAGTAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCT 1

RESULT 160
AAI76185/c
ID AAI76185 standard; DNA; 51 BP.
XX
AC AAI76185;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:3126.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2255 TGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGA 2305
Db 51 TGTATTTTAGTAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGA 1

RESULT 161
AAI76192/c
ID AAI76192 standard; DNA; 51 BP.
XX
AC AAI76192;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:3133.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 43; DB 1; Length 51;
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```
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTG 2312
Db 51 TTAGTAGACAGAGGTTTCACCATGTTGGCCAGGCTGGTCTCGAAGTCTG 1

RESULT 162
AAI79867/c
ID AAI79867 standard; DNA; 51 BP.
XX
AC AAI79867;
XX
DT 09-NOV-2001 (first entry)
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6808.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGAC 2314
Db 51 AGTAGACAGGGCTTCACCGTGTAGCCAGGATGGTCTCAAACTCTCTGAC 1

RESULT 163
AAI79689
ID AAI79689 standard; DNA; 51 BP.
XX
AC AAI79689;
XX
DT 09-NOV-2001 (first entry)
DE Human conservative amino acid changing SNP nucleic acid SEQ:6630.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGGTATCCGCCACCTCGGCTCCCAAAGTCTG 2350
Db 1 TCTGAACCTCTGACCTCAAGATCCGCTCGGCTCCCAAAGTCTG 51

RESULT 164
AAH90176/c
ID AAH90176 standard; cDNA; 51 BP.
XX
AC AAH90176;
XX
DT 08-OCT-2001 (first entry)
DE Human clone cg42869755 SNP site, SEQ ID NO:56.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 1; detection;
KW identification; gene therapy; genetic disorder; ss.

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2308 TCTGACCTCGTATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACA 2358
Db 51 TACTGACCTCGTATCCACCTGCCAGGCTCCCAAAGTCTGGGATTACA 1
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RESULT 165
AAH89484/c
ID AAH89484 standard; DNA; 51 BP.
XX
AC AAH89484;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 265.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCT 2311
Db 51 TTTAGTAGACAGGGTTTACCATGTGGCCAGGCTGGTCTCAAACTCCT 1

RESULT 166
AAH89506
ID AAH89506 standard; DNA; 51 BP.
XX
AC AAH89506;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 287.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGACACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGAC 2314
Db 1 AGTAGACACAGGGTTTACCATGTGGCCAGGCTGGTCTCAAACTCCTGAC 51

RESULT 167
AAH89303
ID AAH89303 standard; DNA; 51 BP.
XX
AC AAH89303;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 84.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTGTACTTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCT 2302
Db 1 TTTGTATTTTAGTAGACAGGGGCTTCCGTGTTATCCAGATGGTCT 51

RESULT 168
ADK19860
ID ADK19860 standard; DNA; 51 BP.
XX
AC ADK19860;
XX

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DT 06-MAY-2004 (first entry)
XX
DE Human mannosyl transferase-related SNP region DNA SeqID62.
XX
KW human; mannosyl transferase; antimanic; antidepressant; gene therapy;
KW fusion protein; chromosome 9 fusion protein; chromosome 11 translocation;
Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2089 TTATTTTTTTGAGACGAGTCTTGCTCTGTTACCCAGGCTGGAGTGCAGT 2139
Db 1 TTTTTTTTTTGAGACAGAGTCTTATTTCTGTTGCCAGGCTGGAGTGCAGT 51

RESULT 169
AAK65537
ID AAK65537 standard; DNA; 49 BP.
XX
AC AAK65537;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20349.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
Query Match 1.8%; Score 42.6; DB 1; Length 49;
Best Local Similarity 91.8%; Pred. No. 2.1e+02;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2267 AGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
Db 1 AGAGACGGGGTTTACCATTTTACCCAGGATGGTCTCGATATCTCCTGACC 49

RESULT 170
AAI62905/c
ID AAI62905 standard; DNA; 49 BP.
XX
AC AAI62905;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human genomic DNA SEQ ID NO 233.
XX
KW Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
Query Match 1.8%; Score 42.6; DB 1; Length 49;
Best Local Similarity 91.8%; Pred. No. 2.1e+02;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2267 AGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
Db 49 AGAGACGGGGTTTACCATTTTACCCAGGATGGTCTCGATATCTCCTGACC 1

RESULT 171
AAI79513
ID AAI79513 standard; DNA; 51 BP.
XX
AC AAI79513;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6454.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

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Query Match      1.8%; Score 42.2; DB 1; Length 51;
Best Local Similarity 93.6%; Pred. No. 2.2e+02;
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTACCGTTGTTAGCCAGGATGGTCTCGATCTCTCTGACCTC 2317
    |||||
Db 1 ACAGGGTTTACCGTTGTTAGCCAGGATGGTCTCTGAACTCTCTGACCTC 47

RESULT 172
ADG84273/c
ID ADG84273 standard; DNA; 50 BP.
XX
AC ADG84273;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human TMD0621 promoter DNA sequence SeqID211.
XX
KW tissue specific gene; tissue specific gene cluster;
KW lq22 immune gene complex; bone marrow specific gene;

Query Match      1.8%; Score 42; DB 1; Length 50;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTCCCAAAGTGGCTGGGATTACAGGCGATGAGCC 2368
    |||||
Db 50 TGATCCACCTCGCTCGGCTCCCAAAGTGGCTGGGATTATAGGCGTGAGCC 1

RESULT 173
AAI75515
ID AAI75515 standard; DNA; 51 BP.
XX
AC AAI75515;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2456.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTACCGTTGTTAGCCAGGATGGTCTCGATCTCTCTGACCTC 2317
    |||||
Db 1 GAGACAGGGTTTACCATGTTGACAGCGCTGGTCTCGAACTCTCTGACCTC 50

RESULT 174
AAI73069/c
ID AAI73069 standard; DNA; 51 BP.
XX
AC AAI73069;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:10.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2089 TTAATTTTTTGGAGACCGAGTCTTGCTCTGTATCCAGGCTGGAGTGCAG 2138
    |||||
Db 50 TTAATTTTTTGGAGACAGAGTCTGCCTCTGTGCGCCAGGCTGGAGTGCAG 1
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RESULT 175
AAI79770
ID AAI79770 standard; DNA; 51 BP.
XX
AC AAI79770;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6711.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2246 CTAATTTTTTGTACTTTTGTAGTAGACAGCGGTTTCACCGTGTAGCCAGG 2295
    |||||
Db 1 CTAATTTTTTGTATTTTGTAGTAGACAGCGGGTTTCGCCATGTGTGCCCAGG 50

RESULT 176
AAI79646/c
ID AAI79646 standard; DNA; 51 BP.
XX
AC AAI79646;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6587.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2241 CCTGGCTAATTTTGTCTTCTTGTAGTAGACAGCGGTTTCACCGTGT 2288
    |||||
Db 48 CCTGGCTAATTTTGTATTTTGTAGTAGACAGCGGGTTTCACCAIGTT 1

RESULT 177
AAI73533/c
ID AAI73533 standard; DNA; 51 BP.
XX
AC AAI73533;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:474.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2324 CGCCACCTCGGCTCCCAAAGTCTGGGATTACAGGATGAGCCACC 2371
    |||||
Db 51 CGCCCGCTCGGCTCCCAAAGTCCCGGATTACAGGCTTGAGTCACC 4

RESULT 178
AAC22417
ID AAC22417 standard; cDNA; 52 BP.
XX
AC AAC22417;
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XX 06-OCT-2000 (first entry)
DT Human secreted protein 5' EST, SEQ ID NO: 26492.
DE Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
KW

Query Match      1.8%; Score 41.6; DB 1; Length 52;
Best Local Similarity 86.5%; Pred. No. 2.4e+02;
Matches 45; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2255 TGTACTTTTGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGAT 2306
DB 1 TGTATTTTGBAGACAGCGGGTTTCGCCATGTTGGCCAGGATGGTCTCGAT 52

RESULT 179
AAA77443
ID AAA77443 standard; cDNA; 51 BP.
XX
AC AAA77443;
XX
DT 16-NOV-2000 (first entry)
DE Human Alusubfamily SQ gene polymorphic site, SEQ ID NO:1126.
XX
KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCT 2302
DB 1 TTTTGTATTTTGTAGACAGCGGGCTTCACCATGTTGGCCAGGCTGGTCT 51

RESULT 180
AAA76989/c
ID AAA76989 standard; cDNA; 51 BP.
XX
AC AAA76989;
XX
DT 16-NOV-2000 (first entry)
DE Human clone cg42924993 polymorphic site, SEQ ID NO:672.
XX
KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCT 2302
DB 51 TTTTGTATTTTGTAGACAGCGGGCTTCACCATGTTGGCCAGGCTGGTCT 1

RESULT 181
AAA77230
ID AAA77230 standard; cDNA; 51 BP.
XX
AC AAA77230;
XX
DT 16-NOV-2000 (first entry)
DE Human clone cg43972482 polymorphic site, SEQ ID NO:913.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 8; detection;
KW identification; gene therapy; ss.

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Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
DB 1 TTAGTAGACAGCGGGTTTCACCATGTTGGTCAAGGCTGGTCTCGAATCCTG 51

RESULT 182
AAI73071/c
ID AAI73071 standard; DNA; 51 BP.
XX
AC AAI73071;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:12.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTAGACCGAGTCTTGCTGTACCCAGGCTGGAGTGCA 2137
DB 51 TTTTCTTTTTTGTAGACAGAGTCTTACTCTGTGCCCCAGGCTGGAGTGCA 1

RESULT 183
AAI76193/c
ID AAI76193 standard; DNA; 51 BP.
XX
AC AAI76193;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:3134.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
DB 51 TTAGTAGACAGCGGGTTTCACCATGCTGCCAGGCTGGTCTCGAATCCTG 1

RESULT 184
AAI79866/c
ID AAI79866 standard; DNA; 51 BP.
XX
AC AAI79866;
XX
DT 09-NOV-2001 (first entry)
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6807.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2264 AGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGAC 2314
DB 1 AGTAGACAGAGGGTTTCACCATGTTGGTCAAGGCTGGTCTCGAATCCTG 51

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Db 51 ACTAGAGACGGGCTTACCGTGTGCTGCCAGGATGGTCTCAAACTCCTGAC 1

RESULT 185
AAI74978/c
ID AAI74978 standard; DNA; 51 BP.
XX
XX
AC AAI74978;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:1919.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
Db 51 TTAGTAGACAGAGGTTTTCATCATGTTGGCCAGGCTGCTTGAATCCTG 1

RESULT 186
AAI74450/c
ID AAI74450 standard; DNA; 51 BP.
XX
XX
AC AAI74450;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:1391.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2320 GATCGCCCACTCGGCTCCCAAAGTCTGGATTACAGCATGAGCCAC 2370
Db 51 GATCCTCTGCTAGCCCTCCCAAAGTCTGGATTACAGCATGAGCCAC 1

RESULT 187
AAI75457/c
ID AAI75457 standard; DNA; 51 BP.
XX
XX
AC AAI75457;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2398.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2292 CAGGATGCTCTCGATCTCTCGACTCGTGATCCGCCACCTCGGCTCCCA 2342
Db 51 CAGGCTGCTCTCAAACTCTCATCTGTCATCCGCCCTCGGCTCCCA 1

RESULT 188
AAI76650/c
ID AAI76650 standard; DNA; 51 BP.
XX
XX
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AC AAI76650;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3591.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2225 GTCATCTGCCACACACACCTGGCTAAATTTTGTACTTTTAGTAGACAGG 2275
Db 51 GGCACCTGCCACCATGCTGGCTAAATTTTGTATTATTTTAGTAGACAGG 1

RESULT 189
AAI75653/c
ID AAI75653 standard; DNA; 51 BP.
XX
XX
AC AAI75653;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2594.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2242 CTGGCTAAATTTTGTACTTTTAGTAGACAGGTTTACCGTGTAGCC 2292
Db 51 CTGGCTGATTTTGTATTATTTTAGTAGACAGGTTTCCCATGTTGGCC 1

RESULT 190
AAI76184/c
ID AAI76184 standard; DNA; 51 BP.
XX
XX
AC AAI76184;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3125.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2255 TGTACTTTTAGTAGACAGGTTTTCACCGTGTAGCCAGGATGCTCGA 2305
Db 51 TGTATTTTAGTAGACAGGTTTACCATGTTGGCCAGGCTGCTCGA 1

RESULT 191
AAI79688
ID AAI79688 standard; DNA; 51 BP.
XX
XX
AC AAI79688;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human conservative amino acid changing SNP nucleic acid SEQ:6629.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
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KW protein therapy; vaccine; probe; diagnostic assay; detection;  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2300 TCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGCTG 2350  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 1 TCTCGAACTCTGACCTCAAGATCCACCTGCTCGGCTCCCAAAGTGCTG 51  
RESULT 192  
AAH90585/c  
ID AAH90585 standard; cDNA; 51 BP.  
XX  
AC AAH90585;  
XX  
DT 08-OCT-2001 (first entry)  
XX  
DE Human clone c943080072 SNP site, SEQ ID NO:465.  
XX  
KW Human; single nucleotide polymorphism; SNP; detection; identification;  
KW gene therapy; genetic disorder; ss.  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2319 TGATCCGCCACCTCGGCTCCCAAAGTGCTGGATTACAGGATGAGCCA 2369  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 51 TGATCCACTCGCTCGGCTCCCAAAGTGCTGGATTATAGGCGTGAGCCA 1  
RESULT 193  
AAH90175/c  
ID AAH90175 standard; cDNA; 51 BP.  
XX  
AC AAH90175;  
XX  
DT 08-OCT-2001 (first entry)  
XX  
DE Human clone c942869755 SNP site, SEQ ID NO:55.  
XX  
KW Human; single nucleotide polymorphism; SNP; chromosome 1; detection;  
KW identification; gene therapy; genetic disorder; ss.  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2308 TCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGCTGGATTACA 2358  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 51 TACTGACCTCGTGATCCACTCGCATGCGCTCCCAAAGTGCTGGATTACA 1  
RESULT 194  
AAH89507  
ID AAH89507 standard; DNA; 51 BP.  
XX  
AC AAH89507;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 288.  
XX  
KW Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression; ds.  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2264 AGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGAC 2314

Db 1 AGTAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCTGAC 51  
RESULT 195  
AAH89485/c  
ID AAH89485 standard; DNA; 51 BP.  
XX  
AC AAH89485;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 266.  
XX  
KW Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression; ds.  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2261 TTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCT 2311  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 51 TTAGTAGACAGGGTTTCACCATATGGCCAGGCTGGTCTCAAACTCTCT 1  
RESULT 196  
AAH89308/c  
ID AAH89308 standard; DNA; 51 BP.  
XX  
AC AAH89308;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 89.  
XX  
KW Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression; ds.  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2279 TCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCGCCCA 2329  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 51 TCATCATGTTGCCAGGATGGTCTTGATTTCTGACCTCGTGATCGCCCA 1  
RESULT 197  
AAH89304  
ID AAH89304 standard; DNA; 51 BP.  
XX  
AC AAH89304;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 85.  
XX  
KW Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression; ds.  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2245 GCTAATTTTGTACTTTTAGTAGACAGGTTTCACCGTGTAGCCAGG 2295  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 1 GCTAATTTTGTATTATTAATAGACGGGGATTACCATGTTGGCCAGG 51  
RESULT 198  
AAH89519/c  
ID AAH89519 standard; DNA; 51 BP.

```
XX AAB89519;
AC
XX
DT 01-OCT-2001 (first entry)
DE
XX Human coding sequence polymorphic site SEQ ID NO: 300.
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
KW
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGCCCTCCCAAGTGTGGATTACAGCATGAGCC 2368
Db 51 GTGATCCATCCGCTTGGCTCCCAAGTGTGGATTACAGCGCGGAGCC 1

RESULT 199
ABL00076/c
ID ABL00076 standard; DNA; 51 BP.
XX
XX ABL00076;
AC
XX
DT 05-MAR-2002 (first entry)
DE
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:67.
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2218 GCTACAGTCATCTGCCACACACCTGGCTAAATTTTGTACTTTTAGTAG 2268
Db 51 GACTACAGGATGCGCCACACCGCTGGCTAAATTTTGTATTTTTAGTAG 1

RESULT 200
ADK19850
ID ADK19850 standard; DNA; 51 BP.
XX
XX ADK19850;
AC
XX
DT 06-MAY-2004 (first entry)
DE
XX Human mannosyl transferase-related SNP region DNA SeqID52.
XX
XX human; mannosyl transferase; antimanic; antidepressant; gene therapy;
KW fusion protein; chromosome 9 fusion protein; chromosome 11 translocation;
KW
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2270 GACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTG 2320
Db 1 GACAGGGTTTCACCATGTTGGCCAGCGCTGGTCTCGAACTCTTGACCTCATG 51

RESULT 201
AAZ66299/c
ID AAZ66299 standard; DNA; 47 BP.
XX
XX AAZ66299;
AC
XX
DT 10-SEP-2001 (first entry)
DE
XX Human map-related biallelic marker SEQ ID NO:646.
XX
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XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX
Query Match 1.7%; Score 41.2; DB 1; Length 47;
Best Local Similarity 93.5%; Pred. No. 2.4e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGAT 2306
Db 47 TTTAGTAGACACGGGGTTTCACCTCTGTAGCCAGGATGGTCTCGAT 2

RESULT 202
AAF89248/c
ID AAF89248 standard; DNA; 47 BP.
XX
XX AAF89248;
AC
XX
DT 10-DEC-2001 (first entry)
DE
XX Sample member clustering method related human polymorphic site #48.
XX
XX Cluster; hierarchical clustering algorithm; population based study;
KW clinical trial; DNA fingerprint; genetic profile analysis; PCR primer;
KW
Query Match 1.7%; Score 41.2; DB 1; Length 47;
Best Local Similarity 93.5%; Pred. No. 2.4e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGAT 2306
Db 47 TTTAGTAGACACGGGGTTTCACCTCTGTAGCCAGGATGGTCTCGAT 2

RESULT 203
AAL31459
ID AAL31459 standard; DNA; 51 BP.
XX
XX AAL31459;
AC
XX
DT 24-JAN-2002 (first entry)
DE
XX Human SNP oligonucleotide #4667.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW
Query Match 1.7%; Score 41.2; DB 1; Length 51;
Best Local Similarity 93.5%; Pred. No. 2.5e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCTCCCAAGTGTGGGATTACAGGATGAGCCACC 2371
Db 1 CCGCGCTTGGCTCCCAAGTGTGGGATTACAGGATGAGCCACC 46

RESULT 204
AAI79699/c
ID AAI79699 standard; DNA; 51 BP.
XX
XX AAI79699;
AC
XX
DT 09-NOV-2001 (first entry)
DE
XX Human conservative amino acid changing SNP nucleic acid SEQ:6640.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW
Query Match 1.7%; Score 41.2; DB 1; Length 51;
Best Local Similarity 93.5%; Pred. No. 2.5e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2096 TTTTGAGACCGAGCTTGTCTGTGTACCCAGGCTGGAGTCCAGTGG 2141
DB 51 TTTTGAGACAGAGCTTGTCTGTGTACCCAGGCTGGAGTACAGTGG 6

RESULT 205
AAH37800/c
ID AAH37800 standard; DNA; 51 BP.
XX
AC
AC AAH37800;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 596.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.7%; Score 41; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.5e+02;
Matches 44; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2096 TTTTGAGACCGAGCTTGTCTGTGTACCCAGGCTGGAGTCCAGTGGTGTAT 2146
DB 51 TTTTGAGACCGAGCTTGTCTGTGTGTGCGCCAGGCTGGAGTCCAGTGGSCGAT 1

RESULT 206
AAI78300
ID AAI78300 standard; DNA; 51 BP.
XX
AC
AC AAI78300;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:5241.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.7%; Score 40.8; DB 1; Length 51;
Best Local Similarity 95.5%; Pred. No. 2.6e+02;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2329 ACCTCGGCCTCCCAAGTGTGGATTACAGGATGAGCCACCG 2372
DB 1 ACCTTGGCCTCCCAAGTGTGGATTACAGGATGAGCAACCG 44

RESULT 207
ABZ09024/c
ID ABZ09024 standard; DNA; 52 BP.
XX
AC
AC ABZ09024;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human oligonucleotide SEQ ID 184.
XX
KW Human; tumour suppressor; virucide; cytostatic; neurotropic;
neuroprotective; neuroleptic; gene therapy; tumour suppression;

Query Match 1.7%; Score 40.8; DB 1; Length 52;
Best Local Similarity 86.5%; Pred. No. 2.6e+02;
Matches 45; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2264 AGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
DB 52 AATAGACAGGGTTTACCATGTGTGGCCAGGCTGGTCTTGAACCTCCTGATC 1

RESULT 208
ABZ78477/c

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ID ABZ78477 standard; DNA; 52 BP.
XX
AC
AC ABZ78477;
XX
DT 24-APR-2003 (first entry)
XX
DE Tumour suppression-related sequence, SEQ ID 184.
XX
KW Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
tumour reversion; apoptosis; virus resistance; viral infection; tumour;

Query Match 1.7%; Score 40.8; DB 1; Length 52;
Best Local Similarity 86.5%; Pred. No. 2.6e+02;
Matches 45; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2264 AGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
DB 52 AATAGACAGGGTTTACCATGTGTGGCCAGGCTGGTCTTGAACCTCCTGATC 1

RESULT 209
AAI78039/c
ID AAI78039 standard; DNA; 51 BP.
XX
AC
AC AAI78039;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4980.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.7%; Score 40.6; DB 1; Length 51;
Best Local Similarity 91.5%; Pred. No. 2.7e+02;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCCTCCCAAGTGTGGATTACAGGATGAGCCACCG 2372
DB 50 CTTGCTCAGCCTCCCAAGTGTGGATTACAGGATGAGCCACTG 4

RESULT 210
AAI79512
ID AAI79512 standard; DNA; 51 BP.
XX
AC
AC AAI79512;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6453.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.7%; Score 40.6; DB 1; Length 51;
Best Local Similarity 91.5%; Pred. No. 2.7e+02;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTC 2317
DB 1 ACAGGGTTTACCGTGTGGCCAGGCTGGTCTTGAACCTCCTGACCTC 47

RESULT 211
AAH89833/c
ID AAH89833 standard; DNA; 50 BP.
XX
AC
AC AAH89833;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 614.

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XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match      1.7%; Score 40.4; DB 1; Length 50;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2294 CGATGGTCTCGATCTCTGACCTGTGATCCGCCACCTCGGCTCCCAA 2343
DB 50 GGATGGTCTCGATCTCTTACCTCATGATCCACCGGCTTGGCTCCCAA 1

RESULT 212
AAA77228
ID AAA77228 standard; cDNA; 51 BP.
XX
AC AAA77228;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human clone c943971764 polymorphic site, SEQ ID NO:911.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 15; detection;
KW identification; gene therapy; ss.

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 97.6%; Pred. No. 2.7e+02;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2330 CCTCGGCTCCCAAAGTCTGGATTACAGGATGAGCCACC 2371
DB 1 CCTGAGCTCCCAAAGTCTGGATTACAGGATGAGCCACC 42

RESULT 213
ADC16930/c
ID ADC16930 standard; DNA; 51 BP.
XX
AC ADC16930;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) region Seq ID32.
XX
KW sequence polymorphism analysis; human identity; human relatedness;
KW single nucleotide polymorphism; SNP; genetic disease; cytostatic;

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTACCGTGTGTAGCCAGGATGGTCTCGATCTCTCGACCTC 2317
DB 51 GAGACGGGGTTTACCATAATTGGCGGGATGGTCTCGAACTCTCGACCTC 2

RESULT 214
AAI79771
ID AAI79771 standard; DNA; 51 BP.
XX
AC AAI79771;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6712.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 2246 CTAATTTTGTACTTTTAGTAGACAGACAGGGTTTACCGTGTGTAGCCAGG 2295
DB 1 CTAATTTTGTATTTTATTAGTAGAGCGGGGTTTTCGCCATGTTGGCCAGG 50

RESULT 215
AAI75514
ID AAI75514 standard; DNA; 51 BP.
XX
AC AAI75514;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2455.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTCCACCGTGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
DB 1 GAGACAGGGTTTCCACCATGTTGACCGGGCTGGTCTCGAACTCTCTGACCTC 50

RESULT 216
AAI73068/c
ID AAI73068 standard; DNA; 51 BP.
XX
AC AAI73068;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:9.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2089 TTATTTTGTAGACCGAGTCTTCTGTTACCCAGGCTGGAGTGCAG 2138
DB 50 TTCTTTTGTAGACAGAGTCTCACTCTGTCGCCAGGCTGGAGTGCAG 1

RESULT 217
ADB73481/c
ID ADB73481 standard; DNA; 48 BP.
XX
AC ADB73481;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human breakpoint region MLL #1.
XX
KW Human; ds; MLL; cancer; AP-4; CDK-6; SEPTIN6; ALL;
KW acute lymphoblastic leukaemia; AML; acute myeloid leukaemia;

Query Match      1.7%; Score 40; DB 1; Length 48;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGACAGCGGTTTCCCGTGTGTAGCCAGGATGGTCTCGATCTCC 2310
DB 48 TAGTAGAGATGGGGTTTTCATGTTGTAGCGAGGATGGTCTCAATCTCC 1

RESULT 218

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AAI79647/c
ID  AAI79647 standard; DNA; 51 BP.
XX
AC  AAI79647;
XX
XX  09-NOV-2001 (first entry)
DT
DE  Human silent SNP containing nucleic acid SEQ:6588.
XX
KW  Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW  protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2241 CCTGGCTAAATTTTGTACCTTTAGTAGACACAGGGTTTCACCGTGT 2288
    |||||
Db  48 CCTGGCTAAATTTTGTATATTTTCAGTAGACACGGGTTTCACCATGTT 1

RESULT 219
AAI73305
ID  AAI73305 standard; DNA; 51 BP.
XX
AC  AAI73305;
XX
XX  09-NOV-2001 (first entry)
DT
DE  Human silent SNP containing nucleic acid SEQ:246.
XX
KW  Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW  protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2318 GTGATCGGCCACCTCGGCCTCCAAAGTCTCGGATTACAGGCATGA 2365
    |||||
Db  4 GTGATCCTCTCGCTCGGCCTCCAAAGTCTCGGATTACAGATATGA 51

RESULT 220
AAH39524
ID  AAH39524 standard; DNA; 51 BP.
XX
AC  AAH39524;
XX
XX  14-AUG-2001 (first entry)
DT
DE  Human SNP flanking oligonucleotide SEQ ID 2320.
XX
KW  Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW  SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2260 TTTTAGTAGACAGAGGTTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
    |||||
Db  2 TTTTAGTAGACAGATGGGGTTTTCACCGTGTGGCCAGGCTGCTCTWGATC 49

RESULT 221
ABZ09598
ID  ABZ09598 standard; DNA; 51 BP.
XX
AC  ABZ09598;
XX
XX  16-JAN-2003 (first entry)
DT
KW  Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW  protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2241 CCTGGCTAAATTTTGTACCTTTAGTAGACACAGGGTTTCACCGTGT 2288
    |||||
Db  48 CCTGGCTAAATTTTGTATATTTTCAGTAGACACGGGTTTCACCATGTT 1
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DE  Human oligonucleotide SEQ ID 758.
XX
XX  Human; tumour suppressor; virucide; cytostatic; nootropic;
KW  neuroprotective; neuroleptic; gene therapy; tumour suppression;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2260 TTTTAGTAGACAGAGGTTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
    |||||
Db  4 TTTTAGTAGAGATGGGGTTTTCACATGTTGGCCAGGATGCTCTCGATC 51

RESULT 222
ABZ79051
ID  ABZ79051 standard; DNA; 51 BP.
XX
AC  ABZ79051;
XX
XX  24-APR-2003 (first entry)
DT
DE  Tumour suppression-related sequence, SEQ ID 758.
XX
KW  Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
KW  tumour reversion; apoptosis; virus resistance; viral infection; tumour;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2260 TTTTAGTAGACAGAGGTTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
    |||||
Db  4 TTTTAGTAGAGATGGGGTTTTCACATGTTGGCCAGGATGCTCTCGATC 51

RESULT 223
AAA77231
ID  AAA77231 standard; cDNA; 51 BP.
XX
AC  AAA77231;
XX
XX  16-NOV-2000 (first entry)
DT
DE  Human clone cg43972482 polymorphic site, SEQ ID NO:914.
XX
KW  Human; single nucleotide polymorphism; SNP; chromosome 8; detection;
KW  identification; gene therapy; ss.

Query Match      1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  2262 TTAGTAGACAGAGGTTTTCACCGTGTAGCCAGGATGCTCTCGATCCTG 2312
    |||||
Db  1 TTAGTAGACAGCGGGTTTTCACCATGCTGTCAGGCTGGTCTCGAACTCCTG 51

RESULT 224
AAC14922/c
ID  AAC14922 standard; cDNA; 51 BP.
XX
AC  AAC14922;
XX
XX  06-OCT-2000 (first entry)
DT
DE  Human secreted protein 5' EST, SEQ ID NO: 18997.
XX
KW  Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW  gene therapy; chromosome mapping; ss.

Query Match      1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
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Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2086 TTAATATTTTTTTTGGAGACCGAGCTTCTCTCTATTACCCAGGCTGGAGTGC 2136
DB 51 TTTTATTTTTTTTGGAGATGGAGTCTCACTCTGTGGCCAGGCTGGAGTGC 1

RESULT 225
AAI74451/c
ID AAI74451 standard; DNA; 51 BP.
XX
AC AAI74451;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:1392.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2320 GATCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGSCATGAGCCAC 2370
DB 51 GATCCTCTGCTCAGCCTCCCAATTGCTGGGATTACAGGSCATGAGCCAC 1

RESULT 226
AAI75652/c
ID AAI75652 standard; DNA; 51 BP.
XX
AC AAI75652;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:2593.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2242 CTGGCTAATTTTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTTAGCC 2292
DB 51 CTGGCTGATTTTTTGTATTTTATTAGTAGAGACGGGGTTTCGCCATGTTGGCC 1

RESULT 227
AAI75456/c
ID AAI75456 standard; DNA; 51 BP.
XX
AC AAI75456;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:2397.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2292 CAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCA 2342
DB 51 CAGGCTGCTCTCAAACTCTGATCTTGTATCCGCCCGCTCGGCTCCCA 1
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RESULT 228
AAI77410/c
ID AAI77410 standard; DNA; 51 BP.
XX
AC AAI77410;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:4351.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2202 CTCCCAATTTAGCTTGGCTTACAGTCTATCTGCCACACACCTGGCTAATTT 2252
DB 51 CTCCCAATTTAGCTTGGACTTACAGGCACAGGCCACACCTGGCTAATTT 1

RESULT 229
AAI75454/c
ID AAI75454 standard; DNA; 51 BP.
XX
AC AAI75454;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:2395.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2294 GGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCA 2344
DB 51 GGCTGCTCTCAAACTCCTGATCTTGTATCCGCCCGCTCGGCTCCCA 1

RESULT 230
AAI77409/c
ID AAI77409 standard; DNA; 51 BP.
XX
AC AAI77409;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:4350.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2320 GATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGATGAGCCAC 2370
DB 51 GATCCTCTGCTTGGCTCCCAAGTCTGGGATTATAGGCATGAGCCGC 1

RESULT 231
AAI74979/c
ID AAI74979 standard; DNA; 51 BP.
XX
AC AAI74979;
XX
DT 09-NOV-2001 (first entry)
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XX DE Human silent SNP containing nucleic acid SEQ:1920.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2262 TTAGTACAGACAGGGTTTACCGGTTAGCCAGGATGCTCGATCTCCCTG 2312
Db 51 TTAGTACAGACAGGGTTTATCATCATGCTGCGCAGGCTGGCTTGAACCTCTG 1

RESULT 232
AAH90586/c
ID AAI73070 standard; DNA; 51 BP.
XX
AC AAI73070;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:11.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2087 TATTATTTTTTTGAGACCGAGTCTTGCTCTGTGTACCCAGGCTGGAGTGCA 2137
Db 51 TTTCCTTTTTTTGAGACAGAGTCTCACTCTGTCGCCACGCTGGAGTGCA 1

RESULT 233
AAH90586/c
ID AAH90586 standard; cDNA; 51 BP.
XX
AC AAH90586;
XX
DT 08-OCT-2001 (first entry)
XX
DE Human clone cg43080072 SNP site, SEQ ID NO:466.
XX
KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; genetic disorder; ss.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2319 TGATCCGCCACCTTCGGCCTCCCAAAGTGTGGGATTACAGGATGAGCCA 2369
Db 51 TGATCCACTCGCTTCGGCCTCCCAAAGTGTGGGATTATAGGCTGAGCCA 1

RESULT 234
AAH89305
ID AAH89305 standard; DNA; 51 BP.
XX
AC AAH89305;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 86.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;

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Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2245 GCTAATTTTTTTGACTTTTAGTAGACAGACAGGGTTTCACCGTGTAGCCAGG 2295
Db 1 GCTAATTTTTTTGATTTTAAATAGAAACGGGGATTCCACCATGTGGCCAGG 51

RESULT 235
AAH89317/c
ID AAH89317 standard; DNA; 51 BP.
XX
AC AAH89317;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 98.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2214 CTTGGCCTACAGTCATCTGCCACACACCTGGCTAATTTTTTGTACTTTTA 2264
Db 51 CTGGGACTACAGCATATGCCACCACGCTGGCTAATTTTTTATATTTTA 1

RESULT 236
AAH89553/c
ID AAH89553 standard; DNA; 51 BP.
XX
AC AAH89553;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 334.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2267 AGAGACAGGGTTTCACCGTGTAGCCAGGATGCTCGATCTCCTGACCTC 2317
Db 51 AGAGACGGGGTTTCCACCATTTTGGCCAGGCTGGTCTTGAACCTCCTGACCTC 1

RESULT 237
AAH89518/c
ID AAH89518 standard; DNA; 51 BP.
XX
AC AAH89518;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 299.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2318 GTGATCCGCCACCTTCGGCCTCCCAAAGTGTGGGATTACAGGATGAGCC 2368
Db 51 GTGATCCATCCGCTTGGGCTCCAGAGTGTGGGATTACAGGCGGAGCC 1

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RESULT 238
AAH89309/c
ID AAH89309 standard; DNA; 51 BP.
XX
AC AAH89309;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 90.
XX
DE Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2279 TCACCGTCTTAGCCAGGATGCTCGATCTCTGACCTCTGATCCGCGCCA 2329
Db 51 TCATCATGTTGCCAGGATGCTCTTAATTTCTGACCTCGTGATCCGCCCA 1

RESULT 239
AAH89566/c
ID AAH89566 standard; DNA; 51 BP.
XX
AC AAH89566;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 347.
XX
DE Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2218 GCCTACAGTCATCGCCACACACACCTGGCTAAATTTTGTACTTTTAGTAG 2268
Db 51 GACTACAGGCATATGCCACCATGCTGCTAAATTTTATATTTTAGTAG 1

RESULT 240
ABL00112/c
ID ABL00112 standard; DNA; 51 BP.
XX
AC ABL00112;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:103.
XX
DE Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2254 TTGTAATTTTATAGTAGAGACAGGGTTTCCCGTGTATCCAGGATGGTCTCG 2304
Db 51 TTGTAATTTTATAGTAGAGATGGGGTTGCACCATGTTGGCCAGGCTGGTCTCG 1

RESULT 241
AAI79698/c
ID AAI79698 standard; DNA; 51 BP.
XX
AC AAI79698;
XX

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DT 09-NOV-2001 (first entry)
XX
DE Human conservative amino acid changing SNP nucleic acid SEQ.6639.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.6; DB 1; Length 51;
Best Local Similarity 91.3%; Pred. No. 3e+02;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2096 TTTTGAGACCGAGTCTTGCTCTTACCCAGGCTGGAGTGCAGTGG 2141
Db 51 TTTAGAGACAGAGTCTTGCTCTTGTCCCGAGGCTGGAGTACAGTGG 6

RESULT 242
ABZ20666/c
ID ABZ20666 standard; DNA; 41 BP.
XX
AC ABZ20666;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human G protein subunit 9-02 coding sequence probe #1.
XX
DE Human; G protein subunit 9.02; cancer; constipation; diarrhoea; cough;
KW cardiac asthma; colic; psychic disease; probe;
Query Match 1.7%; Score 39.4; DB 1; Length 41;
Best Local Similarity 97.6%; Pred. No. 2.8e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2322 TCCGCCACCTCGGCCTCCCAAAGTGTCTGGGATTACAGGCA 2362
Db 41 TCCACCCACCTCGGCCTCCCAAAGTGTCTGGGATTACAGGCA 1

RESULT 243
ABZ49551/c
ID ABZ49551 standard; DNA; 41 BP.
XX
AC ABZ49551;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human glutathione-S-transferase MGST2 gene polymorphic site, #6334.
XX
DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
KW polymorphic site; drug evaluation; drug screening; genotyping;
Query Match 1.7%; Score 39.4; DB 1; Length 41;
Best Local Similarity 97.6%; Pred. No. 2.8e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2298 GGTCTCGATCTCTGACCTCGTATCCGCCACCTCGGCCT 2338
Db 41 GGTCTCGATCTCTGACCTCATGATCCGCCACCTCGGCCT 1

RESULT 244
ABZ43959/c
ID ABZ43959 standard; DNA; 41 BP.
XX
AC ABZ43959;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human glutathione-S-transferase MGST2 gene polymorphic site, #743.
XX
DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
KW polymorphic site; drug evaluation; drug screening; genotyping;

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```
Query Match      1.7%; Score 39.4; DB 1; Length 41;
Best Local Similarity 97.6%; Pred. No. 2.8e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2298 GGTCGTGATCTCTGACCTCGTGTGATCGGCCACCTCGGCCT 2338
      |||||
Db 41 GGTCGTGATCTCTGACCTCGTGTGATCGGCCACCTCGGCCT 1

RESULT 245
AAI79580/c
ID AAI79580 standard; DNA; 51 BP.
XX
AC AAI79580;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:6521.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 39.4; DB 1; Length 51;
Best Local Similarity 97.6%; Pred. No. 3e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 GTGATCGGCCACCTCGGCCTCCCAAAGTCTGGGATTACA 2358
      |||||
Db 41 GTGATCGGCCACCTCGGCCTCCCAAAGTCTGGGATTACA 1

RESULT 246
AAH89818
ID AAH89818 standard; DNA; 51 BP.
XX
AC AAH89818;
XX
DT 01-OCT-2001 (first entry)
DE Human coding sequence polymorphic site SEQ ID NO: 599.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
forensic test; aberrant protein expression; ds.

Query Match      1.7%; Score 39.4; DB 1; Length 51;
Best Local Similarity 87.8%; Pred. No. 3e+02;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2232 GCCACACACCTCGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTC 2280
      |||||
Db 3 GCCACACACCTCGCTAAATTTTGTACTTTTGTATTTTATATAGACAGGGGATTC 51

RESULT 247
ADI12541/c
ID ADI12541 standard; DNA; 44 BP.
XX
AC ADI12541;
XX
DT 22-APR-2004 (first entry)
DE Mutant human BRCA1 genomic DNA resulting from deletion 3 SeqID 24.
XX
KW ds; cancer; human; tumour suppressor;
breast cancer susceptibility gene 1; BRCA1; repetitive Alu;

Query Match      1.7%; Score 39.2; DB 1; Length 44;
Best Local Similarity 93.2%; Pred. No. 2.9e+02;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2316 TCGTGTATCGGCCACCTCGGCCTCCCAAAGTCTGGGATTACAG 2359
      |||||
Db 44 TTGTGATCTGCGCGCTCGGCCTCCCAAAGTCTGGGATTACAG 1

RESULT 248
AAI78301
ID AAI78301 standard; DNA; 51 BP.
XX
AC AAI78301;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:5242.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 39.2; DB 1; Length 51;
Best Local Similarity 93.2%; Pred. No. 3.1e+02;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2329 ACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
      |||||
Db 1 ACCTGGCCTCCCAAAGTCTGGGACTACAGGCATGAGCCACCG 44

RESULT 249
ADI12532
ID ADI12532 standard; DNA; 49 BP.
XX
AC ADI12532;
XX
DT 22-APR-2004 (first entry)
DE Mutant human BRCA1 genomic DNA resulting from deletion 1 SeqID 15.
XX
KW ds; cancer; human; tumour suppressor;
breast cancer susceptibility gene 1; BRCA1; repetitive Alu;

Query Match      1.6%; Score 39; DB 1; Length 49;
Best Local Similarity 89.4%; Pred. No. 3.1e+02;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
      |||||
Db 1 CCCGTCTCGGCCTCCCAAAGTCTGGGATTACAGGTGTGAGCCATCG 47

RESULT 250
AAI78038/c
ID AAI78038 standard; DNA; 51 BP.
XX
AC AAI78038;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:4979.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.6%; Score 39; DB 1; Length 51;
Best Local Similarity 89.4%; Pred. No. 3.2e+02;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
      |||||
Db 50 CCTGCCTCAGCCTCCCAAAGTCTAGGATTACAGGCATGAGCCACTG 4

RESULT 251
AAI77874
ID AAI77874 standard; DNA; 51 BP.
XX
AC AAI77874;
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```
XX 09-NOV-2001 (first entry)
DT Human silent SNP containing nucleic acid SEQ:4815.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.9; DB 1; Length 51;
Best Local Similarity 96.2%; Pred. No. 3.2e+02;
Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2248 AATTTTGTACTTTTGTAGACAGAGGTTTACCGTGTAGCCAGGATGG 2299
Db 1 AATTTTGTATTTTGTAGAGAC-GGGTTTCACCGTGTAGCCAGGATGG 51

RESULT 252
AAI77875
ID AAI77875 standard; DNA; 51 BP.
XX
XX AAI77875;
AC
XX 09-NOV-2001 (first entry)
DT Human silent SNP containing nucleic acid SEQ:4816.
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.9; DB 1; Length 51;
Best Local Similarity 96.2%; Pred. No. 3.2e+02;
Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2248 AATTTTGTACTTTTGTAGACAGAGGTTTACCGTGTAGCCAGGATGG 2299
Db 1 AATTTTGTATTTTGTAGAGACA-GGTTTCACCGTGTAGCCAGGATGG 51

RESULT 253
AAI77229
ID AAI77229 standard; cDNA; 51 BP.
XX
XX AAI77229;
AC
XX 16-NOV-2000 (first entry)
DT Human clone c943971764 polymorphic site, SEQ ID NO:912.
DE Human; single nucleotide polymorphism; SNP; chromosome 15; detection;
KW identification; gene therapy; ss.

Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 95.2%; Pred. No. 3.2e+02;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2330 CCTGGCCTCCAAAGTCTGGGATTACAGCATGACCCACC 2371
Db 1 COTCAGCCTCCAAAGTCTGGGATCATCAGGCATGACCCACC 42

RESULT 254
AAI75651/c
ID AAI75651 standard; DNA; 51 BP.
XX
XX AAI75651;
AC
XX 09-NOV-2001 (first entry)
DT Human silent SNP containing nucleic acid SEQ:2592.
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
```

```
Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 86.0%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2249 ATTTTGTACTTTTGTAGACAGAGGTTTACCGTGTAGCCAGGATG 2298
Db 50 ATTTTGTATTTTGTAGTGAGACAGGTTTCGCCATGTTGGCCGGGCTG 1

RESULT 255
AAI79075
ID AAI79075 standard; DNA; 51 BP.
XX
XX AAI79075;
AC
XX 09-NOV-2001 (first entry)
DT Human silent SNP containing nucleic acid SEQ:6016.
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 86.0%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2089 TTATTTTGTAGACCGAGTCTTGCTGTGTACCCAGGCTGGAGTGCAG 2138
Db 2 TTATTTTGTAAACAGGCTCTCGCTCTGCTGCCAGGCTGGAGTGCAG 51

RESULT 256
AAI74819
ID AAI74819 standard; DNA; 51 BP.
XX
XX AAI74819;
AC
XX 09-NOV-2001 (first entry)
DT Human silent SNP containing nucleic acid SEQ:1760.
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 86.0%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2089 TTATTTTGTAGACCGAGTCTTGCTGTGTACCCAGGCTGGAGTGCAG 2138
Db 2 TTATTTTGTAGACAGAGTCTCGCTCTGCTGCCAGGCTGGAGTGCAG 51

RESULT 257
AAI79530
ID AAI79530 standard; DNA; 51 BP.
XX
XX AAI79530;
AC
XX 09-NOV-2001 (first entry)
DT Human silent SNP containing nucleic acid SEQ:6471.
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 86.0%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2220 CTACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTAGTAGA 2269
Db 1 CTACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTAGTAGA 2269
```



Db 2 CTACAGCACGCGCCACCACCGCGGCTAAATTTTGTATTTTAGTAGTA 51

## RESULT 258

AAI74884  
ID AAI74884 standard; DNA; 51 BP.

XX  
AC AAI74884;

DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:1825.

XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;

Best Local Similarity 86.0%; Pred. No. 3.2e+02; Mismatches 7; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGCGTTTCCCGTGTAGCCAGGATGCTCTCGA 2305

Db 1 GTATTTTCAGTAGACAGCGGTTTACCAATGTTGGCCAGGCTGCTCTCGA 50

## RESULT 259

AAI74965/c  
ID AAI74965 standard; DNA; 51 BP.

XX  
AC AAI74965;

DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:1906.

XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;

Best Local Similarity 86.0%; Pred. No. 3.2e+02; Mismatches 7; Indels 0; Gaps 0;

QY 2268 GAGACAGGTTTCCCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTC 2317

Db 51 GAGACAGGTTTCACTATGTTGGTAGGCTGGTCTCGAATCTCCTGATCTC 2

## RESULT 260

ADK19818/c  
ID ADK19818 standard; DNA; 51 BP.

XX  
AC ADK19818;

DT 06-MAY-2004 (first entry)  
XX  
DE Human mannosyl transferase-related SNP region DNA SeqID20.

XX  
KW human; mannosyl transferase; antimanic; antidepressant; gene therapy;  
KW fusion protein; chromosome 9 fusion protein; chromosome 11 translocation;

Query Match 1.6%; Score 38.8; DB 1; Length 51;

Best Local Similarity 86.0%; Pred. No. 3.2e+02; Mismatches 7; Indels 0; Gaps 0;

QY 2311 TGACCTCGTATCGGCCACCTCGGCTCCCAAAGTCTGGGATTACAGG 2360

Db 50 TGACCTCGTATCGCTCTCGACCTCCCAAAGTACCGGGATTACAGG 1

## RESULT 261

AAI75542  
ID AAI75542 standard; DNA; 51 BP.

XX

AC AAI75542;  
XX  
DT 09-NOV-2001 (first entry)

XX  
DE Human silent SNP containing nucleic acid SEQ:2483.

XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.6; DB 1; Length 51;

Best Local Similarity 91.1%; Pred. No. 3.3e+02; Mismatches 4; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGCA 2362

Db 7 GCGATCCTCCACCCCGGCTCCCAAAGTCTGGGATTACAGCA 51

## RESULT 262

AAV19044/c  
ID AAV19044 standard; DNA; 40 BP.

XX  
AC AAV19044;

DT 28-JUL-1998 (first entry)  
XX  
DE Alu PCR primer 1.

XX  
KW PCR; primer; amplification; Alu repeat sequence; vector;  
KW circular yeast artificial chromosome; YAC; ss.

Query Match 1.6%; Score 38.4; DB 1; Length 40;

Best Local Similarity 97.5%; Pred. No. 3.1e+02; Mismatches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAAGTCTGGGATTACAGCATGAGCCACC 2371

Db 40 TCGGCTCCCAAAGTCTGGGATTACAGCGTGAGCCACC 1

## RESULT 263

AAA97659  
ID AAA97659 standard; DNA; 40 BP.

XX  
AC AAA97659;

DT 15-FEB-2001 (first entry)  
XX  
DE Human MDM2 40mer PCR template.

XX  
KW Pseudocyclic oligonucleotide; functional segment; protective segment;  
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 1.6%; Score 38.4; DB 1; Length 40;

Best Local Similarity 97.5%; Pred. No. 3.1e+02; Mismatches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 659 GGACTCAGGTACATCTGTGAGTGAGAACACAGGTGTACCTT 698

Db 1 GGACCCAGGTACATCTGTGAGTGAGAACACAGGTGTACCTT 40

## RESULT 264

ABL59100/c  
ID ABL59100 standard; DNA; 40 BP.

XX  
AC ABL59100;

DT 27-SEP-2002 (first entry)  
XX  
DE Nucleotide sequence of an Alu PCR primer.

XX  
KW Yeast artificial chromosome; YAC; inter-Alu PCR;

```
KW transformation-associated recombination; PCR; primer; ss.

Query Match      1.6%; Score 38.4; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 3.1e+02;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 2371
      |||||
      40 TCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 1
Db

RESULT 265
ABL60505
ID ABL60505 standard; DNA; 40 BP.
XX
AC ABL60505;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo 17.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      1.6%; Score 38.4; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 3.1e+02;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 659 GGACTCAGGTACATCTGTGAGTGAGACAGGTTGCACCTT 698
      |||||
      1 GGACCCAGGTACATCTGTGAGTGAGACAGGTTGCACCTT 40
Db

RESULT 266
AAI76503
ID AAI76503 standard; DNA; 50 BP.
XX
AC AAI76503;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3444.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.6%; Score 38.4; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2241 CTGGCTAATTTTGTGTTTGTAGTAGACAGGTTTACCGTGT 2288
      |||||
      3 CCCAGCTAATTTTGTGTTTGTAGTAGAGAGTGTACCGTGT 50
Db

RESULT 267
AAI73304
ID AAI73304 standard; DNA; 51 BP.
XX
AC AAI73304;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:245.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.6%; Score 38.4; DB 1; Length 51;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATGA 2365
      |||||
      4 GTGATCTCTGCTCGGCTCTCAAAGTGTGGGATTACAGATGA 51
Db

transformation-associated recombination; PCR; primer; ss.

Query Match      1.6%; Score 38.4; DB 1; Length 51;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGTTTTCACCGTGTAGCCAGGATGTTCTCGATC 2307
      |||||
      4 TTTTAGTAGACAGGTTTTCGCCATGTTGCCAGGCTGTTTGAAC 51
Db

RESULT 269
ABZ20667/C
ID ABZ20667 standard; DNA; 41 BP.
XX
AC ABZ20667;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human G protein subunit 9-02 coding sequence probe #2.
XX
KW Human; G protein subunit 9.02; cancer; constipation; diarrhoea; cough;
KW cardiac asthma; colic; psychic disease; probe;

Query Match      1.6%; Score 37.8; DB 1; Length 41;
Best Local Similarity 95.1%; Pred. No. 3.3e+02;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2322 TCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCA 2362
      |||||
      41 TCCGCCACCTCGGCTCCCGAAGTGTGGGATTACAGGCA 1
Db

RESULT 270
ABZ43958
ID ABZ43958 standard; DNA; 41 BP.
XX
AC ABZ43958;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human glutathione-S-transferase MGST2 gene polymorphic site, #742.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match      1.6%; Score 37.8; DB 1; Length 41;
Best Local Similarity 95.1%; Pred. No. 3.3e+02;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2314 CCTCGTATCCGCCACCTCGGCTCCCAAAGTGTGGGAT 2354
      |||||
      1 CCTCGTATTTGCCACCTCGGCTCCCAAAGTGTGGGAT 41
Db

RESULT 271
ABZ44160
ID ABZ44160 standard; DNA; 41 BP.
```

XX ABZ44160;  
 AC  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human NDUFS5 gene polymorphic site, #944.  
 XX  
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;  
 KW polymorphic site; drug evaluation; drug screening; genotyping;  
 Query Match 1.6%; Score 37.8; DB 1; Length 41;  
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;  
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2264 AGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGCTCTCG 2304  
 DB 1 AGTAGAGACGGGGTTTCACCGTGTAGCCAGCATGCTCTCG 41  
 RESULT 272  
 ABZ49550  
 ID ABZ49550 standard; DNA; 41 BP.  
 XX  
 AC ABZ49550;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human glutathione-S-transferase MGST2 gene polymorphic site, #6333.  
 XX  
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;  
 KW polymorphic site; drug evaluation; drug screening; genotyping;  
 Query Match 1.6%; Score 37.8; DB 1; Length 41;  
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;  
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2314 CCTCGTATCCGCCACCTCGGCTCCCAAAGTCTGGGAT 2354  
 DB 1 CCTCGTATTTGCCACCTCGGCTCCCAAAGTCTGGGAT 41  
 RESULT 273  
 ABZ49631/c  
 ID ABZ49631 standard; DNA; 41 BP.  
 XX  
 AC ABZ49631;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human sulphotransferase SULT1C1 gene polymorphic site, #6413.  
 XX  
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;  
 KW polymorphic site; drug evaluation; drug screening; genotyping;  
 Query Match 1.6%; Score 37.8; DB 1; Length 41;  
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;  
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2328 CACCTCGGCTCCCAAAGTCTGGATTACAGGCATGAGCC 2368  
 DB 41 CGCCTCGGCTCCCAAAGTCTGGATTACAGGCATGAGCC 1  
 RESULT 274  
 ABZ43598/c  
 ID ABZ43598 standard; DNA; 41 BP.  
 XX  
 AC ABZ43598;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human sulphotransferase SULT1C1 gene polymorphic site, #382.  
 XX

KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;  
 KW polymorphic site; drug evaluation; drug screening; genotyping;  
 Query Match 1.6%; Score 37.8; DB 1; Length 41;  
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;  
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2328 CACCTCGGCTCCCAAAGTCTGGATTACAGGCATGAGCC 2368  
 DB 41 CGCCTCGGCTCCCAAAGTCTGGATTACAGGCATGAGCC 1  
 RESULT 275  
 ABZ50172  
 ID ABZ50172 standard; DNA; 41 BP.  
 XX  
 AC ABZ50172;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human NDUFS5 gene polymorphic site, #6954.  
 XX  
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;  
 KW polymorphic site; drug evaluation; drug screening; genotyping;  
 Query Match 1.6%; Score 37.8; DB 1; Length 41;  
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;  
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2264 AGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGCTCTCG 2304  
 DB 1 AGTAGAGACGGGGTTTCACCGTGTAGCCAGCATGCTCTCG 41  
 RESULT 276  
 ADI12523/c  
 ID ADI12523 standard; DNA; 42 BP.  
 XX  
 AC ADI12523;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human BRCA1 DNA junction sequence comprising large deletion SegID 3.  
 XX  
 KW ds: cancer; human; tumour suppressor;  
 KW breast cancer susceptibility Gene 1; BRCA1; repetitive Alu;  
 Query Match 1.6%; Score 37.8; DB 1; Length 42;  
 Best Local Similarity 95.1%; Pred. No. 3.4e+02;  
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2318 GTGATCGGCCACCTCGGCTCCCAAAGTCTGGGATTACA 2358  
 DB 41 GTGATCGGCCCTCGGCTCCCAAAGTCTGGGATTACA 1  
 RESULT 277  
 AAZ68649  
 ID AAZ68649 standard; DNA; 47 BP.  
 XX  
 AC AAZ68649;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Human map-related biallelic marker SEQ ID NO:2999.  
 XX  
 KW Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 Query Match 1.6%; Score 37.4; DB 1; Length 47;  
 Best Local Similarity 87.2%; Pred. No. 3.7e+02;  
 Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 2322 TCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCC 2368
DB 1 TCCGCTGCTCAGCTCCCAAGTCTAGGATTATAGGCGTGAGCC 47

RESULT 278
ABA94091/c
ID ABA94091 standard; DNA; 41 BP.
XX
AC ABA94091;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human tumour suppressor factor 11.77 probe 1 SEQ ID NO:8.
XX
KW Human; tumour suppressor factor 11.77; cytostatic; haemostatic; virucide;
KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;

Query Match 1.5%; Score 36.2; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 4e+02;
Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2322 TCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCC 2362
DB 41 TCCGCCGCTCTTGGCTCCCAAGTCTGGGATTACAGGCA 1

RESULT 279
ADI12521
ID ADI12521 standard; DNA; 42 BP.
XX
AC ADI12521;
XX
DT 22-APR-2004 (first entry)
XX
DE Human BRCA1 DNA junction sequence comprising large deletion SeqID 1.
XX
KW ds; cancer; human; tumour suppressor;
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;

Query Match 1.5%; Score 36.2; DB 1; Length 42;
Best Local Similarity 92.7%; Pred. No. 4e+02;
Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2331 CTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 2371
DB 2 CTCGGCTCCCAAGTCTGGGATTACAGGTGTGAGCCATC 42

RESULT 280
AAK91006/c
ID AAK91006 standard; DNA; 45 BP.
XX
AC AAK91006;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4582.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 1.5%; Score 35.4; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 4.5e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1

RESULT 281
AAK86862/c

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ID AAK86862 standard; DNA; 45 BP.
XX
AC AAK86862;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41674.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 1.5%; Score 35.4; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 4.5e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1

RESULT 282
AAL02933/c
ID AAL02933 standard; DNA; 45 BP.
XX
AC AAL02933;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5621.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.

Query Match 1.5%; Score 35.4; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 4.5e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1

RESULT 283
AAS32041/c
ID AAS32041 standard; DNA; 45 BP.
XX
AC AAS32041;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #215.
XX
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;

Query Match 1.5%; Score 35.4; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 4.5e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1

RESULT 284
ABN90396/c
ID ABN90396 standard; DNA; 45 BP.
XX
AC ABN90396;
XX
DT 24-JUL-2002 (first entry)
XX
DE Human liver antigen HLD8E09 genomic sequence, SEQ ID NO:517.

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XX Human; liver antigen; liver disorder; hepatic disorder; infection;  
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;  
Query Match 1.5%; Score 35.4; DB 1; Length 45;  
Best Local Similarity 86.7%; Pred. No. 4.5e+02;  
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131  
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1  
RESULT 285  
ABZ74161/c  
ID ABZ74161 standard; DNA; 45 BP.  
XX  
AC ABZ74161;  
XX  
DT 12-MAY-2003 (first entry)  
XX  
DE Secreted protein gene 198 genomic fragment HMCIP65, SEQ ID NO:1308.  
DE  
KW Human; secreted protein; cancer; tumour; hyperproliferative disorder;  
KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;  
Query Match 1.5%; Score 35.4; DB 1; Length 45;  
Best Local Similarity 86.7%; Pred. No. 4.5e+02;  
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131  
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1  
RESULT 286  
ABZ73706/c  
ID ABZ73706 standard; DNA; 45 BP.  
XX  
AC ABZ73706;  
XX  
DT 12-MAY-2003 (first entry)  
XX  
DE Secreted protein gene 1 genomic fragment H6BSF56, SEQ ID NO:853.  
DE  
KW Human; secreted protein; cancer; tumour; hyperproliferative disorder;  
KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;  
Query Match 1.5%; Score 35.4; DB 1; Length 45;  
Best Local Similarity 86.7%; Pred. No. 4.5e+02;  
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131  
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1  
RESULT 287  
ADA98416/c  
ID ADA98416 standard; DNA; 45 BP.  
XX  
AC ADA98416;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human secreted protein-related DNA sequence #9.  
DE  
KW human; secreted protein; cardiovascular disorder; arrhythmia;  
KW atherosclerosis; stroke; endocarditis; congestive heart failure;  
Query Match 1.5%; Score 35.4; DB 1; Length 45;  
Best Local Similarity 86.7%; Pred. No. 4.5e+02;  
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131  
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1  
RESULT 288  
ADA44446/c  
ID ADA44446 standard; DNA; 45 BP.  
XX  
AC ADA44446;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human secreted protein DNA SEQ ID 639.  
DE  
KW Gene therapy; human; Antidiabetic; Anorectic; Ophthalmological;  
KW Neuroprotective; Cerebroprotective; Antianemic; ds.  
Query Match 1.5%; Score 35.4; DB 1; Length 45;  
Best Local Similarity 86.7%; Pred. No. 4.5e+02;  
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131  
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1  
RESULT 289  
ABZ67723/c  
ID ABZ67723 standard; DNA; 45 BP.  
XX  
AC ABZ67723;  
XX  
DT 26-MAR-2003 (first entry)  
XX  
DE Human secreted protein encoding genomic DNA SEQ ID NO 1246.  
DE  
KW Human; secreted protein; neurotropic; neuroprotective; cytostatic;  
KW virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV;  
Query Match 1.5%; Score 35.4; DB 1; Length 45;  
Best Local Similarity 86.7%; Pred. No. 4.5e+02;  
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131  
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1  
RESULT 290  
ABZ67302/c  
ID ABZ67302 standard; DNA; 45 BP.  
XX  
AC ABZ67302;  
XX  
DT 26-MAR-2003 (first entry)  
XX  
DE Human secreted protein encoding genomic DNA SEQ ID NO 825.  
DE  
KW Human; secreted protein; neurotropic; neuroprotective; cytostatic;  
KW virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV;  
Query Match 1.5%; Score 35.4; DB 1; Length 45;  
Best Local Similarity 86.7%; Pred. No. 4.5e+02;  
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2087 TATTATTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 2131  
DB 45 TTTTGTGAGACCGAGTCTGCTCTGTGTACCCAGGCTGG 1  
RESULT 291





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XX Human silent SNP containing nucleic acid SEQ:3331.
DE
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.4%; Score 33.6; DB 1; Length 44;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2316 TCGTGATCCGCCACCTCGGCTCCCAAGTGTGGATT 2355
Db      |||||
5 TCATGATCCGCCCTCTCGGCTCTCAAGTGTGGATT 44

RESULT 305
AAQ27391
ID AAQ27391 standard; DNA; 35 BP.
XX
AC AAQ27391;
XX
DT 25-MAR-2003 (revised)
DE 27-JAN-1993 (first entry)
DE Inter-Alu specific primer PDJ33.
XX
KW Polymerase chain reaction; PCR; repetitive element; ss.

Query Match      1.4%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 5.1e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGTGGATTACAGGATGAGCCA 2369
Db      |||||
1 GCCTCCCAAGTGTGGATTACAGGCTGAGCCA 35

RESULT 306
AAS15951/c
ID AAS15951 standard; DNA; 41 BP.
XX
AC AAS15951;
XX
DT 14-FEB-2002 (first entry)
DE Human proteolytic enzyme regulatory protein 11, probe #2.
XX
KW Human; proteolytic enzyme regulatory protein 11; cytosolic; virucidal;
KW immunomodulatory; antiinflammatory; haemostatic; cancer; haemopathy;

Query Match      1.4%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 5.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2107 AGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
Db      |||||
40 AGTCTTGCTCTGTGCCAGGCTGGAGTGCAGTGG 6

RESULT 307
AAS15950/c
ID AAS15950 standard; DNA; 41 BP.
XX
AC AAS15950;
XX
DT 14-FEB-2002 (first entry)
DE Human proteolytic enzyme regulatory protein 11, probe #1.
XX
KW Human; proteolytic enzyme regulatory protein 11; cytosolic; virucidal;
KW immunomodulatory; antiinflammatory; haemostatic; cancer; haemopathy;

Query Match      1.4%; Score 33.4; DB 1; Length 41;
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Best Local Similarity 97.1%; Pred. No. 5.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2107 AGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
Db      |||||
40 AGTCTTGCTCTGTGTGCCAGGCTGGAGTGCAGTGG 6

RESULT 308
ADP12341/c
ID ADP12341 standard; DNA; 33 BP.
XX
AC ADP12341;
XX
DT 12-AUG-2004 (first entry)
DE Tagman probe set 2 #199.
DE
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; probe.

Query Match      1.4%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1559 GGAAGAAACCCAGACAAAGAGAGAGTGTGGA 1591
Db      |||||
33 GGAAGAAACCCAGACAAAGAGAGAGTGTGGA 1

RESULT 309
ABZ50127/c
ID ABZ50127 standard; DNA; 41 BP.
XX
AC ABZ50127;
XX
DT 26-JUN-2003 (first entry)
DE Human NDUFS1 gene polymorphic site, #6909.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match      1.4%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 5.6e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTAATTTTAGTAGAGACGGGTTTCCCGTGTAGCC 2292
Db      |||||
41 TTTTGTAATTTTAGTAGAGACGGGTTTCCCGATGTGGCC 1

RESULT 310
ABZ44117/c
ID ABZ44117 standard; DNA; 41 BP.
XX
AC ABZ44117;
XX
DT 26-JUN-2003 (first entry)
DE Human NDUFS1 gene polymorphic site, #901.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match      1.4%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 5.6e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTAATTTTAGTAGAGACGGGTTTCCCGTGTAGCC 2292
Db      |||||
41 TTTTGTAATTTTAGTAGAGACGGGTTTCCCGATGTGGCC 1
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RESULT 311
ADP75520/c
ID ADP75520 standard; DNA; 41 BP.
XX
XX
AC ADP75520;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human ADAM19 gene, sequence surrounding SNP 16.
XX
KW Human; ds; ADAM19; Endophilin 1; Endophilin 2; NRG2; ADAMTS2;
KW a disintegrin and metalloprotease; neuroregulin 2; SNP;

Query Match 1.4%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 5.6e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2327 CCACCTGGCTCCCAAGTGTGGGATTACAGGCATGAGC 2367
Db 41 CCGCCTTGCCCAACCAAGTGTGGGATTACAGGCATGAGC 1

RESULT 312
ADL64280/c
ID ADL64280 standard; DNA; 41 BP.
XX
XX
AC ADL64280;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) #203.
XX
KW ss; human; single nucleotide polymorphism; SNP;
KW C1 S subcomponent protein; CIS; alanyl aminopeptidase protein; ANPEP;

Query Match 1.4%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 5.6e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCTGACCTGCTGATCGCCACCTCGGCCT 2338
Db 41 GGTCTTGAACCTCTTAACCTCATGATCCACCCACCTCGGCCT 1

RESULT 313
ABA96570
ID ABA96570 standard; DNA; 41 BP.
XX
XX
AC ABA96570;
XX
DT 19-MAR-2002 (first entry)
XX
DE Human tyrosinase 9 probe, SEQ ID NO:8.
XX
KW Human; tyrosinase 9; recombinant production; malignant tumour; cancer;
KW blood disease; HIV infection; gene therapy; human immunodeficiency virus;

Query Match 1.4%; Score 32.8; DB 1; Length 41;
Best Local Similarity 94.4%; Pred. No. 5.7e+02;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATCCAGGCTGGAGTGCACTGG 2141
Db 3 GAGTCTTACTCTGTCTACCCAGGCTGGAGTGCACTGG 38

RESULT 314
ABA96571
ID ABA96571 standard; DNA; 41 BP.
XX
XX
AC ABA96571;
XX

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DT 19-MAR-2002 (first entry)
XX
XX
DE Human tyrosinase 9 probe, SEQ ID NO:9.
XX
XX
KW Human; tyrosinase 9; recombinant production; malignant tumour; cancer;
KW blood disease; HIV infection; gene therapy; human immunodeficiency virus;

Query Match 1.4%; Score 32.8; DB 1; Length 41;
Best Local Similarity 94.4%; Pred. No. 5.7e+02;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATCCAGGCTGGAGTGCACTGG 2141
Db 3 GAGTCTTACTCTGTCTACCCAGGCTGGAGTGCACTGG 38

RESULT 315
ADC59511
ID ADC59511 standard; DNA; 41 BP.
XX
XX
AC ADC59511;
XX
DT 18-DEC-2003 (first entry)
XX
DE Polypeptide-respiratory chain dehydrogenase-11.55 specific probe, #1.
XX
KW Polypeptide-respiratory chain dehydrogenase-11.55; cancer;
KW malignant tumour; haemopathy; human immunodeficiency virus infection;

Query Match 1.4%; Score 32.8; DB 1; Length 41;
Best Local Similarity 94.4%; Pred. No. 5.7e+02;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATCCAGGCTGGAGTGCACTGG 2141
Db 3 GAGTCTTACTCTGTCTACCCAGGCTGGAGTGCACTGG 38

RESULT 316
AAH91207/c
ID AAH91207 standard; DNA; 40 BP.
XX
XX
AC AAH91207;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #282.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match 1.4%; Score 32.6; DB 1; Length 40;
Best Local Similarity 87.5%; Pred. No. 5.8e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2277 TTTACCGTGTAGCAGGATGCTCTCGATCTCTCGACCT 2316
Db 40 TTTACCAATGTAGTCAGGCTGTCTCNAACCTCTGACCT 1

RESULT 317
ABL60966/c
ID ABL60966 standard; DNA; 41 BP.
XX
XX
AC ABL60966;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human retinoblastoma bindin (RBBP9) 13.31 cDNA specific probe 1.
XX
KW Human; retinoblastoma bindin 13.31; RBBP9; retinoblastoma; cancer; probe;
KW ss.

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Query Match      1.4%; Score 32.6; DB 1; Length 41;
Best Local Similarity 89.7%; Pred. No. 5.9e+02;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTCTGCTGTACCCAGGCTGGAGTGCAGTGG 2141
    |||||||
DB 41 ACTGAGTCTCTGCTGTACCCAGGCTGGAGTGCAGTGG 3

RESULT 318
ABA97057
ID ABA97057 standard; DNA; 41 BP.
XX
AC ABA97057;
XX
DT 18-MAR-2002 (first entry)
XX
DE Human 2-hydroxy acid dehydrogenase 16 probe SEQ ID 9.
XX
KW Human; 2-hydroxy acid dehydrogenase 16; cancer; haemopathy; HIV;
KW human immunodeficiency virus; infection; probe; ss.

Query Match      1.4%; Score 32.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 6e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2108 GTCTTGCTCTGTTACCCAGGCTGGAGTGCAGTGG 2141
    |||||||
DB 5 GTCTTGCTCTGTCACCCAGGCTGGAGTGCAGTGG 38

RESULT 319
ABA97056
ID ABA97056 standard; DNA; 41 BP.
XX
AC ABA97056;
XX
DT 18-MAR-2002 (first entry)
XX
DE Human 2-hydroxy acid dehydrogenase 16 probe SEQ ID 8.
XX
KW Human; 2-hydroxy acid dehydrogenase 16; cancer; haemopathy; HIV;
KW human immunodeficiency virus; infection; probe; ss.

Query Match      1.4%; Score 32.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 6e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2108 GTCTTGCTCTGTTACCCAGGCTGGAGTGCAGTGG 2141
    |||||||
DB 5 GTCTTGCTCTGTCACCCAGGCTGGAGTGCAGTGG 38

RESULT 320
AAH91831/c
ID AAH91831 standard; DNA; 38 BP.
XX
AC AAH91831;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #906.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match      1.4%; Score 32.2; DB 1; Length 38;
Best Local Similarity 89.5%; Pred. No. 6e+02;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGTATCCGCCACCTCGGCTCCCAA 2344
    |||||||
DB 38 CTCCTGACCTCTGATCCNCCACCTCACCTCCCAA 1
```

```
RESULT 321
ABZ72304/c
ID ABZ72304 standard; DNA; 41 BP.
XX
AC ABZ72304;
XX
DT 03-APR-2003 (first entry)
XX
DE Gene 216 SNP reference sequence SEQ ID NO 276.
XX
KW Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;

Query Match      1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2315 CTCGTGATCGCCACCTCGGCTCCCAAAGTGTGGAT 2354
    |||||||
DB 40 CTGCTGATCTCTTACCCCGGCTTCCCAAAGTGTGGAT 1

RESULT 322
ABZ49727/c
ID ABZ49727 standard; DNA; 41 BP.
XX
AC ABZ49727;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human sulphotransferase TPST2 gene polymorphic site, #6509.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match      1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2302
    |||||||
DB 41 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2

RESULT 323
ABZ43574/c
ID ABZ43574 standard; DNA; 41 BP.
XX
AC ABZ43574;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human sulphotransferase TPST2 gene polymorphic site, #358.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match      1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2302
    |||||||
DB 41 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2

RESULT 324
ABX75157/c
ID ABX75157 standard; DNA; 41 BP.
XX
AC ABX75157;
```

```
XX 25-MAR-2003 (first entry)
DT Human gene 216 DNA sequence flanking SNP #43.
DE Human; mouse; ds; gene 216; antiasthmatic; antiinflammatory; anorectic;
KW chromosome 20p13-p12; single nucleotide polymorphism; SNP; gene therapy;
KW

Query Match 1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2315 CTGGTGATCGCCCACTCGGCTCCCAAGTCTGGGAT 2354
Db ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
40 CTGGTGATCTCTTACCCTCCCGGCTTCCCAAGTCTGGGAT 1

RESULT 325
ADJ36885/C
ID ADJ36885 standard; DNA; 41 BP.
XX AC ADJ36885;
XX
XX 22-APR-2004 (first entry)
DT Gene 216 single nucleotide polymorphism seq id 276.
XX antiasthmatic; respiratory; gene therapy; asthma;
KW bronchial hyperresponsiveness; atopy; chronic obstructive lung disease;
KW

Query Match 1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2315 CTGGTGATCGCCCACTCGGCTCCCAAGTCTGGGAT 2354
Db ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
40 CTGGTGATCTCTTACCCTCCCGGCTTCCCAAGTCTGGGAT 1

RESULT 326
ADL81463/C
ID ADL81463 standard; DNA; 41 BP.
XX AC ADL81463;
XX
XX 20-MAY-2004 (first entry)
DT Gene 216 single nucleotide polymorphism #36.
XX asthma; bronchial hyperresponsiveness; obesity;
KW inflammatory bowel disease; human; gene 216; ds;
KW

Query Match 1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2315 CTGGTGATCGCCCACTCGGCTCCCAAGTCTGGGAT 2354
Db ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
40 CTGGTGATCTCTTACCCTCCCGGCTTCCCAAGTCTGGGAT 1

RESULT 327
AAH49727/C
ID AAH49727 standard; DNA; 41 BP.
XX AC AAH49727;
XX
XX 25-SEP-2001 (first entry)
DT Human DNA mismatch repair protein 11 coding sequence probe #1.
XX Human; DNA repair mismatch protein 11; cancer; haemopathy; HIV infection;
KW immunological disease; inflammation; gene therapy; probe; ss.
KW
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```
Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2322 TCGGCCCACTCGGCTCCCAAGTCTGGGATTACAGGCA 2362
Db ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
41 TCTTCTGCTCGCGGCTCCCAAGTCTGGGATTACAGGCA 1

RESULT 328
ABV74811/C
ID ABV74811 standard; DNA; 41 BP.
XX AC ABV74811;
XX
XX 31-JAN-2003 (first entry)
DT Signalase 11.22 probe #1.
XX Signalase 11.22; enzyme; tumour; haemopathy; HIV infection;
KW immunological disease; inflammation; cytostatic; anti-HIV; probe; ss.
KW

Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 97.0%; Pred. No. 6.7e+02;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2109 TCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
Db ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
41 TCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 9

RESULT 329
ABL40963/C
ID ABL40963 standard; DNA; 41 BP.
XX AC ABL40963;
XX
XX 03-JUL-2002 (first entry)
DT Transcription regulation factor ZFM1 isomer 19.47 cDNA specific probe 1.
XX Transcription regulation factor ZFM1 isomer 19.47; human; ZFM1;
KW transcription regulation factor; cytostatic; haemostatic; virucide;
KW

Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2188 TTCTCTGCTCAGCCTCCCAATTAGCTTGGCCTACAGTCA 2228
Db ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
41 TTCTCTGCTCAACCTCCGAGTAGCTGGACTACAGGCA 1

RESULT 330
ABL40964/C
ID ABL40964 standard; DNA; 41 BP.
XX AC ABL40964;
XX
XX 03-JUL-2002 (first entry)
DT Transcription regulation factor ZFM1 isomer 19.47 cDNA specific probe 2.
XX Transcription regulation factor ZFM1 isomer 19.47; human; ZFM1;
KW transcription regulation factor; cytostatic; haemostatic; virucide;
KW

Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2188 TTCTCTGCTCAGCCTCCCAATTAGCTTGGCCTACAGTCA 2228
Db ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

Db 41 TTCTCTGCTCAACTCCGAGTAGCTGGGACTACAGGCA 1

RESULT 331  
ABZ47125/c  
ID ABZ47125 standard; DNA; 41 BP.  
XX  
XX AC ABZ47125;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human ATP-binding cassette ABCB4 gene polymorphic site, #3909.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 7;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
XX

Query Match 1.3%; Score 31.4; DB 1; Length 41;  
Best Local Similarity 85.4%; Pred. No. 6.7e+02;  
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2092 TTTTITTTGACCGAGTCTTGCTCTGTACCCAGGCTGGA 2132  
|||||  
Db 41 TTTTITTTGAGTGAAGTCTTACTCTGTCTCACCACCAAGCTGGA 1

RESULT 332  
ABZ43249/c  
ID ABZ43249 standard; DNA; 41 BP.  
XX  
XX AC ABZ43249;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human ATP-binding cassette ABCB4 gene polymorphic site, #33.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 7;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
XX

Query Match 1.3%; Score 31.4; DB 1; Length 41;  
Best Local Similarity 85.4%; Pred. No. 6.7e+02;  
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2092 TTTTITTTGACCGAGTCTTGCTCTGTACCCAGGCTGGA 2132  
|||||  
Db 41 TTTTITTTGAGTGAAGTCTTACTCTGTCTCACCACCAAGCTGGA 1

RESULT 333  
ABZ49403  
ID ABZ49403 standard; DNA; 41 BP.  
XX  
XX AC ABZ49403;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human UDP glycosyltransferase UGT2B15 gene polymorphic site, #6186.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
KW drug evaluation; drug screening; genotyping; genetic profiling;  
XX

Query Match 1.3%; Score 31.4; DB 1; Length 41;  
Best Local Similarity 85.4%; Pred. No. 6.7e+02;  
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2272 CAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTCG 2312  
|||||  
Db 1 CAGAGTTTACCATGTTGGCCAGGCTGGTCTTGACTCTCG 41

RESULT 334  
AAL51683/c  
ID AAL51683 standard; DNA; 41 BP.  
XX

AC AAL51683;  
XX  
DT 17-APR-2003 (first entry)  
XX  
DE PC6 protease 9-9 (AIDS-associated protein) nucleotide probe #1.  
XX  
KW Probe; ss; PC6 protease; 9.9; AIDS-associated protein; diabetes; AIDS.  
XX

Query Match 1.3%; Score 31.2; DB 1; Length 41;  
Best Local Similarity 91.7%; Pred. No. 6.8e+02;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATACCCAGGCTGGAGTGCAGTGG 2141  
|||||  
Db 41 GAGTCTGCTCTGTGCGCCAGGCTGGAGTGCAGTGG 6

RESULT 335  
AAF88864/c  
ID AAF88864 standard; DNA; 41 BP.  
XX  
XX AC AAF88864;  
XX  
DT 07-JAN-2003 (first entry)  
XX  
DE Saccharophosphotransferase 9.46 PCR primer SEQ ID 8.  
XX  
KW Phosphoenolpyruvate dependent saccharophosphotransferase 9.46;  
KW malignant tumour; haemopathy; HIV infection; immunological disease;

Query Match 1.3%; Score 31.2; DB 1; Length 41;  
Best Local Similarity 91.7%; Pred. No. 6.8e+02;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATACCCAGGCTGGAGTGCAGTGG 2141  
|||||  
Db 38 GAGTCTGCTCTGTGTCACCCAGGCTGGAGTGCAGTGG 3

RESULT 336  
ADC59512  
ID ADC59512 standard; DNA; 41 BP.  
XX  
XX AC ADC59512;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Polypeptide-respiratory chain dehydrogenase-11.55 specific probe, #2.  
XX  
KW Polypeptide-respiratory chain dehydrogenase-11.55; cancer;  
KW malignant tumour; haemopathy; human immunodeficiency virus infection;

Query Match 1.3%; Score 31.2; DB 1; Length 41;  
Best Local Similarity 91.7%; Pred. No. 6.8e+02;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATACCCAGGCTGGAGTGCAGTGG 2141  
|||||  
Db 3 GAGTCTTGCTCTGTGCTAGGCTGGAGTGCAGTGG 38

RESULT 337  
ABZ57501/c  
ID ABZ57501 standard; DNA; 41 BP.  
XX  
XX AC ABZ57501;  
XX  
DT 05-APR-2003 (first entry)  
XX  
DE Ser/Thr protein kinase 9.79 probe, SEQ ID NO:9.  
XX  
KW Ser/Thr protein kinase 9.79; recombinant production; gene therapy;

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KW  tumour; cancer; diabetes; cytostatic; probe; ss.

Query Match      1.3%; Score 31.2; DB 1; Length 41;
Best Local Similarity 91.7%; Pred. No. 6.8e+02;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2248 AATTTTGTACTTTTAGTAGACAGCGGTTTCACC 2283
    ( 37 ACTTTTGTATTATTAGTAGACAGCGGTTTCACC 2
    )

Db

RESULT 338
ADK66044
ID  ADK66044 standard; DNA; 31 BP.
XX
AC  ADK66044;
XX
DT  06-MAY-2004 (first entry)
XX
DE  Standardized polynucleotide system polynucleotide #9 probe.
XX
KW  ss; standardized polynucleotide system; medical diagnosis;
KW  functional genomics; sample analysis; pharmacogenomics; sample analysis;

Query Match      1.3%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1606 TTAATGCCATTGAACCTTGTTGTGATTGTGCA 1636
    1 TTAATGCCATTGAACCTTGTTGTGATTGTGCA 31
Db

RESULT 339
AAZ89377
ID  AAZ89377 standard; DNA; 33 BP.
XX
AC  AAZ89377;
XX
DT  15-JUN-2000 (first entry)
XX
DE  Human mdm-2 probe mdm2probe.
XX
KW  Human; mdm-2; probe; reaction container; quantitation; diagnosis;
KW  food analysis; ss.

Query Match      1.3%; Score 31; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1606 TTAATGCCATTGAACCTTGTTGTGATTGTGCA 1636
    1 TTAATGCCATTGAACCTTGTTGTGATTGTGCA 31
Db

RESULT 340
ABZ48532
ID  ABZ48532 standard; DNA; 40 BP.
XX
AC  ABZ48532;
XX
DT  26-JUN-2003 (first entry)
XX
DE  Human oligopeptide transporter PEPT1 gene polymorphic site, #5315.
XX
KW  Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
KW  drug evaluation; drug screening; genotyping; genetic profiling;

Query Match      1.3%; Score 31; DB 1; Length 40;
Best Local Similarity 87.2%; Pred. No. 6.9e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2257 TACTTTTAGTAGACAGCGGTTTCACCGTTGTAGCCAGG 2295

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Db  1 TATTTTATAGACAGCGGTTTCACCATATTGCCAGG 39

RESULT 341
ABQ83633
ID  ABQ83633 standard; DNA; 41 BP.
XX
AC  ABQ83633;
XX
DT  26-JAN-2003 (first entry)
XX
DE  Human mPer3-10.01 probe 1 SEQ ID NO:8.
XX
KW  Human; mPer3-10.01; vegetative nervous dysfunction; psychic disease;
KW  endocrinopathy; growth development disturbance disease; tumour; probe;

Query Match      1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 87.2%; Pred. No. 6.9e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2274 GGGTTTCACCGTGTAGCCAGGATGCTCTCGATCTCCTG 2312
    3 GGGTTTCACCATGTTGGCAGGCTGTCTCGAACTCCTG 41
Db

RESULT 342
ABQ83634
ID  ABQ83634 standard; DNA; 41 BP.
XX
AC  ABQ83634;
XX
DT  26-JAN-2003 (first entry)
XX
DE  Human mPer3-10.01 probe 2 SEQ ID NO:9.
XX
KW  Human; mPer3-10.01; vegetative nervous dysfunction; psychic disease;
KW  endocrinopathy; growth development disturbance disease; tumour; probe;

Query Match      1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 87.2%; Pred. No. 6.9e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2274 GGGTTTCACCGTGTAGCCAGGATGCTCTCGATCTCCTG 2312
    3 GGGTTTCACCATGTTGGCAGGCTGTCTCGAACTCCTG 41
Db

RESULT 343
ABS55669/c
ID  ABS55669 standard; DNA; 41 BP.
XX
AC  ABS55669;
XX
DT  27-DEC-2002 (first entry)
XX
DE  cAMP dependent kinase regulation subunit 8.8 probe #1.
XX
KW  Human; cAMP dependent kinase regulation subunit 8.8; cyclic AMP;
KW  malignant tumour; inflammation; antagonist; probe; ss.

Query Match      1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 87.2%; Pred. No. 6.9e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2331 CTCGGCCTCCCAAGTGTGGGATTACAGGCATGACCA 2369
    39 CTCGGCCTCCCAAGATGTTAGGATTACAGGCATGAACCA 1
Db

RESULT 344
ABL60967/c
ID  ABL60967 standard; DNA; 41 BP.

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XX ABL60967;
AC
XX
DT 23-SEP-2002 (first entry)
XX
DE Human retinoblastoma bindin (RBBP9) 13.31 cDNA specific probe 2.
XX
KW Human; retinoblastoma bindin 13.31; RBBP9; retinoblastoma; cancer; probe;
KW 88.

Query Match 1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 87.2%; Pred. No. 6.9e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTTCTCTCTTTACCCAGGCTGGAGTGAGTGG 2141
DB 41 ACTGAGTCTTCTCTCTGTCCAGCAGGCTTGAGTGTAGTGG 3

RESULT 345
ADE24786/c
ID ADE24786 standard; DNA; 36 BP.
XX
AC ADE24786;
XX
DT 29-JAN-2004 (first entry)
XX
DE Genetic analysis method associated target DNA seq id 11.
XX
KW genetic analysis; complementary strand extension;
KW fluorophore-tagged DNA strand; DNA analysis; genetic testing;

Query Match 1.3%; Score 30.8; DB 1; Length 36;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 32; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2305 ATCTCTGACCTCGTGATCCGCCACCTCGGCTCC 2340
DB 36 AACTCTTAACCTCGTGATCCGCCACCTCGGCTCC 1

RESULT 346
ACC84461
ID ACC84461 standard; DNA; 33 BP.
XX
AC ACC84461;
XX
DT 28-AUG-2003 (first entry)
XX
DE NTP peptide encoding sequence #8.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.

Query Match 1.3%; Score 29.8; DB 1; Length 33;
Best Local Similarity 93.9%; Pred. No. 7.4e+02;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2331 CTCGGCTCCCAAGTGTCTGGATTACAGGCAT 2363
DB 1 CTCAGCTCCCAAGTGTCTGGATTACAGGCGT 33

RESULT 347
AAA97662/c
ID AAA97662 standard; DNA; 29 BP.
XX
AC AAA97662;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human MDM2 hybridisation probe.
XX

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KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 1.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 AGGAATCATCGGACTCAGGTACATCTGTG 677
DB 29 AGGAATCATCGGACTCAGGTACATCTGTG 1

RESULT 348
ABL60508/c
ID ABL60508 standard; DNA; 29 BP.
XX
AC ABL60508;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA hybridising probe.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match 1.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 AGGAATCATCGGACTCAGGTACATCTGTG 677
DB 29 AGGAATCATCGGACTCAGGTACATCTGTG 1

RESULT 349
AAK91040
ID AAK91040 standard; DNA; 32 BP.
XX
AC AAK91040;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4616.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 1.2%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTGTGTTTGTAGTAGACAGGGTTTCA 2281
DB 1 TTTTGTGTTTGTAGTAGACAGGGTTTCA 32

RESULT 350
AAS32075
ID AAS32075 standard; DNA; 32 BP.
XX
AC AAS32075;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #249.
XX
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;

Query Match 1.2%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2250 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 2281
DB 1 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 32

RESULT 351
ABN90430
ID ABN90430 standard; DNA; 32 BP.
XX AC
XX ABN90430;
XX
XX 24-JUL-2002 (first entry)
XX Human liver antigen HLDV38 genomic sequence, SEQ ID NO:551.
XX Human; liver antigen; liver disorder; hepatic disorder; infection;
XX hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;
XX

Query Match 1.2%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 2281
DB 1 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 32

RESULT 352
ADJ15343
ID ADJ15343 standard; DNA; 32 BP.
XX AC
XX ADJ15343;
XX
XX 20-MAY-2004 (first entry)
XX Human liver-related genomic DNA - SEQ ID 551.
XX
XX liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
XX antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;
XX

Query Match 1.2%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 2281
DB 1 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 32

RESULT 353
AAL47196
ID AAL47196 standard; DNA; 30 BP.
XX AC
XX AAL47196;
XX
XX 22-AUG-2002 (first entry)
XX Human rheumatoid arthritis associated DR3 gene related oligo #9.
XX
XX Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
XX gene therapy; PCR; primer; ss.

Query Match 1.2%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 8.3e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2295 GATGGTCTCGATCTCTGACCTCGTGATCC 2324
DB 1 GATGGTCTCTGATCTCTGACCTCGTGATCC 30

RESULT 354
AAL47197/c
ID AAL47197/c standard; DNA; 30 BP.
XX AC
XX AAL47197;
XX
XX 22-AUG-2002 (first entry)
XX Human rheumatoid arthritis associated DR3 gene related oligo #10.
XX
XX Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
XX gene therapy; PCR; primer; ss.

Query Match 1.2%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 8.3e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2295 GATGGTCTCGATCTCTGACCTCGTGATCC 2324
DB 30 GATGGTCTTGTGATCTCTGACCTCGTGATCC 1

RESULT 355
ADE14248/c
ID ADE14248 standard; DNA; 32 BP.
XX AC
XX ADE14248;
XX
XX 29-JAN-2004 (first entry)
XX Optineurin promoter motif, repeat element or regulatory region #357.
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX SNP; glaucoma; progressive ocular hypertensive disorder;

Query Match 1.2%; Score 28.4; DB 1; Length 32;
Best Local Similarity 96.7%; Pred. No. 8.5e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2343 AAGTGTCTGGATTACAGGCATGAGCCACCG 2372
DB 32 AAGTGTCTGGATTACAGGCATGAGCCACCG 3

RESULT 356
ADE14029/c
ID ADE14029 standard; DNA; 32 BP.
XX AC
XX ADE14029;
XX
XX 29-JAN-2004 (first entry)
XX Optineurin promoter motif, repeat element or regulatory region #138.
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX SNP; glaucoma; progressive ocular hypertensive disorder;

Query Match 1.2%; Score 28.4; DB 1; Length 32;
Best Local Similarity 96.7%; Pred. No. 8.5e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2343 AAGTGTCTGGATTACAGGCATGAGCCACCG 2372
DB 32 AAGTGTCTGGATTACAGGCATGAGCCACCG 3

RESULT 357
AAA97658
ID AAA97658 standard; DNA; 28 BP.
XX AC
XX AAA97658;
XX
XX 15-FEB-2001 (first entry)
XX Human MDM2 gene target oligonucleotide.
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KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match      1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 ATCTGTGAGTGAGACAGGTTGCACCTT 698
Db 1 ATCTGTGAGTGAGACAGGTTGCACCTT 28

RESULT 358
ABK65940/c
ID ABK65940 standard; DNA; 28 BP.
XX
AC ABK65940;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human gene specific PCR primer #28.
XX
KW Primer; ss; DNA microarray; differential expression analysis; human.
XX

Query Match      1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 CCTTAGCTGACTATTGGAAATGCACCTC 1231
Db 28 CCTTAGCTGACTATTGGAAATGCACCTC 1

RESULT 359
ABK65939
ID ABK65939 standard; DNA; 28 BP.
XX
AC ABK65939;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human gene specific PCR primer #27.
XX
KW Primer; ss; DNA microarray; differential expression analysis; human.
XX

Query Match      1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 GGAGATATGTTGTGAAGAAGCAGTAGC 947
Db 1 GGAGATATGTTGTGAAGAAGCAGTAGC 28

RESULT 360
ABL60504
ID ABL60504 standard; DNA; 28 BP.
XX
AC ABL60504;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo 16.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 671 ATCTGTGAGTGAGACAGGTTGCACCTT 698
Db 1 ATCTGTGAGTGAGACAGGTTGCACCTT 28

RESULT 361
ADP11597/c
ID ADP11597 standard; DNA; 28 BP.
XX
AC ADP11597;
XX
DT 12-AUG-2004 (first entry)
XX
DE Tagman probe of the invention #280.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; probe.

Query Match      1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TGGCCTGCTTTACATGTGCAAGAAGCT 1714
Db 28 TGGCCTGCTTTACATGTGCAAGAAGCT 1

RESULT 362
AAI62688/c
ID AAI62688 standard; DNA; 33 BP.
XX
AC AAI62688;
XX
DT 19-OCT-2001 (first entry)
XX
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 338.
XX
KW Human; breast antigen; ovarian antigen; cancer; metastasis; gene therapy;
KW ds.

Query Match      1.2%; Score 27.8; DB 1; Length 33;
Best Local Similarity 93.5%; Pred. No. 9.1e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTTACCCAGGCTGGAGTGCAGTGG 2141
Db 33 TCGCTCTGTTGCCAGGCTGGAGTGCAGTGG 3

RESULT 363
AAL06807/c
ID AAL06807 standard; DNA; 33 BP.
XX
AC AAL06807;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 9495.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.

Query Match      1.2%; Score 27.8; DB 1; Length 33;
Best Local Similarity 93.5%; Pred. No. 9.1e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTTACCCAGGCTGGAGTGCAGTGG 2141
Db 33 TCGCTCTGTTGCCAGGCTGGAGTGCAGTGG 3

RESULT 364

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AAH91537/c  
 ID AAH91537 standard; DNA; 35 BP.  
 XX  
 AC  
 AAH91537;  
 XX  
 DT 09-OCT-2001 (first entry)  
 DE Human inflammatory bowel disease associated polymorphic site #612.  
 XX  
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 Query Match 1.2%; Score 27.6; DB 1; Length 35;  
 Best Local Similarity 85.7%; Pred. No. 9.4e+02;  
 Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 2233 CCACACACCTGGCTAAATTTTGTACTTTTACTA 2267  
 DB 35 CCACAACGCCGCCGCTAAATTTTGTATTTTGGTA 1  
 RESULT 365  
 AAQ73572  
 ID AAQ73572 standard; DNA; 31 BP.  
 XX  
 AC  
 AAQ73572;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 25-JUN-1995 (first entry)  
 XX  
 DE Enhancer element ex-4 conserved basepair sequence.  
 KW Enhancer element; carcinoma; tumor; cancer; SLPI gene;  
 Query Match 1.2%; Score 27.4; DB 1; Length 31;  
 Best Local Similarity 90.3%; Pred. No. 9.3e+02;  
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2331 CTGGGCTCCCAAGTGTGGGATTACAGGC 2361  
 DB 1 CTCAGCTCCCAANGTGTGGGANTACAGGC 31  
 RESULT 366  
 AAQ27389  
 ID AAQ27389 standard; DNA; 32 BP.  
 XX  
 AC  
 AAQ27389;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-JAN-1993 (first entry)  
 XX  
 DE Inter-Alu specific primer PDJ33A.  
 KW Polymerase chain reaction; PCR; repetitive element; ss.  
 Query Match 1.2%; Score 27.4; DB 1; Length 32;  
 Best Local Similarity 96.6%; Pred. No. 9.4e+02;  
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2332 TCGGCTCCCAAGTGTGGGATTACAGG 2360  
 DB 4 TCGGCTCCCAAGTGTGGGATTACAGG 32  
 RESULT 367  
 AAA04371  
 ID AAA04371 standard; DNA; 29 BP.  
 XX  
 AC  
 AAA04371;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX

DE Polymorphic fragment of hypertension associated gene HSTSCENE.  
 XX  
 KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 Query Match 1.1%; Score 27; DB 1; Length 29;  
 Best Local Similarity 93.1%; Pred. No. 9.5e+02;  
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2339 CCCAAGTCTGGGATTACAGGCATGAGC 2367  
 DB 1 CCCAAGTCTGGGRTTACAGGCCTGAGC 29  
 RESULT 368  
 AAA04313  
 ID AAA04313 standard; DNA; 29 BP.  
 XX  
 AC  
 AAA04313;  
 XX  
 DT 22-MAY-2000 (first entry)  
 DE Polymorphic fragment of hypertension associated gene GLUT4.  
 XX  
 KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 Query Match 1.1%; Score 27; DB 1; Length 29;  
 Best Local Similarity 93.1%; Pred. No. 9.5e+02;  
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2281 ACGTGTAGCCAGGATGCTCGATCTC 2309  
 DB 1 ACCATGTAGCCAGRATGCTCTCGATCTC 29  
 RESULT 369  
 AAA03996  
 ID AAA03996 standard; DNA; 29 BP.  
 XX  
 AC  
 AAA03996;  
 XX  
 DT 22-MAY-2000 (first entry)  
 DE Polymorphic fragment of hypertension associated gene APOC4.  
 XX  
 KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 Query Match 1.1%; Score 27; DB 1; Length 29;  
 Best Local Similarity 93.1%; Pred. No. 9.5e+02;  
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2332 TCGGCTCCCAAGTGTGGGATTACAGG 2360  
 DB 1 TTGGCTCCCAAGGCTGGGATTACAGG 29  
 RESULT 370  
 ADE14206/c  
 ID ADE14206 standard; DNA; 32 BP.  
 XX  
 AC  
 ADE14206;  
 XX  
 DT 29-JAN-2004 (first entry)  
 DE Optineurin promoter motif, repeat element or regulatory region #315.  
 XX  
 KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;  
 KW SNP; glaucoma; progressive ocular hypertensive disorder;  
 Query Match 1.1%; Score 26.8; DB 1; Length 32;  
 Best Local Similarity 93.3%; Pred. No. 1e+03;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2343 AAGTCTGGGATTACAGCATGAGCCACCG 2372  
 DB 32 AAGTCTGGGATTACAGGTGTGAGCCACCG 3

RESULT 371  
 ID AA237740 standard; DNA; 26 BP.  
 XX AA237740;  
 AC  
 XX  
 DT 07-JAN-2000 (first entry)  
 DE Human mdm2 real-time reverse PCR primer #270.  
 DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 1.1%; Score 26; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 TGAAGTTATTAAAGTCTGTGGTGCA 440  
 DB 26 TGAAGTTATTAAAGTCTGTGGTGCA 1

RESULT 372  
 ID AAA97660 standard; DNA; 26 BP.  
 XX AAA97660;  
 AC  
 XX  
 DT 15-FEB-2001 (first entry)  
 DE Human MDM2 forward RT-PCR primer.  
 DE Pseudocyclic oligonucleotide; functional segment; protective segment;  
 KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 1.1%; Score 26; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 ACAGGAATCTGGTAGTCAATCAG 647  
 DB 1 ACAGGAATCTGGTAGTCAATCAG 26

RESULT 373  
 ID AAA50949 standard; DNA; 26 BP.  
 XX AAA50949;  
 AC  
 XX  
 DT 27-OCT-2000 (first entry)  
 DE Human mdm2 PCR primer #1.  
 DE Fluorescent protein; fluorescence labelling; fusion protein; human;  
 KW PCR primer; ss.

Query Match 1.1%; Score 26; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAATGCTGTGTACC 337  
 DB 1 ATGTGCAATACCAATGCTGTGTACC 26

RESULT 374  
 ID AAD03619 standard; DNA; 26 BP.  
 XX AAD03619;  
 AC  
 XX  
 DT 19-JUN-2001 (first entry)  
 DE Human marathon cDNA library (Burke's lymphoma) amplifying PCR primer #1.  
 DE Anthozoa; Chromoprotein; fluorescent protein; sunscreen; biosensor;  
 KW analyte detection assay; selectable marker; recombinant DNA application;

Query Match 1.1%; Score 26; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAATGCTGTGTACC 337  
 DB 1 ATGTGCAATACCAATGCTGTGTACC 26

RESULT 375  
 ID AAF80894/c standard; DNA; 26 BP.  
 XX AAF80894;  
 AC  
 XX  
 DT 02-MAY-2001 (first entry)  
 DE Human mdm2 reverse primer.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 1.1%; Score 26; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 TGAAGTTATTAAAGTCTGTGGTGCA 440  
 DB 26 TGAAGTTATTAAAGTCTGTGGTGCA 1

RESULT 376  
 ID AAS29509/c standard; DNA; 26 BP.  
 XX AAS29509;  
 AC  
 XX  
 DT 21-NOV-2001 (first entry)  
 DE Reverse PCR primer used to amplify human mdm2 mRNA.  
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 1.1%; Score 26; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 TGAAGTTATTAAAGTCTGTGGTGCA 440  
 DB 26 TGAAGTTATTAAAGTCTGTGGTGCA 1

RESULT 377  
 ID ABL60506 standard; DNA; 26 BP.  
 XX ABL60506;  
 AC  
 XX  
 DT 12-AUG-2002 (first entry)

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XX Human MDM2 mRNA amplifying RT-PCR forward primer.
DE Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;
KW Query Match 1.1%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 622 ACAGGAACCTTGGTAGTAGTCAATCAG 647
DB 1 ACAGGAACCTTGGTAGTAGTCAATCAG 26

RESULT 378
ADD21705/c
ID ADD21705 standard; DNA; 26 BP.
XX
AC ADD21705;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2-specific PCR primer #2.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 1.1%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 415 TGAAGTTATTAAAGTCGTGGTGCA 440
DB 26 TGAAGTTATTAAAGTCGTGGTGCA 1

RESULT 379
AAA04303
ID AAA04303 standard; DNA; 29 BP.
XX
AC AAA04303;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.1%; Score 26; DB 1; Length 29;
Best Local Similarity 92.9%; Pred. No. 1.e+03;
Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2345 GTGCTGGATTACAGGCATGAGCACCG 2372
DB 1 GTGCTGGATTACAGGCATGAGCACCG 28

RESULT 380
AAD42705
ID AAD42705 standard; DNA; 30 BP.
XX
AC AAD42705;
XX
DT 15-NOV-2002 (first entry)
DE Hdm2 cDNA amplifying PCR primer.
XX
KW Human; detection; cancer; ARF-p19 protein; cell cycle regulator; tumour;
KW cell cycle arrest; cell growth; hyperproliferative signal; therapeutic;
Query Match 1.1%; Score 25.8; DB 1; Length 30;

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Best Local Similarity 93.1%; Pred. No. 1.e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 312 ATGTGCAATACCAACATGTCTGTACCTAC 340
DB 1 ATGTGCAATACCAACATGTCTGTGTCTAC 29

RESULT 381
AAA03956
ID AAA03956 standard; DNA; 29 BP.
XX
AC AAA03956;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene APOC1.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.1%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.e+03;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2254 TTGTACTTTTAGTAGAGACAGGGTTTTCAC 2282
DB 1 TTGTATTTTCAGTAKAGACAGGGTTTTCAC 29

RESULT 382
AAA04312
ID AAA04312 standard; DNA; 29 BP.
XX
AC AAA04312;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.1%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.e+03;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2275 GGTTCACCGTGTAGCCAGGATGGTCTC 2303
DB 1 GGTTCACCATGTTRGCCAGATGGTCTC 29

RESULT 383
AAA03995
ID AAA03995 standard; DNA; 29 BP.
XX
AC AAA03995;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene APOC4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.1%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.e+03;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2326 CCCACCTCGGCTCCCAAGTCTGGAT 2354
DB 1 CCCGCTTGGCTCTCYCAAAGTCTGGAT 29

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RESULT 384
AA04505
ID AAA04505 standard; DNA; 29 BP.
XX AC
XX AAA04505;
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.1%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.1e+03;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTCCCAAGTG 2347
DB 1 TGAATGCCCGCTTGGCTCCCAAGTG 29

RESULT 385
AAQ73570
ID AAQ73570 standard; DNA; 32 BP.
XX AC
XX AAQ73570;
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Enhancer element er-3 conserved basepair sequence.
XX
KW Enhancer element; carcinoma; tumor; cancer; SLPI gene;

Query Match 1.1%; Score 25.2; DB 1; Length 32;
Best Local Similarity 87.1%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCA 2281
DB 2 TTTTGTATTTTAGTAGAGATGGGINTCA 32

RESULT 386
AAH79009/c
ID AAH79009 standard; DNA; 33 BP.
XX AC
XX AAH79009;
DT 09-NOV-2001 (first entry)
XX
DE Human signal peptidase 9 PCR primer 4.
XX
KW Human; signal peptidase 9; malignant tumour; haemopathy; HIV; infection;
KW human immunodeficiency virus; immunological disease; inflammation;

Query Match 1.1%; Score 25.2; DB 1; Length 33;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGCATGAGCCACC 2371
DB 33 AAAGTCTGGGATTACAGGCATGAGATCC 4

RESULT 387
ABK50423/c
ID ABK50423 standard; DNA; 33 BP.
XX AC
XX ABK50423;
XX

QY 30-JUL-2002 (first entry)
XX
DE Human transfer down-regulation protein 9.79 cDNA PCR primer #2.
XX
KW Human; transfer down-regulation protein 9.79; primer; ss; tumour; cancer;
KW DNA recombination; PCR.

Query Match 1.1%; Score 25.2; DB 1; Length 33;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGCATGAGCCACC 2371
DB 33 AAAGTCTGGGATTACAGGCATGAGATCC 4

RESULT 388
AAZ37741
ID AAZ37741 standard; DNA; 25 BP.
XX AC
XX AAZ37741;
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 real-time reverse PCR probe #271.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCACCTCACAGATTCAGCTTCGGA 379
DB 1 CCACCTCACAGATTCAGCTTCGGA 25

RESULT 389
AAF80895
ID AAF80895 standard; DNA; 25 BP.
XX AC
XX AAF80895;
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 amplification probe.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCACCTCACAGATTCAGCTTCGGA 379
DB 1 CCACCTCACAGATTCAGCTTCGGA 25

RESULT 390
AAH38447/c
ID AAH38447 standard; DNA; 25 BP.
XX AC
XX AAH38447;
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1243.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

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Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2185 CCATTCTCCTGCTCAGCCTCCCAA 2209
DB 25 CCATTCTCCTGCTCAGCCTCCCAA 1

RESULT 391
AAS29510
ID AAS29510 standard; DNA; 25 BP.
XX
AC AAS29510;
XX
DT 21-NOV-2001 (first entry)
DE Fluorescent labelled human mdm2 probe.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCACCTCACAGATTCCAGCTTCGGA 379
DB 1 CCACCTCACAGATTCCAGCTTCGGA 25

RESULT 392
AAS15700
ID AAS15700 standard; DNA; 25 BP.
XX
AC AAS15700;
XX
DT 29-JAN-2002 (first entry)
DE Human Alu sequence PCR primer #2.
XX
KW Human; Alu sequence; ss; PCR primer; human immunodeficiency virus;
KW Latent HIV detection; LTR; long terminal repeat;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAAGTGCTGGGATTACAG 2359
DB 1 GCCTCCCAAAGTGCTGGGATTACAG 25

RESULT 393
ADB04775
ID ADB04775 standard; DNA; 25 BP.
XX
AC ADB04775;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5761.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2283 CGTGTAGCCAGGATGCTCGATC 2307
DB 1 CGTGTAGCCAGGATGCTCGATC 25

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGGATG 2298
DB 1 GGGTTTCACCGTGTAGCCAGGATG 25

RESULT 394
ADB04766
ID ADB04766 standard; DNA; 25 BP.
XX
AC ADB04766;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5752.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCG 2304
DB 1 CACCGTGTAGCCAGGATGCTCG 25

RESULT 396
ADB04781
ID ADB04781 standard; DNA; 25 BP.
XX
AC ADB04781;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5767.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2289 AGCCAGGATGCTCGATCTCTCGA 2313
DB 1 AGCCAGGATGCTCGATCTCTCGA 25

RESULT 397
ADB04770
ID ADB04770 standard; DNA; 25 BP.
XX
AC ADB04770;

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```
XX 20-NOV-2003 (first entry)
DT Human MDZ7 scanning oligonucleotide SEQ ID 5756.
DE Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2278 TTCACCGTGTAGCCAGGATGGTCT 2302
DB 1 TTCACCGTGTAGCCAGGATGGTCT 25
RESULT 398
ADB04773
ID ADB04773 standard; DNA; 25 BP.
XX
AC ADB04773;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5759.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2281 ACCGTGTAGCCAGGATGGTCTCGA 2305
DB 1 ACCGTGTAGCCAGGATGGTCTCGA 25
RESULT 399
ADB04771
ID ADB04771 standard; DNA; 25 BP.
XX
AC ADB04771;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5757.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2279 TCACCGTGTAGCCAGGATGGTCTC 2303
DB 1 TCACCGTGTAGCCAGGATGGTCTC 25
RESULT 400
ADB04780
ID ADB04780 standard; DNA; 25 BP.
XX
AC ADB04780;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5766.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
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Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2288 TAGCCAGGATGGTCTCGATCTCCTG 2312
DB 1 TAGCCAGGATGGTCTCGATCTCCTG 25
RESULT 401
ADB04767
ID ADB04767 standard; DNA; 25 BP.
XX
AC ADB04767;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5753.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2275 GGTTCACCGTGTAGCCAGGATGG 2299
DB 1 GGTTCACCGTGTAGCCAGGATGG 25
RESULT 402
ADB04769
ID ADB04769 standard; DNA; 25 BP.
XX
AC ADB04769;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5755.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2277 TTTCACCGTGTAGCCAGGATGGTC 2301
DB 1 TTTCACCGTGTAGCCAGGATGGTC 25
RESULT 403
ADB04776
ID ADB04776 standard; DNA; 25 BP.
XX
AC ADB04776;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5762.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2284 GTGTTAGCCAGGATGGTCTCGATCT 2308
DB 1 GTGTTAGCCAGGATGGTCTCGATCT 2308
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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
 Query Match 1.1%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 355 CCACCTCACAGATTCAGCTTCGGA 379  
 DB 1 CCACCTCACAGATTCAGCTTCGGA 25  
 RESULT 411  
 AAA04503  
 ID AAA04503 standard; DNA; 29 BP.  
 XX  
 XX  
 AC AAA04503;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DE Polymorphic fragment of hypertension associated gene PGIS.  
 KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 Query Match 1.1%; Score 25; DB 1; Length 29;  
 Best Local Similarity 92.6%; Pred. No. 1.2e+03;  
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2274 GGGTTTCACCGTTGTTAGCCAGGATGGT 2300  
 DB 3 GGATTTACCGTTRTTAGCCAGGATGGT 29  
 RESULT 412  
 ABA94089/c  
 ID ABA94089 standard; DNA; 33 BP.  
 XX  
 AC ABA94089;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Human tumour suppressor factor 11.77 PCR primer 3 SEQ ID NO:5.  
 KW Human; tumour suppressor factor 11.77; cytostatic; haemostatic; virucide;  
 KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;  
 Query Match 1.1%; Score 25; DB 1; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2340 CCAAGTCTGGGATTACAGGCATG 2364  
 DB 33 CCAAGTCTGGGATTACAGGCATG 9  
 RESULT 413  
 ABL54842/c  
 ID ABL54842 standard; DNA; 33 BP.  
 XX  
 AC ABL54842;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Human G-protein subunit 12.65 related primer#4.  
 KW Human; G-protein subunit 12.65; cytostatic; analgesic; antiasthmatic;  
 KW antidiarrhoeal; antiinflammatory; nootropic; hormone receptor; tumour;  
 Query Match 1.1%; Score 25; DB 1; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2342 AAAGTCTGGGATTACAGGCATGAG 2366

DB 33 AAAGTCTGGGATTACAGGCATGAG 9  
 RESULT 414  
 AAA27185  
 ID AAA27185 standard; DNA; 28 BP.  
 XX  
 AC AAA27185;  
 XX  
 DT 11-SEP-2000 (first entry)  
 XX  
 DE Reverse primer IL10 for target sequence human interleukin 10.  
 XX P2; CX5C chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;  
 KW allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;  
 Query Match 1.0%; Score 24.8; DB 1; Length 28;  
 Best Local Similarity 92.9%; Pred. No. 1.2e+03;  
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2111 TTGCTCTGTTCACCCAGGCTGGAGTGCGAG 2138  
 DB 1 TTGCTCTGTTCACCCAGGCTGGAGTGCGAG 28  
 RESULT 415  
 AAH39586/c  
 ID AAH39586 standard; DNA; 31 BP.  
 XX  
 AC AAH39586;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE SNP specific lower PCR primer SEQ ID 2382.  
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 Query Match 1.0%; Score 24.6; DB 1; Length 31;  
 Best Local Similarity 87.1%; Pred. No. 1.2e+03;  
 Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2256 GTACTTTTAGTAGACAGACAGGTTTCACCGTG 2286  
 DB 31 GTACTTTTAGTAGACAGACAGGTTTCATTATG 1  
 RESULT 416  
 AAH91712/c  
 ID AAH91712 standard; DNA; 32 BP.  
 XX  
 AC AAH91712;  
 XX  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human inflammatory bowel disease associated polymorphic site #787.  
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 Query Match 1.0%; Score 24.6; DB 1; Length 32;  
 Best Local Similarity 84.4%; Pred. No. 1.2e+03;  
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 2300 TCTCGATCTCCTGACCTCGTGATCCGCCACC 2331  
 DB 32 TCTGATCTCTTGACCTCTGATCCGCCCTGCC 1  
 RESULT 417  
 AAH40071  
 ID AAH40071 standard; DNA; 27 BP.



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XX AAH40071;
AC
XX
DT 14-AUG-2001 (first entry)
DE
DE SNP specific SNPE primer SEQ ID 2867.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match 1.0%; Score 24.4; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.2e+03;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 GATCTCTGACCTGCTGATCGGCCAC 2330
Db 1 GATCTCTGACCTGCTGATCGGCCAC 27

RESULT 418
AAH404504
ID AAA04504 standard; DNA; 29 BP.
AC
AC AAA04504;
XX
XX 22-MAY-2000 (first entry)
XX
XX Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 24.4; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.2e+03;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGGATGGTC 2301
Db 2 GGATTTTACCGTATYTAGCCAGGATGGTC 29

RESULT 419
AAH404498
ID AAA04498 standard; DNA; 29 BP.
AC
AC AAA04498;
XX
XX 22-MAY-2000 (first entry)
XX
XX Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 24.4; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.2e+03;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2140 GGGTGATCTTGGCTCACTGCAAGCTCTG 2167
Db 2 GCGTGATCTCGGCTCACTGCAAGCTCTG 29

RESULT 420
AAH403993
ID AAA03993 standard; DNA; 29 BP.
AC
AC AAA03993;
XX
XX 22-MAY-2000 (first entry)
XX
XX Polymorphic fragment of hypertension associated gene APOC4.

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KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 24.4; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.2e+03;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2343 AAGTGTGGGATTACAGGCATGAGCCAC 2370
Db 1 AAGTGTAGGATTAYAGGCGTGAGCCAC 28

RESULT 421
AAH91563/c
ID AAQ29012 standard; DNA; 25 BP.
XX
XX AAQ29012;
AC
XX
XX 25-MAR-2003 (revised)
DT 23-FEB-1993 (first entry)
XX
XX Alu family consensus sequence-derived probe #1.
XX
KW Low frequency repeat; AluI restriction digest; genetic mapping; ss.
Query Match 1.0%; Score 24.2; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.2e+03;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGTCTGGGATTACAGGCATGAGCCAC 2370
Db 25 TGTCTGGGATTACAGGYRTGAGCCAC 1

RESULT 422
AAH91563/c
ID ACA62537 standard; DNA; 29 BP.
XX
XX ACA62537;
AC
XX
XX 18-AUG-2003 (first entry)
XX
XX Human MDM2 mutant 156-221 PCR primer #1.
XX
XX Human; ss; PCR; primer; MDM2; cancer; tumour; cytostatic; p19(ARF); p53;
XX Rb; oncoprotein; oncogenic transformation; proteosomal degradation.
Query Match 1.0%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 964 CGCCATCGAATCCGGATCTTGATGCTGGT 992
Db 1 CGCCATCTAGACCGGATCTTGATGCTGGT 29

RESULT 423
AAH91563/c
ID AAH91563 standard; DNA; 30 BP.
XX
XX AAH91563;
AC
XX
XX 09-OCT-2001 (first entry)
XX
XX Human inflammatory bowel disease associated polymorphic site #638.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
Query Match 1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 2090 TATTTTGTGAGCCGAGTCTTGCTCTGT 2119
DB 30 TTTTGTGAGCCGAGTCTCGCTCTGT 1

RESULT 424
AAD42698
ID AAD42698 standard; DNA; 30 BP.
XX
AC AAD42698;
XX
DT 15-NOV-2002 (first entry)
XX
DE Primer #4 used to construct Hdm2 mutant plasmid.
XX
KW Human; detection; cancer; ARP-p19 protein; cell cycle regulator; tumour;
KW cell cycle arrest; cell growth; hyperproliferative signal; therapeutic;

Query Match 1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 89.7%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 934 AAAGAAGCAGTAGCAGTGAATCTACAGG 962
DB 2 ATATGAGCAGTAGCAGTGAATCTACAGG 30

RESULT 425
AAQ73573
ID AAQ73573 standard; DNA; 31 BP.
XX
AC AAQ73573;
XX
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Enhancer element er-3 conserved basepair sequence.
XX
KW Enhancer element; carcinoma; tumor; cancer; SLP1 gene;

Query Match 1.0%; Score 24.2; DB 1; Length 31;
Best Local Similarity 83.9%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2197 CTCAGCCTCCCAANTAGTTCGCTACAGTC 2227
DB 1 CTCAGCCTCCCAANTAGTTCGGANTACAGGC 31

RESULT 426
AAZ89375
ID AAZ89375 standard; DNA; 24 BP.
XX
AC AAZ89375;
XX
DT 15-JUN-2000 (first entry)
XX
DE Human mdm-2 PCR primer mdm2Pr11.
XX
KW Human; mdm-2; PCR primer; reaction container; quantitation; diagnosis;
KW food analysis; ss.

Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1581 GAGAGTGTGGAATCTAGTTTGGCCC 1604
DB 1 GAGAGTGTGGAATCTAGTTTGGCCC 24

RESULT 427
AAH45830/c

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ID AAH45830 standard; DNA; 24 BP.
XX
AC AAH45830;
XX
DT 11-SEP-2001 (first entry)
XX
DE Telomere size determination method related oligonucleotide #3.
XX
KW Telomere size determination; chromosomal DNA; probe; primer;
KW repetitive sequence; tissue aging; cancer progression; ds.

Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACA 2358
DB 24 GCCTCCCAAGTCTGGGATTACA 1

RESULT 428
AAH45828
ID AAH45828 standard; DNA; 24 BP.
XX
AC AAH45828;
XX
DT 11-SEP-2001 (first entry)
XX
DE Telomere size determination method related oligonucleotide #1.
XX
KW Telomere size determination; chromosomal DNA; probe; primer;
KW repetitive sequence; tissue aging; cancer progression; ds.

Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACA 2358
DB 1 GCCTCCCAAGTCTGGGATTACA 24

RESULT 429
AAI69885/c
ID AAI69885 standard; DNA; 24 BP.
XX
AC AAI69885;
XX
DT 14-DEC-2001 (first entry)
XX
DE Human transglutaminase 12 PCR primer #1.
XX
KW Human; transglutaminase 12; cytostatic; virucidal; immunomodulatory;
KW antiinflammatory; haemostatic; gene therapy; malignant tumour;

Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTGTGGGATTACAGGCATG 2364
DB 24 CAAAGTGTGGGATTACAGGCATG 1

RESULT 430
ADK66042
ID ADK66042 standard; DNA; 24 BP.
XX
AC ADK66042;
XX
DT 06-MAY-2004 (first entry)
XX
DE Standardized polynucleotide system polynucleotide #9 PCR primer #1.

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XX ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis;

Query Match      1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1581 GAGAGTGTGGAATCTAGTTTGCCC 1604
DB 1 GAGAGTGTGGAATCTAGTTTGCCC 24

RESULT 431
AAQ25353/c
ID AAQ25353 standard; DNA; 25 BP.
XX
AC AAQ25353;
XX
DT 21-NOV-1992 (first entry)
XX
DE Sequence of probe Alu 1.
XX
KW Hybridisation rate; chondroitin sulphate; probe; probe cocktail; Alu 1;
KW ss.

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGTGGGATTACA 2358
DB 24 GCCTCCCAAGTGTGGGATTACA 1

RESULT 432
ADB04765
ID ADB04765 standard; DNA; 25 BP.
XX
AC ADB04765;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5751.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGGAT 2297
DB 2 GGGTTTCACCGTGTAGCCAGGAT 25

RESULT 433
ADB04783
ID ADB04783 standard; DNA; 25 BP.
XX
AC ADB04783;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5769.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2291 CCAGGATGCTCTCGATCTCTCTGAC 2314
DB 1 CCAGGATGCTCTCGATCTCTCTGAC 24

RESULT 434
AAA04506
ID AAA04506 standard; DNA; 29 BP.
XX
AC AAA04506;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.0%; Score 24; DB 1; Length 29;
Best Local Similarity 92.3%; Pred. No. 1.3e+03;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2347 GCTGGATTACAGCATGAGCCACCG 2372
DB 1 GCTGGATTACAGGYGTGAGCCACCG 26

RESULT 435
AAA03879/c
ID AAA03879 standard; DNA; 29 BP.
XX
AC AAA03879;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene AEL.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2098 TTGAGACCGAGTCTTGCTCTGTATCCAG 2126
DB 29 TTGAGACAGGGTCTGCTCTGTGCCCCAG 1

RESULT 436
AAA03958
ID AAA03958 standard; DNA; 29 BP.
XX
AC AAA03958;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene APOC1.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2303 CGATCTCTGACCTCGTGATCCGCCACC 2331
DB 1 CGATCTCTGACTTGTGTGATCCGCTGCC 29

RESULT 437

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AAA04485/c
ID AAA04485 standard; DNA; 29 BP.
XX
AC AAA04485;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2267 AGAGACGGGTTTCCACCGTGTAGCCAGG 2295
DB 29 AGAGACGGGTTTCCACCGTGTAGCCAGG 1

RESULT 438
AAA03985/c
ID AAA03985 standard; DNA; 29 BP.
XX
AC AAA03985;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene APOC3.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2110 CTTGCTCTGTACCCAGGCTGGAGTGCGAG 2138
DB 29 CTTGCTCTGTACCCAGGCTGGAGTGCGAG 1

RESULT 439
AAA04389/c
ID AAA04389 standard; DNA; 29 BP.
XX
AC AAA04389;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene IAPP.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2105 CGAGTCTGTCTGTACCCAGGCTGGAG 2133
DB 29 CGAGTCTGTCTGTACCCAGGCTGGAG 1

RESULT 440
AAA04314
ID AAA04314 standard; DNA; 29 BP.
XX
AC AAA04314;
XX
DT 22-MAY-2000 (first entry)
XX

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DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2303 CGATCTCTCGACCTCGTGATCCGCCACC 2331
DB 1 CGATCTCTCGACCTCGTGATCTGCTGCC 29

RESULT 441
AAV19047
ID AAV19047 standard; DNA; 30 BP.
XX
AC AAV19047;
XX
DT 28-JUL-1998 (first entry)
XX
DE Alu PCR primer 4.
XX
KW PCR; primer; amplification; Alu repeat sequence; vector;
KW circular yeast artificial chromosome; YAC; ss.

Query Match 1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.4e+03;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTGCTCTGTATACCCAG 2126
DB 1 TTTGAGACCGAGTCTGCTCTGTGCCCCAG 30

RESULT 442
ABL59103
ID ABL59103 standard; DNA; 30 BP.
XX
AC ABL59103;
XX
DT 27-SEP-2002 (first entry)
XX
DE PCR primer used to amplify an 82 bp Alu probe.
XX
KW Yeast artificial chromosome; YAC; pPD39;
KW transformation-associated recombination; PCR; primer; ss.

Query Match 1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.4e+03;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTGCTCTGTATACCCAG 2126
DB 1 TTTGAGACCGAGTCTGCTCTGTGCCCCAG 30

RESULT 443
ACC85703
ID ACC85703 standard; DNA; 30 BP.
XX
AC ACC85703;
XX
DT 22-APR-2004 (first entry)
XX
DE Human protease MDT9 related DNA sequence SEQ ID NO: 18.
XX
KW Promoter; human; protease; MDT9; chronic kidney failure; nephrotropic;
KW gene; ds.

Query Match 1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.4e+03;

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```
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2097 TTTGAGACCGAGTCTTCTGTGTACCCAG 2126
DB 1 TTTGAGACCGAGTCTCTGTGTGCCAG 30

RESULT 444
AAH40799
ID AAH40799 standard; DNA; 25 BP.
XX AC
XX AAH40799;
XX
DT 14-AUG-2001 (first entry)
DE
DE SNP specific SNPE primer SEQ ID 3595.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2343 AAGTGTGGGATTACAGCGATGAGC 2367
DB 1 AAGTGTGGGATTACAGCGGTGAGC 25

RESULT 445
AAS14584
ID AAS14584 standard; DNA; 25 BP.
XX AC
XX AAS14584;
XX
DT 18-DEC-2001 (first entry)
DE
DE Human SNAP23 SNP region #2 PCR primer #1.
KW Human; single-nucleotide polymorphism; SNP; SNAP23; ss; PCR primer;
KW synaptosome associated protein of 23 kilodaltons; diabetes; obesity;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2336 CCTCCCAAGTCTGGGATTACAGG 2360
DB 1 CCTCCCAAGTACTGGGATTACAGG 25

RESULT 446
AAS14581
ID AAS14581 standard; DNA; 25 BP.
XX AC
XX AAS14581;
XX
DT 18-DEC-2001 (first entry)
DE
DE Human SNAP23 SNP region #1 PCR primer #1.
KW Human; single-nucleotide polymorphism; SNP; SNAP23; ss; PCR primer;
KW synaptosome associated protein of 23 kilodaltons; diabetes; obesity;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2336 CCTCCCAAGTCTGGGATTACAGG 2360
DB 1 CCTCCCAAGTACTGGGATTACAGG 25

Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2097 TTTGAGACCGAGTCTTCTGTGTACCCAG 2126
DB 1 TTTGAGACCGAGTCTCTGTGTGCCAG 30

RESULT 444
AAH40799
ID AAH40799 standard; DNA; 25 BP.
XX AC
XX AAH40799;
XX
DT 14-AUG-2001 (first entry)
DE
DE SNP specific SNPE primer SEQ ID 3595.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2343 AAGTGTGGGATTACAGCGATGAGC 2367
DB 1 AAGTGTGGGATTACAGCGGTGAGC 25

RESULT 445
AAS14584
ID AAS14584 standard; DNA; 25 BP.
XX AC
XX AAS14584;
XX
DT 18-DEC-2001 (first entry)
DE
DE Human SNAP23 SNP region #2 PCR primer #1.
KW Human; single-nucleotide polymorphism; SNP; SNAP23; ss; PCR primer;
KW synaptosome associated protein of 23 kilodaltons; diabetes; obesity;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2336 CCTCCCAAGTCTGGGATTACAGG 2360
DB 1 CCTCCCAAGTACTGGGATTACAGG 25

RESULT 446
AAS14581
ID AAS14581 standard; DNA; 25 BP.
XX AC
XX AAS14581;
XX
DT 18-DEC-2001 (first entry)
DE
DE Human SNAP23 SNP region #1 PCR primer #1.
KW Human; single-nucleotide polymorphism; SNP; SNAP23; ss; PCR primer;
KW synaptosome associated protein of 23 kilodaltons; diabetes; obesity;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2336 CCTCCCAAGTCTGGGATTACAGG 2360
DB 1 CCTCCCAAGTACTGGGATTACAGG 25
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RESULT 447
ABT03658
ID ABT03658 standard; DNA; 25 BP.
XX AC
XX ABT03658;
XX
DT 13-SEP-2002 (first entry)
DE
DE Human Med-6 gene PCR primer SEQ ID NO: 179.
KW Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
KW transcription factor; PCR; primer; ss.
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2341 CAAAGTCTGGGATTACAGCGATGA 2365
DB 1 CAAAGTCTGGGATTACAGCGGTGA 25

RESULT 448
AD117385
ID AD117385 standard; DNA; 25 BP.
XX AC
XX AD117385;
XX
DT 15-APR-2004 (first entry)
DE
DE PCR primer used for exon linking to confirm human NOVX DNA SeqID921.
KW human; PCR; primer; ss; exon linking; NOVX; cardiomyopathy;
KW atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2295 GATGGTCTCGATCTCCTGACCTCGT 2319
DB 1 GATGGTCTCGATCTCCTGACCTCTT 25

RESULT 449
ADN42474
ID ADN42474 standard; DNA; 25 BP.
XX AC
XX ADN42474;
XX
DT 17-JUN-2004 (first entry)
DE
DE Human NOV22c exon linking PCR primer #2.
KW Human; ss; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis; PCR;
KW primer; exon linking.
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2295 GATGGTCTCGATCTCCTGACCTCGT 2319
DB 1 GATGGTCTCGATCTCCTGACCTCTT 25

RESULT 450
AAH40327
ID AAH40327 standard; DNA; 27 BP.
XX AC
XX AAH40327;
XX
DT 14-AUG-2001 (first entry)
```

XX SNP specific SNPE primer SEQ ID 3123.  
DE  
XX  
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
Query Match 1.0%; Score 23.4; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 1.4e+03;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2302 TCGATCTCTGACCTCGTGATCCGCC 2328  
DB 1 TCGNTCTCTGACCTCGTGNTCCGTCC 27

RESULT 451  
ABX15004/c  
ID ABX15004 standard; DNA; 29 BP.  
XX  
AC ABX15004;  
XX  
DT 14-MAR-2003 (first entry)  
XX Human delta opioid receptor OPRD1-7 SNP genotyping PCR probe #2.  
DE  
XX Human; delta opioid receptor; OPRD1-7; ss; PCR; probe; SNP;  
KW single nucleotide polymorphism; eating disorder; anorexia nervosa;  
KW  
Query Match 1.0%; Score 23.2; DB 1; Length 29;  
Best Local Similarity 89.3%; Pred. No. 1.4e+03;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2249 ATTCTTTGCTACTTTAGTAGACAGG 2276  
DB 28 AATTTTGTACTTTTAGTAAGATAGG 1

RESULT 452  
ABT34292/c  
ID ABT34292 standard; DNA; 29 BP.  
XX  
AC ABT34292;  
XX  
DT 12-JUN-2003 (first entry)  
XX Opioid receptor D1 probe SEQ ID No 78.  
DE  
XX Eating disorder; polymorphism; dataset; allele; HGBASE identification;  
KW serotonin receptor 1D; delta-opioid receptor; dopamine receptor D2;  
KW  
Query Match 1.0%; Score 23.2; DB 1; Length 29;  
Best Local Similarity 89.3%; Pred. No. 1.4e+03;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2249 ATTCTTTGCTACTTTAGTAGACAGG 2276  
DB 28 AATTTTGTACTTTTAGTAAGATAGG 1

RESULT 453  
AAH40734  
ID AAH40734 standard; DNA; 30 BP.  
XX  
AC AAH40734;  
XX  
DT 14-AUG-2001 (first entry)  
XX SNP specific lower PCR primer SEQ ID 3530.  
DE  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
KW  
Query Match 1.0%; Score 23.2; DB 1; Length 30;

Best Local Similarity 89.3%; Pred. No. 1.4e+03;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2249 ATTCTTTGCTACTTTAGTAGACAGG 2276  
DB 3 AATTTTGTACTTTTAGTAGACAGG 30

RESULT 454  
AAF77571/c  
ID AAF77571 standard; DNA; 23 BP.  
XX  
AC AAF77571;  
XX  
DT 29-MAY-2001 (first entry)  
XX Human mdm2 RNA PCR primer #2.  
DE  
XX Human; p53; proliferative disease; diterpenoid triepoxides;  
KW multi-drug resistance; cancer; restenosis; atherosclerosis; psoriasis;  
KW  
Query Match 1.0%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1374 GAGGGCTTTGATGTTCTGATTG 1396  
DB 23 GAGGGCTTTGATGTTCTGATTG 1

RESULT 455  
ADE12183/c  
ID ADE12183 standard; DNA; 23 BP.  
XX  
AC ADE12183;  
XX  
DT 29-JAN-2004 (first entry)  
XX PCR primer #2 for mdm2 cDNA from human MCF-7 (breast cancer) cell line.  
DE  
XX Tumour; synergistic combination therapy; tumour cell; p21waf1/cip1;  
KW diterpenoid triepoxide; vinca alkaloid; triptolide; anti-proliferative;  
KW  
Query Match 1.0%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1374 GAGGGCTTTGATGTTCTGATTG 1396  
DB 23 GAGGGCTTTGATGTTCTGATTG 1

RESULT 456  
ADG72450/c  
ID ADG72450 standard; DNA; 23 BP.  
XX  
AC ADG72450;  
XX  
DT 11-MAR-2004 (first entry)  
XX PCR primer #2 for human mdm2 cDNA.  
DE  
XX Hyperproliferative disorder; antiproliferative; diterpenoid triepoxide;  
KW tumour; p21; waf1/cip1; carcinoma; cancer; multi-drug resistance; p53;  
KW  
Query Match 1.0%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1374 GAGGGCTTTGATGTTCTGATTG 1396  
DB 23 GAGGGCTTTGATGTTCTGATTG 1

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RESULT 457
ADP11845
ID ADP11845 standard; DNA; 23 BP.
XX
XX
AC ADP11845;
XX
DT 12-AUG-2004 (first entry)
DE
DE Set 2 left PCR primer for marker probe #197.
XX
XX
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

Query Match 1.0%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GCAGCCCAAGAAGATGTGAAAGAG 1550
Db 1 GCAGCCCAAGAAGATGTGAAAGAG 23

RESULT 458
ABI99962
ID ABI99962 standard; DNA; 24 BP.
XX
XX
AC ABI99962;
XX
DT 31-MAY-2002 (first entry)
DE
DE Human phosphatidic acid phosphatase 2-12 RT-PCR primer, SEQ ID NO:4.
XX
XX
XX
KW Human; phosphatidic acid phosphatase 2-12; recombinant production;
KW cancer; HIV infection; human immunodeficiency virus; gene therapy;

Query Match 1.0%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACACAGGGTTTCAC 2282
Db 2 TTTTAGTAGACACAGGGTTTCAC 24

RESULT 459
ACA90127
ID ACA90127 standard; DNA; 24 BP.
XX
XX
AC ACA90127;
XX
DT 10-JUL-2003 (first entry)
DE
DE Human kinesin gene(s) antisense oligonucleotide #10.
XX
XX
XX
KW Human; ss; antisense; kinesin; CNRP-E; Eg5; MCAK; colon cancer; stroke;
KW T cell cancer; B cell lymphoma; pancreatic cancer; breast cancer;

Query Match 1.0%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2350 GGGATTACAGCATGAGCCACCG 2372
Db 1 GGGATTACAGCATGAGCCACCG 23

RESULT 460
ADB04764
ID ADB04764 standard; DNA; 25 BP.
XX
XX
AC ADB04764;
XX

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DT 20-NOV-2003 (first entry)
XX
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5750.
XX
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 1.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGGA 2296
Db 3 GGGTTTCACCGTGTAGCCAGGA 25

RESULT 461
ADO56443/C
ID ADO56443 standard; DNA; 30 BP.
XX
XX
AC ADO56443;
XX
DT 12-AUG-2004 (first entry)
DE
DE Human cyclin-dependent kinase 10, CDK10 proximal SNP PCR primer #166.
XX
XX
XX
KW gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;

Query Match 1.0%; Score 23; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTGCTGGGATTACAGGCAT 2363
Db 30 CAAAGTGCTGGGATTACAGGCAT 8

RESULT 462
ADO56349/C
ID ADO56349 standard; DNA; 30 BP.
XX
XX
AC ADO56349;
XX
DT 12-AUG-2004 (first entry)
DE
DE Human cyclin-dependent kinase 10, CDK10 proximal SNP PCR primer #72.
XX
XX
XX
KW gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;

Query Match 1.0%; Score 23; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTGCTGGGATTACAGGCAT 2363
Db 30 CAAAGTGCTGGGATTACAGGCAT 8

RESULT 463
AAV59189
ID AAV59189 standard; DNA; 26 BP.
XX
XX
AC AAV59189;
XX
DT 21-DEC-1998 (first entry)
DE
DE Human bak gene promoter NF-kappa B site 2.
XX
XX
XX
KW Bak gene; promoter; human; apoptosis; ischaemia; tumour; cancer;
KW infection; HIV; neurodegenerative disorder; hair loss;

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Query Match 1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2264 AGTAGAGACAGGGTTTCACCGTGTTA 2289
DB 1 AGTAGAGACGGGGTTTCACCATGTTA 26

RESULT 464
ABK65978
ID ABK65978 standard; DNA; 26 BP.
XX
AC ABK65978;
XX
DT 02-JUL-2002 (first entry)
DE Human gene specific PCR primer #66.
XX
KW Primer; ss; DNA microarray; differential expression analysis; human.
XX

Query Match 1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTGCTGGGATTACAGGCATGAGC 2367
DB 1 AAAGTGCTAGGATTACAGGCGTGAGC 26

RESULT 465
AAH40487
ID AAH40487 standard; DNA; 27 BP.
XX
AC AAH40487;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific SNPE primer SEQ ID 3283.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.0%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAGTGTGGGATTACA 2358
DB 1 TTGGCTCNCACAGTGTGGGATTACA 27

RESULT 466
AAH39279
ID AAH39279 standard; DNA; 27 BP.
XX
AC AAH39279;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific SNPE primer SEQ ID 2075.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.0%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2344 AGTGCTGGGATTACAGGCATGAGCCAC 2370
DB 1 AGTCTGGGATTACAGGCATGAGCCAC 27
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RESULT 467
AAA04311
ID AAA04311 standard; DNA; 29 BP.
XX
AC AAA04311;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.0%; Score 22.8; DB 1; Length 29;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTCACCGTGTAGCCAGGATG 2298
DB 2 ACGCGTTTCACCGTGTAGCCAGGATG 29

RESULT 468
AAA04497
ID AAA04497 standard; DNA; 29 BP.
XX
AC AAA04497;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.0%; Score 22.8; DB 1; Length 29;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2106 GAGTCTGTCTCTTACCCAGGCTGGAG 2133
DB 2 GAGTCTGTCTGTGTCGCCAGGCTAGAG 29

RESULT 469
AAH38989
ID AAH38989 standard; DNA; 30 BP.
XX
AC AAH38989;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific upper PCR primer SEQ ID 1785.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.0%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTGTACTTTTAGTAGAGACAGG 2275
DB 5 TTTTGTATTATTTTAGTAGAGACGGG 30

RESULT 470
ADO56348/c
ID ADO56348 standard; DNA; 30 BP.
XX
AC ADO56348;
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XX 12-AUG-2004 (first entry)
DT Human cyclin-dependent kinase 10, CDK10 proximal SNP PCR primer #71.
DE gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;

Query Match 1.0%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTCTGGGATTACAGCA 2362
DB 30 CTCCCAAAGTCTGGGATTACATCCA 5

RESULT 471
ADP08583/c
ID ADP08583 standard; DNA; 30 BP.
XX
AC ADP08583;
XX
DT 26-AUG-2004 (first entry)
DE PCR primer 167 used to genotype human glycoprotein VI (GP6) polymorphism.
KW breast cancer; cytostatic; gene therapy; human; platelet glycoprotein VI;
KW GP6; GPIV; GPII; chromosome 19q13.4; ss; PCR; primer; SNP;

Query Match 1.0%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTCTGGGATTACAGCA 2362
DB 30 CTCCCAAAGTCTGGGATTACATCCA 5

RESULT 472
ADP08583/c
ID ADP08583 standard; DNA; 30 BP.
XX
AC ADP08583;
XX
DT 26-AUG-2004 (first entry)
DE PCR primer 167 used to genotype human glycoprotein VI (GP6) polymorphism.
KW breast cancer; cytostatic; gene therapy; human; platelet glycoprotein VI;
KW GP6; GPIV; GPII; chromosome 19q13.4; ss; PCR; primer; SNP;

Query Match 1.0%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTCTGGGATTACAGCA 2362
DB 30 CTCCCAAAGTCTGGGATTACATCCA 5

RESULT 473
AAQ77890/c
ID AAQ77890 standard; cDNA; 30 BP.
XX
AC AAQ77890;
XX
DT 25-MAR-2003 (revised)
DE 06-JUL-1995 (first entry)
KW Neural thread protein AD10-7 cDNA 5' antisense oligonucleotide.
KW Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;

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Query Match 1.0%; Score 22.6; DB 1; Length 30;
Best Local Similarity 86.2%; Pred. No. 1.5e+03;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTGCGACCAATTCCTGCTCAGCCTCC 2207
DB 30 TTCAAGCGATTCTCTGCTCAGCCTCC 2

RESULT 474
AAT27744/c
ID AAT27744 standard; DNA; 30 BP.
XX
AC AAT27744;
XX
DT 14-NOV-1996 (first entry)
DE Neural thread protein antisense sequence.
KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;

Query Match 1.0%; Score 22.6; DB 1; Length 30;
Best Local Similarity 86.2%; Pred. No. 1.5e+03;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTGCGACCAATTCCTGCTCAGCCTCC 2207
DB 30 TTCAAGCGATTCTCTGCTCAGCCTCC 2

RESULT 475
AAF92888
ID AAF92888 standard; DNA; 24 BP.
XX
AC AAF92888;
XX
DT 17-MAY-2001 (first entry)
DE Human ABC1 transcription factor binding site #49.
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

Query Match 0.9%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTGATCC 2324
DB 1 CTCGATCTCTGACCTCGTGATCC 24

RESULT 476
ABA03268/c
ID ABA03268 standard; DNA; 24 BP.
XX
AC ABA03268;
XX
DT 14-FEB-2002 (first entry)
DE Human chorine ion channel 9 PCR primer #1.
KW Human; chorine ion channel 9; cytostatic; virucide; immunomodulator;
KW antiinflammatory; haemostatic; gene therapy; tumour; haemopathy;

Query Match 0.9%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2265 GTAGACAGGGTTTCCCGTGT 2288
DB 1 GTAGACAGGGTTTCCCGTGT 2288

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Db      24 GTAGAGACGGGGTTTCCACCGTGT 1

RESULT 477
ABA05118/c
ID ABA05118 standard; DNA; 24 BP.
XX
XX
AC ABA05118;
XX
XX
DT 04-MAR-2002 (first entry)
XX
XX Human Pax protein 22 coding sequence PCR primer #2.
DE Human; Pax protein 22; cancer; haemopathy; HIV infection; cytostatic;
KW haemostatic; virucide; immunomodulatory; antiinflammatory; inflammation;
KW

Query Match      0.9%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2307 CTCCTGACCTCGTGATCGGCCAC 2330
Db      24 CTCCTGACCTCGTGATCGGCCGC 1

RESULT 478
ADL07545/c
ID ADL07545 standard; DNA; 24 BP.
XX
XX
AC ADL07545;
XX
XX
DT 06-MAY-2004 (first entry)
XX
XX DE Sec24 protein-31.35 RT-PCR primer #1.
DE ss; primer; Sec24 protein-31.35; cancer; HIV infection; PCR; RT-PCR;
KW reverse transcriptase PCR.

Query Match      0.9%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2347 GCTGGGATTACAGGCATGAGCCAC 2370
Db      24 GCTGGGATTACAGGCATGAGCCAC 1

RESULT 479
AAQ63846/c
ID AAQ63846 standard; DNA; 25 BP.
XX
XX
AC AAQ63846;
XX
XX
DT 25-MAR-2003 (revised)
DT 29-JAN-1995 (first entry)
XX
XX PCR primer ALU for tumour specific DNA.
XX
XX Arbitrary primers; AP-PCR; amplification; tumour cells; cancer;

Query Match      0.9%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2260 TTTTAGTAGACAGCGGTTTCACC 2283
Db      24 TTTTAGTAGACAGCGGTTTCACC 1

RESULT 480
AAK24391
ID AAK24391 standard; DNA; 25 BP.
XX
XX

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AC AAX24391;
XX
XX 07-JUN-1999 (first entry)
XX
XX Chemokine receptor CCR8 PCR primer CY6.
XX
XX Chemokine receptor; CCR8; human; G protein coupled receptor; HIV;
KW infection; therapy; immunomodulator; chemotaxis; apoptosis; PCR; primer;

Query Match      0.9%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2347 GCTGGGATTACAGGCATGAGCCAC 2370
Db      1 GCTAGGATTACAGGCATGAGCCAC 24

RESULT 481
ADB97611/c
ID ADB97611 standard; DNA; 25 BP.
XX
XX
AC ADB97611;
XX
XX
DT 04-DEC-2003 (first entry)
XX
XX Tumour tissue arbitrary PCR primer #10.
XX
XX ss; PCR; primer; tumour; tumour tissue; colorectal tumour cell;
KW stomach tumour cell; pancreatic tumour cell; cancer risk; cancer.

Query Match      0.9%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2260 TTTTAGTAGACAGCGGTTTCACC 2283
Db      24 TTTTAGTAGACAGCGGTTTCACC 1

RESULT 482
ADO04045/c
ID ADO04045 standard; DNA; 25 BP.
XX
XX
AC ADO04045;
XX
XX
DT 29-JUL-2004 (first entry)
XX
XX AP-PCR primer J, used to identify deletions in human gene.
XX
XX Neoplasm identification; tumour; colorectal; stomach; pancreatic;
KW arbitrarily primed; AP; PCR; primer; human; ss.

Query Match      0.9%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2260 TTTTAGTAGACAGCGGTTTCACC 2283
Db      24 TTTTAGTAGACAGCGGTTTCACC 1

RESULT 483
AAH91455/c
ID AAH91455 standard; DNA; 29 BP.
XX
XX
AC AAH91455;
XX
XX
DT 09-OCT-2001 (first entry)
XX
XX Human inflammatory bowel disease associated polymorphic site #530.
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;

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KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match      0.9%; Score 22.4; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2230 CTGCACACACACCTGGCTAATTTT 2254
DB 25 CTGCCACCNCACCTGGCTAATTTT 1

RESULT 484
AAA04010/c
ID AAA04010 standard; DNA; 29 BP.
XX
AC AAA04010;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene APOC4.
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22.2; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGCTGGGATTACGGCAT 2363
DB 29 GCCTCCCGAGTAGCGGGATTACAGGCAT 1

RESULT 485
AAA04663
ID AAA04663 standard; DNA; 29 BP.
XX
AC AAA04663;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene TBXA2R.
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22.2; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTGCACCATTCCTCGCTCAGCTCCC 2207
DB 1 TTCAGCGATTCCTGCTGCTCAGCTCCC 29

RESULT 486
AAA04486/c
ID AAA04486 standard; DNA; 29 BP.
XX
AC AAA04486;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene PGIS.
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22.2; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGGGTTTCACCGTGTAG 2290

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DB 29 TTAGTAGACAGGGRTTTCGCATGTGG 1

RESULT 487
AAA04496
ID AAA04496 standard; DNA; 29 BP.
XX
AC AAA04496;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene PGIS.
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22.2; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2098 TTGAGACCGAGCTTGCTCTGTACCAG 2126
DB 1 TTGAGATGGAGTCTGTCTGTGCCCCAG 29

RESULT 488
AAA04500
ID AAA04500 standard; DNA; 29 BP.
XX
AC AAA04500;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene PGIS.
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22.2; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2193 CTGCTCAGCTCCCAATTAGCTTGGCCT 2221
DB 1 CTGCTCAGCTCCCTCGAGTAGTGGGACT 29

RESULT 489
AAA04009/c
ID AAA04009 standard; DNA; 29 BP.
XX
AC AAA04009;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene APOC4.
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22.2; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2222 ACAGTCATCTGCCACACACCTGGCTAAT 2250
DB 29 ACAGGTCATCTGCCAYCATGCCCGCTAAT 1

RESULT 490
AAA03983/c
ID AAA03983 standard; DNA; 29 BP.

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XX AAA03983;  
 AC  
 DT 22-MAY-2000 (first entry)  
 XX  
 DE Polymorphic fragment of hypertension associated gene APOC3.  
 XX  
 KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 KW  
 Query Match 0.9%; Score 22.2; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 1.5e+03;  
 Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 2270 GACAGGGTTTACCGGTGTAGCCAGGATG 2298  
 Db 29 GATGGGGTTTCACRGTGTGGCCAGGTG 1  
 RESULT 491  
 AAV29285  
 ID AAV29285 standard; cDNA; 22 BP.  
 XX  
 AC AAV29285;  
 XX  
 DT 21-AUG-1998 (first entry)  
 XX  
 DE Nucleotide sequence of PCR primer P2.  
 XX  
 KW Human; tumorigenesis gene; T-gene; PLAG2; PLAG1; CTNNB1; antibody;  
 KW benign tumour; malignant tumour; leukaemia; lymphoma; cancer; inhibition;  
 KW  
 Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2338 TCCCAAGTGTGGGATTACAG 2359  
 Db 1 TCCCAAGTGTGGGATTACAG 22  
 RESULT 492  
 AAC69376/c  
 ID AAC69376 standard; DNA; 22 BP.  
 XX  
 AC AAC69376;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 BAC contig polymorphic site, SEQ ID NO:275.  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW  
 Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2188 TTCTCTGCTCAGCTCCCAA 2209  
 Db 22 TTCTCTGCTCAGCTCCCAA 1  
 RESULT 493  
 AAZ89376/c  
 ID AAZ89376 standard; DNA; 22 BP.  
 XX  
 AC AAZ89376;  
 XX  
 DT 15-JUN-2000 (first entry)  
 XX  
 DE Human mdm-2 PCR primer mdm2Pr21.  
 XX

KW Human; mdm-2; PCR primer; reaction container; quantitation; diagnosis;  
 KW food analysis; ss.  
 Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1638 GGTGCGACCTAAAAAATGGTTGCA 1659  
 Db 22 GGTGCGACCTAAAAAATGGTTGCA 1  
 RESULT 494  
 AA97661/c  
 ID AA97661 standard; DNA; 22 BP.  
 XX  
 AC AA97661;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Human MDM2 reverse RT-PCR primer 1.  
 XX  
 KW Pseudocyclic oligonucleotide; functional segment; protective segment;  
 KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;  
 KW  
 Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 679 GTGAGAACAGGTGTCACTTGA 700  
 Db 22 GTGAGAACAGGTGTCACTTGA 1  
 RESULT 495  
 AAF77570  
 ID AAF77570 standard; DNA; 22 BP.  
 XX  
 AC AAF77570;  
 XX  
 DT 29-MAY-2001 (first entry)  
 XX  
 DE Human mdm2 RNA PCR primer #1.  
 XX  
 KW Human; p53; proliferative disease; diterpenoid triepoxides;  
 KW multi-drug resistance; cancer; restenosis; atherosclerosis; psoriasis;  
 KW  
 Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 639 GTCAATCAGCAGGAATCATCGG 660  
 Db 1 GTCAATCAGCAGGAATCATCGG 22  
 RESULT 496  
 AAC87596  
 ID AAC87596 standard; DNA; 22 BP.  
 XX  
 AC AAC87596;  
 XX  
 DT 16-MAR-2001 (first entry)  
 XX  
 DE Human Alu sequence PCR primer, CL1.  
 XX  
 KW Human; keratinocyte growth factor; KGF; chromosome 9p11; abnormality;  
 KW cancer; miscarriage; spontaneous abortion; genetic susceptibility;  
 KW  
 Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2338 TCCCAAAAGTGTGGGATTACAG 2359
Db 1 TCCCAAAAGTGTGGGATTACAG 22

RESULT 497
AAF88160
ID AAF88160 standard; DNA; 22 BP.
XX
AC
XX
AC AAF88160;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human thyroid malfunction-associated protein RITA PCR primer #1.
KW KRAB domain; hyperplasia; thyroid; tumor; zinc finger motif; primer;
KW cytosstatic; antithyroid; gene therapy; chromosome 19; 19q13; ss.

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAAAGTGTGGGATTACAG 2359
Db 1 TCCCAAAAGTGTGGGATTACAG 22

RESULT 498
ABL60507/c
ID ABL60507 standard; DNA; 22 BP.
XX
AC ABL60507;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA amplifying RT-PCR reverse primer.
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 679 GTGAGAACAGGTGCACCTTGA 700
Db 22 GTGAGAACAGGTGCACCTTGA 1

RESULT 499
ADE12182
ID ADE12182 standard; DNA; 22 BP.
XX
AC ADE12182;
XX
DT 29-JAN-2004 (first entry)
XX
DE PCR primer #1 for mdm2 cDNA from human MCF-7 (breast cancer) cell line.
KW Tumour; synergistic combination therapy; tumour cell; p21waft1/cipl;
KW diterpenoid triepoxide; vinca alkaloid; triptolide; anti-proliferative;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 GTCAATCAGCAGGAATCATCGG 660
Db 1 GTCAATCAGCAGGAATCATCGG 22

RESULT 500
ADK66043/c
ID ADK66043 standard; DNA; 22 BP.
XX
AC
XX
DT 06-MAY-2004 (first entry)
XX
DE Standardized polynucleotide system polynucleotide #9 PCR primer #2.
KW ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1638 GGTCGACCTAAAAAATGTTGCA 1659
Db 22 GGTCGACCTAAAAAATGTTGCA 1

RESULT 501
ADK66047/c
ID ADK66047 standard; DNA; 22 BP.
XX
AC
XX
DT 06-MAY-2004 (first entry)
XX
DE Standardized polynucleotide system polynucleotide #10 PCR primer #2.
KW ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1253 CCTTCCATCACATTCGACACAGA 1274
Db 22 CCTTCCATCACATTCGACACAGA 1

RESULT 502
ADG72449
ID ADG72449 standard; DNA; 22 BP.
XX
AC
XX
DT 11-MAR-2004 (first entry)
XX
DE PCR primer #1 for human mdm2 cDNA.
KW Hyperproliferative disorder; antiproliferative; diterpenoid triepoxide;
KW tumour; p21; waf1/cipl; carcinoma; cancer; multi-drug resistance; p53;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 GTCAATCAGCAGGAATCATCGG 660
Db 1 GTCAATCAGCAGGAATCATCGG 22

RESULT 503
AAF69748
ID AAF69748 standard; DNA; 23 BP.
XX
AC AAF69748;
XX
DT 18-APR-2001 (first entry)
XX
DE Human IL4Ralpha gene PCR primer #84.

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XX Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; PCR primer; ss.

Query Match      0.9%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2233 CCACCACACCTGGCTAAATTTT 2254
Db 1 CCACCACACCTGGCTAAATTTT 22

RESULT 504
AAL56647/c
ID AAL56647 standard; DNA; 24 BP.
XX
AC AAL56647;
XX
DT 09-OCT-2003 (first entry)
DE
DE HS2+ primer nested for HS3+, which amplifies the human tp53 gene.
XX
KW Genomics; DNA sequencing; random fragmentation; primer linked fragment;
KW HS3+; positional amplification; PCR; primer; ss; human; tp53; HS2+.

Query Match      0.9%; Score 22; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTACCCAGGATGGTCTCGATC 2307
Db 22 GTTACCCAGGATGGTCTCGATC 1

RESULT 505
ADB04763
ID ADB04763 standard; DNA; 25 BP.
XX
AC ADB04763;
XX
DT 20-NOV-2003 (first entry)
DE
DE Human MDZ7 scanning oligonucleotide SEQ ID 5749.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGG 2295
Db 4 GGGTTTCACCGTGTAGCCAGG 25

RESULT 506
AAA04309
ID AAA04309 standard; DNA; 29 BP.
XX
AC AAA04309;
XX
DT 22-MAY-2000 (first entry)
DE
DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22; DB 1; Length 29;
Best Local Similarity 91.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 2231 TGCACACACCTGGCTAAATTTT 2254
Db 6 TGCACACACCTGGCTAAATTTT 29

RESULT 507
AAA03981/c
ID AAA03981 standard; DNA; 29 BP.
XX
AC AAA03981;
XX
DT 22-MAY-2000 (first entry)
DE
DE Polymorphic fragment of hypertension associated gene APOC3.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22; DB 1; Length 29;
Best Local Similarity 91.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2349 TGGGATTACAGGCATGAGCCACCG 2372
Db 29 TGGGATTACAGGCATGAGCCACCTG 6

RESULT 508
AAF84351/c
ID AAF84351 standard; DNA; 25 BP.
XX
AC AAF84351;
XX
DT 20-JUN-2001 (first entry)
DE
DE Human CYP2C18i PCR primer #7.
XX
KW Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C18i; ss.

Query Match      0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2269 AGACAGGGTTTCACCGTGTAGCCA 2293
Db 25 AGACAGGGTTTCACCATGTTGGCCA 1

RESULT 509
ADB04739
ID ADB04739 standard; DNA; 25 BP.
XX
AC ADB04739;
XX
DT 20-NOV-2003 (first entry)
DE
DE Human MDZ7 scanning oligonucleotide SEQ ID 5725.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2248 AATTTTGTACTTTTAGTAGACAC 2272
Db 1 AATATTTTGTATTTTAGTAGACAC 25

RESULT 510

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ADB04737
ID ADB04737 standard; DNA; 25 BP.
XX
AC ADB04737;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5723.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2246 CTAATTTTGTACTTTTAGTAGAG 2270
Db 1 CTAATATTTGTATTTTAGTAGAG 25

RESULT 511
ADB04667
ID ADB04667 standard; DNA; 25 BP.
XX
AC ADB04667;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5653.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2176 GGGTTCGACCACTTCCTGCCTCA 2200
Db 1 GGGTTCACACCACTTCCTGCTCA 25

RESULT 512
ADB04738
ID ADB04738 standard; DNA; 25 BP.
XX
AC ADB04738;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5724.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2247 TAATTTTGTACTTTTAGTAGAGA 2271
Db 1 TAATATTTGTATTTTAGTAGAGA 25

RESULT 513
ADB04743
ID ADB04743 standard; DNA; 25 BP.
XX
AC ADB04743;
XX
DT 20-NOV-2003 (first entry)
XX
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DE Human MD27 scanning oligonucleotide SEQ ID 5729.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGG 2276
Db 1 TTTTGTATTTTAGTAGACAGGG 25

RESULT 514
ADB04674
ID ADB04674 standard; DNA; 25 BP.
XX
AC ADB04674;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5660.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2183 CACCATTCCTCGCTCAGCTCCC 2207
Db 1 CACCATTCCTCGCTCAGCTCCC 25

RESULT 515
ADB04668
ID ADB04668 standard; DNA; 25 BP.
XX
AC ADB04668;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5654.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2177 GGTTCGACCACTTCCTGCCTCAG 2201
Db 1 GGTTCACACCACTTCCTGCTTCAG 25

RESULT 516
AAH91552
ID AAH91552 standard; DNA; 27 BP.
XX
AC AAH91552;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #627.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
Query Match 0.9%; Score 21.8; DB 1; Length 27;
Best Local Similarity 88.5%; Pred. No. 1.6e+03;
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Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2335 GCCTCCCAAGTCTGGGATTACAGG 2360
Db 1 GCCTCCCAAGTCTGGGATTACAGG 26

RESULT 517
ADO12902
ID ADO12902 standard; DNA; 29 BP.
XX
AC ADO12902;
XX
DT 15-JUL-2004 (first entry)
DE Single multiplex PCR primer #2274.
XX
KW ss; primer; simultaneous amplification;
KW single multiplex polymerase chain reaction; multifactorial disease;
Query Match 0.9%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2332 TCGGCTCCCAAGTCTGGGATTA 2356
Db 5 TCGGCTCCCAAAATCTGGGATTA 29

RESULT 518
ADO12945/c
ID ADO12945 standard; DNA; 29 BP.
XX
AC ADO12945;
XX
DT 15-JUL-2004 (first entry)
DE Single multiplex PCR primer #2317.
XX
KW ss; primer; simultaneous amplification;
KW single multiplex polymerase chain reaction; multifactorial disease;
Query Match 0.9%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2332 TCGGCTCCCAAGTCTGGGATTA 2356
Db 25 TCGGCTCCCAAAATCTGGGATTA 1

RESULT 519
AAT12509
ID AAT12509 standard; DNA; 28 BP.
XX
AC AAT12509;
XX
DT 09-SEP-1996 (first entry)
DE
DE Primer Alu B corresp. to bases 294-267.
KW Primer; PCR; polymerase chain reaction; amplification; Alu repeat; ss;
KW quantitation; internal standard; plasmid; contamination; therapeutic.
Query Match 0.9%; Score 21.6; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2100 GAGACCGAGTCTGCTGTACCCAGG 2127
Db 1 GAGACAGAGTCTGCTGTGCGCCAGG 28

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RESULT 520
AAX83037/c
ID AAX83037 standard; DNA; 23 BP.
XX
AC AAX83037;
XX
DT 31-AUG-1999 (first entry)
DE
DE Primer E2C to isolate human WRN gene 3' exons.
KW Human; WRN; Werner's syndrome; detection; diagnosis; autosomal;
KW recessive disorder; phenotype; primer; RT-PCR; amplification; ss.
Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2336 CCTCCCAAGTCTGGGATTACA 2358
Db 23 CCTCCCAAGTCTGGGATTACA 1

RESULT 521
ADH47847
ID ADH47847 standard; DNA; 23 BP.
XX
AC ADH47847;
XX
DT 25-MAR-2004 (first entry)
DE
DE NOV14 PCR primer, SEQ ID 260.
XX
KW Antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2097 TTTGAGACCGAGTCTTGCTGT 2119
Db 1 TTTGAGACCGAGTCTTGCTGT 23

RESULT 522
ADA74797/c
ID ADA74797 standard; DNA; 23 BP.
XX
AC ADA74797;
XX
DT 20-NOV-2003 (first entry)
DE
DE PCR primer F1209 used to sequence human LDLR DNA.
KW discriminant function coefficient; DC; ethnic affiliation; haplotype;
KW descent predictor; forensic analysis; Alu repeat; hot spot; diversity;
Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2344 AGTGCTGGGATTACAGCGATGAG 2366
Db 23 AGTGCTGGGATTACAGCGGTGAG 1

RESULT 523
ADP68378
ID ADP68378 standard; DNA; 23 BP.
XX
AC ADP68378;
XX
DT 12-AUG-2004 (first entry)

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XX PCR primer used to amplify human NOV14 DNA (Ag210) SeqID 262.
DE human; PCR; ss; NOVX; Alzheimer's disease; Huntington's; inflammatory;
KW Crohn's disease; rheumatoid arthritis; immunological; endocrine;
KW

Query Match      0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTTGCTCTGT 2119
DB 1 TTTGAGACCGAGTCTTGCTCTGT 23

RESULT 524
ADL25729
ID ADL25729 standard; DNA; 23 BP.
XX
AC ADL25729;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOVX gene, reverse PCR primer #29.
XX
KW ss; PCR; primer; Cytostatic; Neuroprotective; Immunosuppressive;
KW Gene therapy; Vaccine; human; neurodegenerative disorder;

Query Match      0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTTGCTCTGT 2119
DB 1 TTTGAGACCGAGTCTTGCTCTGT 23

RESULT 525
ABV75668/c
ID ABV75668 standard; DNA; 24 BP.
XX
AC ABV75668;
XX
DT 28-JAN-2003 (first entry)
XX
DE Human FD16.06 PCR primer 2.
XX
KW Human; FD16.06; cancer; HIV; PCR; primer; ss.
XX

Query Match      0.9%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2108 GTCTTGCTCTGTACCCAGGCTG 2130
DB 24 GTCTTGCTCTGTGCCAGGCTG 2

RESULT 526
ABQ83396
ID ABQ83396 standard; DNA; 24 BP.
XX
AC ABQ83396;
XX
DT 21-JAN-2003 (first entry)
XX
DE Human proteasome p40.5 subunit 20.24 PCR primer 2 SEQ ID NO:4.
XX
KW Human; proteasome p40.5 subunit 20.24; malignant tumour; haemopathy;
KW Human immunodeficiency virus infection; HIV infection; inflammation;

Query Match      0.9%; Score 21.4; DB 1; Length 24;
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Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2266 TAGAGACAGGGTTTTCACCGTGT 2288
DB 1 TAGAGACAGGGTTTTCACCGTGT 23

RESULT 527
ADE43814/c
ID ADE43814 standard; DNA; 24 BP.
XX
AC ADE43814;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human LIPA PCR primer, SEQ ID 419.
XX
KW Neurodegenerative disease; uPA; SNGG; IDE; KNSL1; LIPA; TNFRSF6;
KW Alzheimer's disease; neuroprotective; neurotropic; gene therapy;

Query Match      0.9%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACAGCGGTTTCACC 2283
DB 23 TTTAGTAGATACAGGGTTTCACC 1

RESULT 528
ADL06343/c
ID ADL06343 standard; DNA; 24 BP.
XX
AC ADL06343;
XX
DT 06-MAY-2004 (first entry)
XX
DE RT-PCR primer #1 for cDNA encoding human protein-13.2.
XX
KW Human; protein-13.2; site-specific recombinase;
KW growth development disorder; tumour; reverse transcriptase-PCR; RT-PCR;

Query Match      0.9%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCCTCCC 2207
DB 24 CGATTCTCTGCTCAGCCTCCC 2

RESULT 529
ADH54292/c
ID ADH54292 standard; DNA; 24 BP.
XX
AC ADH54292;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human neurodegenerative disease-related PCR primer SeqID419.
XX
KW human; neurodegenerative disease; urokinase plasminogen activator; uPA;
KW gamma-synuclein; SNGG; insulin degrading enzyme; IDE;

Query Match      0.9%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACAGCGGTTTCACC 2283
DB 23 TTTAGTAGATACAGGGTTTCACC 1
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RESULT 530
AAH16609
ID AAX16609 standard; DNA; 25 BP.
XX AC
XX AAX16609;
DT 29-APR-1999 (first entry)
XX AC
DE Interleukin 1 (44112332) haplotype PCR primer #3.
KW Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata;
KW coronary artery disease; osteoporosis; nephropathy; diabetes mellitus;

Query Match 0.9%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGGAGCCACCG 2372
DB 1 GGGATTACAGGCGTGGAGCCACCG 23

RESULT 531
AAD27391
ID AAD27391 standard; DNA; 25 BP.
XX AC
XX AAD27391;
DT 18-APR-2002 (first entry)
XX AC
DE PCR primer #1, used for genotyping human IL-1A (gz5/gz6) marker.
KW Human; interleukin-1; inflammatory disorder; coronary artery disease;
KW periodontal disease; Alzheimer's disease; atherosclerosis; osteoporosis;

Query Match 0.9%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGGAGCCACCG 2372
DB 1 GGGATTACAGGCGTGGAGCCACCG 23

RESULT 532
ADN48862
ID ADN48862 standard; DNA; 25 BP.
XX AC
XX ADN48862;
DT 15-JUL-2004 (first entry)
XX AC
DE Human interleukin-1A (gz5/gz6) amplifying PCR primer #1.
KW Early-onset menopause; EOM; diagnosis; therapy; human; interleukin-1A;
KW IL-1A; PCR; primer; ss.

Query Match 0.9%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGGAGCCACCG 2372
DB 1 GGGATTACAGGCGTGGAGCCACCG 23

RESULT 533
AAH39523
ID AAH39523 standard; DNA; 27 BP.
XX AC
XX AAH39523;

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DT 14-AUG-2001 (first entry)
XX AC
XX SNP specific SNPE primer SEQ ID 2319.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 21.2; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.7e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2257 TACTTTTAGTAGACAGAGGTTTCACC 2283
DB 1 TATTTTAGTAGAGATGGGNTTTCACC 27

RESULT 534
AAH38059/c
ID AAH38059 standard; DNA; 27 BP.
XX AC
XX AAH38059;
DT 14-AUG-2001 (first entry)
XX AC
DE SNP specific SNPE primer SEQ ID 855.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 21.2; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.7e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2142 GTGATCTTGCTCACTGCAAGCTCTGC 2168
DB 27 GTGATCTTAGTCACTGCAACCTCCGC 1

RESULT 535
AAH40803
ID AAH40803 standard; DNA; 27 BP.
XX AC
XX AAH40803;
DT 14-AUG-2001 (first entry)
XX AC
DE SNP specific SNPE primer SEQ ID 3599.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 21.2; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.7e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2344 AGTGTGGGATTACAGGCATGCCAC 2370
DB 1 AGTGCTGAAATTAACAGNCGTGACCCAC 27

RESULT 536
AAV27991/c
ID AAV27991 standard; DNA; 21 BP.
XX AC
XX AAV27991;
DT 25-SEP-1998 (first entry)
XX AC
DE Ataxia telangiectasia exon 17 primer 2.
KW ss; PCR; primer; amplification; ataxia telangiectasia; diagnosis; human;
KW radiation; breast cancer.

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Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGGG 2142
    |||||
Db 21 CCCAGGCTGGAGTGCAGTGGG 1

RESULT 537
AAZ37739
ID AAZ37739 standard; DNA; 21 BP.
XX
AC AAZ37739;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 real-time forward PCR primer #269.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCATAATGTGCAATACCAACA 327
    |||||
Db 1 GGCATAATGTGCAATACCAACA 21

RESULT 538
AAX35114
ID AAX35114 standard; DNA; 21 BP.
XX
AC AAX35114;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S7-3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
    inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1007 AGGTGATTGGTTGGATCAGGA 1027
    |||||
Db 1 AGGTGATTGGTTGGATCAGGA 21

RESULT 539
AAX35136/c
ID AAX35136 standard; DNA; 21 BP.
XX
AC AAX35136;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7-3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
    inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1007 AGGTGATTGGTTGGATCAGGA 1027
    |||||
Db 21 AGGTGATTGGTTGGATCAGGA 1

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RESULT 540
AAA62471/c
ID AAA62471 standard; DNA; 21 BP.
XX
AC AAA62471;
XX
DT 21-NOV-2000 (first entry)
XX
DE Human SECX 2826468 forward primer.
XX
KW Human; secreted protein; SECX; cancer; cytostatic; vaccine; primer;
    expression analysis; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCCTGACCTCGTG 2320
    |||||
Db 21 TCTCGATCTCCTGACCTCGTG 1

RESULT 541
AAA97663/c
ID AAA97663 standard; DNA; 21 BP.
XX
AC AAA97663;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human MDM2 reverse RT-PCR primer 2.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
    nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 726 GTACAAGAGCTTCAGGAAGAG 746
    |||||
Db 21 GTACAAGAGCTTCAGGAAGAG 1

RESULT 542
AAA50950/c
ID AAA50950 standard; DNA; 21 BP.
XX
AC AAA50950;
XX
DT 27-OCT-2000 (first entry)
XX
DE Human mdm2 PCR primer #2.
XX
KW Fluorescent protein; fluorescence labelling; fusion protein; human;
    PCR primer; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 GTGCTAACTATTTCCTCCCTAG 1787
    |||||
Db 21 GTGCTAACTATTTCCTCCCTAG 1

RESULT 543
AAD03620/c
ID AAD03620 standard; DNA; 21 BP.
XX
AC AAD03620;

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XX 19-JUN-2001 (first entry)
DT
XX Human marathon cDNA library (Burke's lymphoma) amplifying PCR primer #2.
DE
XX Anthozoa; Chromoprotein; fluorescent protein; sunscreen; biosensor;
KW analyte detection assay; selectable marker; recombinant DNA application;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 GTGCTAACTATTTCCTCCCTAG 1787
DB 21 GTGCTAACTATTTCCTCCCTAG 1

RESULT 544
AAF95738
ID AAF95738 standard; DNA; 21 BP.
XX
AC AAF95738;
XX
DT 06-JUN-2001 (first entry)
DE Human gene single nucleotide polymorphism #499.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2336 CCTCCCAAAGTCTGGGATTA 2356
DB 1 CCTCCCAAAGTCTGGGATTA 21

RESULT 545
AAF80893
ID AAF80893 standard; DNA; 21 BP.
XX
AC AAF80893;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 forward primer.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAATGTGCAATACCAACA 327
DB 1 GGCAATGTGCAATACCAACA 21

RESULT 546
AAH40326
ID AAH40326 standard; DNA; 21 BP.
XX
AC AAH40326;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific lower PCR primer SEQ ID 3122.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

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Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGCTCTCGAT 2306
DB 1 GTTAGCCAGGATGCTCTCGAT 21

RESULT 547
AAH22714/c
ID AAH22714 standard; DNA; 21 BP.
XX
AC AAH22714;
XX
DT 07-SEP-2001 (first entry)
DE Human secreted protein (SECX) specific oligo.
XX
KW Secreted protein; SECX; cancer; human; cytostatic; gene therapy;
KW PCR primer; probe; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGTG 2320
DB 21 TCTCGATCTCTGACCTCGTG 1

RESULT 548
AAS29508
ID AAS29508 standard; DNA; 21 BP.
XX
AC AAS29508;
XX
DT 21-NOV-2001 (first entry)
DE Forward PCR primer used to amplify human mdm2 mRNA.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAATGTGCAATACCAACA 327
DB 1 GGCAATGTGCAATACCAACA 21

RESULT 549
ABS98157
ID ABS98157 standard; DNA; 21 BP.
XX
AC ABS98157;
XX
DT 23-DEC-2002 (first entry)
DE Human multidrug resistance gene polymorphic sequence #59.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTAGCCAGGATG 2298
DB 1 TTCACCGTGTAGCCAGGATG 2298

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Db      1  TTCACCGTGTAGCCAGGATG 21

RESULT 550
ABL60509/c
ID  ABL60509 standard; DNA; 21 BP.
XX
AC  ABL60509;
XX
DT  12-AUG-2002 (first entry)
XX
DE  Human MDM2 mRNA amplifying RT-PCR reverse primer 2.
XX
KW  Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
    nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;
    MDM2;
    anticisense therapy; human; antisense; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      726  GTACAAGAGCTTCAGGAAGAG 746
        |||||
Db      21  GTACAAGAGCTTCAGGAAGAG 1

RESULT 551
ADD21704
ID  ADD21704 standard; DNA; 21 BP.
XX
AC  ADD21704;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2-specific PCR primer #1.
XX
KW  anticisense oligonucleotide; human; mdm2; hyperproliferation;
    hyperproliferative disorder; cancer; psoriasis; fibrosis;
    anticisense therapy; human; antisense; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      307  GGCAAAATGTGCAATACCAACA 327
        |||||
Db      1  GGCAAAATGTGCAATACCAACA 21

RESULT 552
AAD64997
ID  AAD64997 standard; DNA; 21 BP.
XX
AC  AAD64997;
XX
DT  11-MAR-2004 (first entry)
XX
DE  Human mouse double minute (MDM2) sense oligonucleotide S7-3.
XX
KW  MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
    therapeutic; antisense therapy; human; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1007  AGGTGATTGGTTGGATCAGGA 1027
        |||||
Db      1  AGGTGATTGGTTGGATCAGGA 21

RESULT 553
AAD65018/c
ID  AAD65018 standard; DNA; 21 BP.
XX

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AC  AAD65018;
XX
DT  11-MAR-2004 (first entry)
XX
DE  Human mouse double minute (MDM2) antisense oligonucleotide AS7-3.
XX
KW  MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
    therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1007  AGGTGATTGGTTGGATCAGGA 1027
        |||||
Db      21  AGGTGATTGGTTGGATCAGGA 1

RESULT 554
ADK66046
ID  ADK66046 standard; DNA; 21 BP.
XX
AC  ADK66046;
XX
DT  06-MAY-2004 (first entry)
XX
DE  Standardized polynucleotide system polynucleotide #10 PCR primer #1.
XX
KW  ss; standardized polynucleotide system; medical diagnosis;
    functional genomics; sample analysis; pharmacogenomics; sample analysis;
    anticisense therapy; human; antisense; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      359  CTCACAGATTCACGCTTCGGA 379
        |||||
Db      1  CTCACAGATTCACGCTTCGGA 21

RESULT 555
ADI23732
ID  ADI23732 standard; DNA; 21 BP.
XX
AC  ADI23732;
XX
DT  06-MAY-2004 (first entry)
XX
DE  Human LPDLR PCR primer #12.
XX
KW  lipase; LPDL; LPDLR; lipase deficiency; atherosclerosis;
    fatty liver disease; dyslipidaemia; hypercholesterolaemia;
    anticisense therapy; human; antisense; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2346  TGCTGGGATTACGGCATGAG 2366
        |||||
Db      1  TGCTGGGATTACGGCATGAG 21

RESULT 556
AAF93028/c
ID  AAF93028 standard; DNA; 22 BP.
XX
AC  AAF93028;
XX
DT  17-MAY-2001 (first entry)
XX
DE  Polymorphic sequence for ABC1 polymorphic site #38.
XX
KW  High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

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XX
Query Match      0.9%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2188 TTCTCTGCTCAGCTGCCCA 2209
DB 22 TTCTCTGCTTACGCTGCCCA 1

RESULT 557
ADB04762
ID ADB04762 standard; DNA; 25 BP.
XX
AC ADB04762;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5748.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTTAGCCAG 2294
DB 5 GGGTTTCACCGTGTTAGCCAG 25

RESULT 558
AAF92891
ID AAF92891 standard; DNA; 24 BP.
XX
AC AAF92891;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 transcription factor binding site #52.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTGATCC 2324
DB 1 CTCGATCTCTGACCTCGTGATCC 24

RESULT 559
AAF92843
ID AAF92843 standard; DNA; 24 BP.
XX
AC AAF92843;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 transcription factor binding site #6.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2293 AGGATGGTCTCGATCTCTGACCT 2316
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Db 1 AGCTGGTCTCGAAGTCTCTGACCT 24

RESULT 560
AAI65098
ID AAI65098 standard; DNA; 24 BP.
XX
AC AAI65098;
XX
DT 28-NOV-2001 (first entry)
XX
DE Human zinc finger protein 15 PCR primer #1.
XX
KW Human; zinc finger protein 15; cytostatic; virucidal; immunomodulatory;
KW antiinflammatory; haemostatic; gene therapy; malignant neoplasm;

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2349 TGGGATTACAGGCATGAGCCACCG 2372
DB 1 TGGGATTACAGGTGTGAGCCACCG 24

RESULT 561
ABK51390
ID ABK51390 standard; DNA; 24 BP.
XX
AC ABK51390;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human Mch2 protein 9.57, RT-PCR primer 2.
XX
KW Human; Mch2 protein 9.57; cancer; human immunodeficiency virus infection;
KW HIV; reverse transcriptase PCR; RT-PCR; primer; ss.

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2102 GACCGAGTCTTGCTCTGTACCCA 2125
DB 1 GACAGAGTCTTGCTCTGTGCCCA 24

RESULT 562
ABL56667
ID ABL56667 standard; DNA; 24 BP.
XX
AC ABL56667;
XX
DT 30-JUL-2002 (first entry)
XX
DE PCR primer #2 for human prollyl oligomeric peptidase 13.2 cDNA.
XX
KW Human; prollyl oligomeric peptidase 13.2; enzyme; angiocardiodiopathy;
KW nervous system retrograde disease; gene therapy; PCR; primer; ss.

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTTGCTCTGTACC 2123
DB 1 GAGACAGAGTCTTGCTCTGTGCC 24

RESULT 563
AAL46337/c
ID AAL46337 standard; DNA; 24 BP.
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XX AAL46337;
AC
XX
DT 19-JUL-2002 (first entry)
XX
XX Human M30 protein coding sequence PCR primer hm30_nn_s5.
XX
XX Neurodegenerative disease; M30; M31; M32; M33; stroke;
KW fragile X syndrome; Huntington's disease; Parkinson's disease;
KW
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2106 GAGTCTTGCTCTGTACCCAGGCT 2129
|||||
Db 24 GAGTCTTGCTCTGTGCTAGGCT 1

RESULT 564
AAS20575
ID AAS20575 standard; DNA; 24 BP.
XX
XX AAS20575;
AC
XX
DT 23-APR-2002 (first entry)
XX
XX Human uterine globulin 12 cDNA RT-PCR primer #2.
XX
XX Human; uterine globulin 12; malignant tumour; cancer; haemopathy;
KW human immunodeficiency virus; HIV; immunological disease; inflammation;
KW
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2264 AGTAGACAGCGGTTTCCCGTGT 2287
|||||
Db 1 AGTAGAACAGCGGTTTCCACCATGT 24

RESULT 565
ABQ77823
ID ABQ77823 standard; DNA; 24 BP.
XX
XX ABQ77823;
AC
XX
DT 20-DEC-2002 (first entry)
XX
XX Human protein phosphatase 13.64 RT-PCR primer, SEQ ID NO:3.
XX
XX Human; protein phosphatase 13.64; recombinant production; gene therapy;
KW female genital development disorder; abnormal female sex characteristic;
KW
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2265 GTAGACAGCGGTTTCCCGTGT 2288
|||||
Db 1 GTAGAGATGGGGTTTCCCGGTGT 24

RESULT 566
ABT08420
ID ABT08420 standard; DNA; 24 BP.
XX
XX ABT08420;
AC
XX
DT 27-NOV-2002 (first entry)
XX
XX Human PSF promoter PCR primer SEQ ID NO: 55.
XX
XX

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KW Human; cyclin-dependent kinase; CDK; cyclin-dependent kinase inhibitor;
KW inhibitor; cancer; age-related disease; promoter; atherosclerosis;
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2342 AAAGTCTGGGATTACAGGCATGA 2365
|||||
Db 1 AAAGTCTGGGATTAGAGGGGTGA 24

RESULT 567
ABZ57256/c
ID ABZ57256 standard; DNA; 24 BP.
XX
XX ABZ57256;
AC
XX
DT 01-APR-2003 (first entry)
XX
XX Human RAGE4 renal cancer antigen 11.44 RT-PCR primer, SEQ ID NO:3.
XX
XX Human; RAGE4 renal cancer antigen 11.44; recombinant production;
KW gene therapy; renal tumour; renal cancer; cytostatic;
KW
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2260 TTTTGTAGACAGCGGTTTTCACC 2283
|||||
Db 24 TTTTGTAGACAGCGGATTTCACC 1

RESULT 568
ACA90120
ID ACA90120 standard; DNA; 24 BP.
XX
XX ACA90120;
AC
XX
DT 10-JUL-2003 (first entry)
XX
XX Human kinesin gene(s) antisense oligonucleotide #3.
XX
XX Human; ss; antisense; kinesin; CENP-E; Eg5; MCAK; colon cancer; stroke;
KW T cell cancer; B cell lymphoma; pancreatic cancer; breast cancer;
KW
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2100 GAGACCGAGTCTTGCTCTGTTCACC 2123
|||||
Db 1 GAGACCGACTCTTGCTCTGTGTGCC 24

RESULT 569
ACF35685/c
ID ACF35685 standard; DNA; 24 BP.
XX
XX ACF35685;
AC
XX
DT 13-OCT-2003 (first entry)
XX
XX Human TGNP promoter amplifying forward primer.
XX
XX Trans-Golgi network integral membrane protein; TGNP; chromosome 2p11.2;
KW cytostatic; antiinflammatory; immunomodulator; neuroprotective; human;
KW
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2114 CTCTGTTACCCAGGCTGGAGTGCA 2137
DB 24 CTCTGTCACCCAGGCTTGAGTGCA 1

RESULT 570
ADG28972
ID ADG28972 standard; DNA; 24 BP.
XX
AC
XX ADG28972;
XX
DT 26-FEB-2004 (first entry)
XX
DE PCR primer SEQ ID 55 used to amplify human PSF promoter DNA.
XX
KW recombinant expression construct; cyclin-dependent kinase inhibitor; CDK;
KW virucide; cytostatic; neuroprotective; nootropic; antiarteriosclerotic;

Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTGTGGGATTACAGGCATGA 2365
DB 1 AAAGTGTGGGATTACAGGCATGA 24

RESULT 571
ADQ30417/c
ID ADQ30417 standard; DNA; 24 BP.
XX
AC ADQ30417;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human VRI exon 1d transcription factor binding fragment #136.
DE ds; VRI receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;

Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2340 CCAAGTGTGGATTACAGGCAT 2363
DB 24 CCAAGTGTGGATTACAGGCAT 1

RESULT 572
AAH38671
ID AAH38671 standard; DNA; 25 BP.
XX
AC AAH38671;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1467.
DE
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2249 ATTTTGTACTTTTAGTAGAGAC 2272
DB 1 AATTTTGTATTTTAGTAGAGAC 24

RESULT 573
AAH38231
ID AAH38231 standard; DNA; 25 BP.
XX
AC AAH38231;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1027.
DE
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2249 ATTTTGTACTTTTAGTAGAGAC 2272
DB 1 AATTTTGTATTTTAGTAGAGAC 24

RESULT 574
ADB04675
ID ADB04675 standard; DNA; 25 BP.
XX
AC ADB04675;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5661.
DE
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2184 ACCATTCTCTGCTCAGCTCCC 2207
DB 1 ACCATTCTCTGCTCAGCTCCC 24

RESULT 575
ADB04744
ID ADB04744 standard; DNA; 25 BP.
XX
AC ADB04744;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5730.
DE
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2253 TTGTGTAATTTTAGTAGAGACGGG 2276
DB 1 TTGTGTAATTTTAGTAGAGACGGG 24

RESULT 576
ADB04673
ID ADB04673 standard; DNA; 25 BP.
XX
AC ADB04673;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5659.

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XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2183 CACCAATTCCTCTGCTCAGCCTCC 2206
DB 2 CACCAATTCCTCTGCTCAGCCTCC 25

RESULT 577
ADB04664
ID ADB04664 standard; DNA; 25 BP.
XX
AC ADB04664;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5650.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 CCGGGTTCGACCAATTCCTCTGC 2196
DB 1 CCGGGTTCGACCAATTCCTCTGC 24

RESULT 578
ADB04736
ID ADB04736 standard; DNA; 25 BP.
XX
AC ADB04736;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5722.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2246 CTAATTTTGTACTTTTAGTAGA 2269
DB 2 CTAATTTTGTACTTTTAGTAGA 25

RESULT 579
ADB04740
ID ADB04740 standard; DNA; 25 BP.
XX
AC ADB04740;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5726.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 2249 ATTTTGTACTTTTAGTAGAGAC 2272
DB 1 ATATTTTGTATTTTAGTAGAGAC 24

RESULT 580
ADB04666
ID ADB04666 standard; DNA; 25 BP.
XX
AC ADB04666;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5652.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2176 GGGTTCGACCAATTCCTCTGCCTC 2199
DB 2 GGGTTCGACCAATTCCTCTGCCTC 25

RESULT 581
ADB04669
ID ADB04669 standard; DNA; 25 BP.
XX
AC ADB04669;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5655.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2178 GTTCGACCAATTCCTCTGCCTCAG 2201
DB 1 GTTCGACCAATTCCTCTGCCTCAG 24

RESULT 582
ADB04663
ID ADB04663 standard; DNA; 25 BP.
XX
AC ADB04663;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5649.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 CCGGGTTCGACCAATTCCTCTGC 2196
DB 2 CCGGGTTCGACCAATTCCTCTGC 25

RESULT 583
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ADB04742
ID ADB04742 standard; DNA; 25 BP.
XX
AC ADB04742;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5728.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGAGACAGG 2275
DB 2 TTTTGTATTTTAGTAGAGACGG 25

RESULT 584
ADJ94629
ID ADJ94629 standard; DNA; 25 BP.
XX
AC ADJ94629;
XX
XX 06-MAY-2004 (first entry)
XX
XX Promoter related PCR primer, SEQ ID 7.
XX
XX Promoter; human; fat cell; PCR; primer; ss.

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTCACC 2283
DB 1 TTTTAGTAGAGACAGGGTTTCACC 24

RESULT 585
AAZ37279/c
ID AAZ37279 standard; DNA; 27 BP.
XX
AC AAZ37279;
XX
XX 01-FEB-2000 (first entry)
XX
XX PCR primer for SGRF coding sequence.
XX
KW SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;
KW immune system; haematopoietic system; therapy; PCR primer; ss.

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2192 CCTGCTCAGCTCCCAATTAGCT 2215
DB 27 CCTGCTCAGCTCCCAAGCAGCT 4

RESULT 586
AAH39267
ID AAH39267 standard; DNA; 27 BP.
XX
AC AAH39267;
XX
XX 14-AUG-2001 (first entry)
XX
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DE SNP specific SNPE primer SEQ ID 2063.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2346 TGCTGGATTACAGGCATGAGCCACC 2371
DB 1 TGCTGNGATTATAGNCACGAGCCACC 26

RESULT 587
AAH91322/c
ID AAH91322 standard; DNA; 27 BP.
XX
AC AAH91322;
XX
XX 09-OCT-2001 (first entry)
XX
XX Human inflammatory bowel disease associated polymorphic site #397.
XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2185 CGATTCTCTGCTCAGCCTCCCAA 2209
DB 25 CGATTCTCTGCTCAGCCTCCCAA 1

RESULT 588
ACC84460
ID ACC84460 standard; DNA; 27 BP.
XX
AC ACC84460;
XX
XX 28-AUG-2003 (first entry)
XX
XX NTP peptide encoding sequence #7.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.

Query Match 0.9%; Score 20.6; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.8e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2331 CTGGGCTCCCAAGTGTGGATTAC 2357
DB 1 CTCAGCCTCCCAAGCAGCTGGATTAC 27

RESULT 589
AAC69375/c
ID AAC69375 standard; DNA; 22 BP.
XX
AC AAC69375;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human ABC1 BAC contig polymorphic site, SEQ ID NO:274.
XX
XX Human ABC1 cholesterol transporter; chromosome 9q31;
XX ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2188 TTCTCTGCTCAGCCTCCCA 2209
Db 22 TTCTCTGCTTAGCCTCCCA 1

RESULT 590
AAF84349/c
ID AAF84349 standard; DNA; 22 BP.
XX
AC AAF84349;
XX
XX 20-JUN-2001 (first entry)
XX
DE Human CYP2C181 PCR primer #5.
XX
KW Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C181; ss.
XX

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2344 AGTCTGGGATTACAGGCATGA 2365
Db 22 AATGCTGGGATTACAGGCATGA 1

RESULT 591
AAD31453/c
ID AAD31453 standard; DNA; 22 BP.
XX
AC AAD31453;
XX
XX 31-MAY-2002 (first entry)
XX
DE Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt1R.
KW Human; Van Buchem's disease; genomic deletion; craniofacial dysmorphism;
KW autosomal recessive disorder; chromosome 17; chromosome 17q21;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2187 ATTCTCTGCTCAGCCTCCCA 2208
Db 22 ATTCTCTGCTCAGCCTCCCA 1

RESULT 592
AAD31457/c
ID AAD31457 standard; DNA; 22 BP.
XX
AC AAD31457;
XX
XX 31-MAY-2002 (first entry)
XX
DE Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt3R.
KW Human; Van Buchem's disease; genomic deletion; craniofacial dysmorphism;
KW autosomal recessive disorder; chromosome 17; chromosome 17q21;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2187 ATTCTCTGCTCAGCCTCCCA 2208
Db 22 ATTCTCTGCTCAGCCTCCCA 1
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RESULT 593
ADB88578
ID ADB88578 standard; DNA; 22 BP.
XX
AC ADB88578;
XX
XX 04-DEC-2003 (first entry)
XX
DE Frizzled-4 (FZD4) modulating agent related oligo, SEQ ID No 25.
XX
KW Frizzled-4; FZD4; immunomodulatory compound; ophthalmological; vasotropic;
KW antiinflammatory; vulnery; osteopathic; antimicrobial; antipsoriatic;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2109 TCTTGCTCTGTACCCAGGCTG 2130
Db 1 TCTTGCTCTGTACCCAGGCTG 22

RESULT 594
ADB88579
ID ADB88579 standard; DNA; 22 BP.
XX
AC ADB88579;
XX
XX 04-DEC-2003 (first entry)
XX
DE Frizzled-4 (FZD4) modulating agent related oligo, SEQ ID No 26.
KW Frizzled-4; FZD4; immunomodulatory compound; ophthalmological; vasotropic;
KW antiinflammatory; vulnery; osteopathic; antimicrobial; antipsoriatic;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2109 TCTTGCTCTGTACCCAGGCTG 2130
Db 1 TCTTGCTCTGTACCCAGGCTG 22

RESULT 595
ADM65599
ID ADM65599 standard; DNA; 22 BP.
XX
AC ADM65599;
XX
XX 03-JUN-2004 (first entry)
XX
DE NRY polymorphism detection primer #505.
KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2092 TTTTCTTGTGAGACCGAGTCTTG 2113
Db 1 TTTTCTTGTGAGACCGAGTCTTG 22

RESULT 596
ADM65602
ID ADM65602 standard; DNA; 22 BP.
XX
AC ADM65602;
XX
XX 03-JUN-2004 (first entry)
XX
DT
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XX NRY polymorphism detection primer #507.
DE ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match      0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2092 TTTTGTGAGCCGAGTCTTG 2113
DB 1 TTTTGTGAGCCGAGTCTTG 22

RESULT 597
ADM65605
ID ADM65605 standard; DNA; 22 BP.
XX AC
XX ADM65605;
XX
DT 03-JUN-2004 (first entry)
XX
DE NRY polymorphism detection primer #509.
KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match      0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2092 TTTTGTGAGCCGAGTCTTG 2113
DB 1 TTTTGTGAGCCGAGTCTTG 22

RESULT 598
ABS58183/c
ID ABS58183 standard; DNA; 24 BP.
XX AC
XX ABS58183;
XX
DT 26-FEB-2003 (first entry)
XX
DE RT-PCR primer #1 for cDNA encoding human zinc finger protein 10.01.
KW Human; zinc finger protein 10.01; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection; inflammation;
Query Match      0.9%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCGTGAGCCACCG 2372
DB 24 GGATTACAGGCGTGAGCCACCG 3

RESULT 599
ABA96912/c
ID ABA96912 standard; DNA; 24 BP.
XX AC
XX ABA96912;
XX
DT 15-MAY-2002 (first entry)
XX
DE Human arginase 9 RT-PCR primer, SEQ ID NO:3 version #1.
KW Human; arginase 9; recombinant production; argininaemia;
KW arginine metabolism disorder; urea metabolism disorder;
Query Match      0.9%; Score 20.4; DB 1; Length 24;

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Best Local Similarity 95.5%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCGTGAGCCACCG 2372
DB 24 GGATTACAGGCGTGAGCCACCG 3

RESULT 600
ABX15537
ID ABX15537 standard; DNA; 25 BP.
XX AC
XX ABX15537;
XX
DT 11-APR-2003 (first entry)
XX
DE Human IL-1 genotyping marker gz51gz6 primer #1.
KW Human; ss; PCR; primer; interleukin-1; IL-1; marker gz51gz6; nephropathy;
KW inflammatory disease; Systemic Inflammatory Response; SIRS; genotyping;
Query Match      0.9%; Score 20.4; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGAGCCACCG 2372
DB 1 GGGATTACAGGCGTGAGCCACCG 23

RESULT 601
AAH38991/c
ID AAH38991 standard; DNA; 25 BP.
XX AC
XX AAH38991;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1787.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCTCCCAAGTGCTG 2350
DB 25 CCCGCTTGACCTCCCAAGTGCTG 1

RESULT 602
AAH37598
ID AAH37598 standard; DNA; 25 BP.
XX AC
XX AAH37598;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific lower PCR primer SEQ ID 394.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2090 TATTTTGTGAGCCGAGTCTTG 2114
DB 1 TTTTGTGAGTGGAGTCTTG 25

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RESULT 603
AAH38423
ID AAH38423 standard; DNA; 25 BP.
XX
XX
AC AAH38423;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1219.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2185 CCATTCTCTGCTCAGCTCCCAA 2209
Db 1 CAATTCTCTGCTCAGCTCCCAA 25

RESULT 604
AAH40563/c
ID AAH40563 standard; DNA; 25 BP.
XX
XX
AC AAH40563;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 3359.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCTGCTCAGCTCCCAATTA 2212
Db 25 TTGTCCTGCTCAGCTCCCGATTA 1

RESULT 605
AAH37859
ID AAH37859 standard; DNA; 25 BP.
XX
XX
AC AAH37859;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 655.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCTGCTCAGCTCCCAATTA 2212
Db 25 TTGTCCTGCTCAGCTCCCGATTA 1

RESULT 606
AAH40067/c
ID AAH40067 standard; DNA; 25 BP.
XX
XX
AC AAH40067;
XX

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DT 14-AUG-2001 (first entry)
XX
XX
DE SNP specific SNPE primer SEQ ID 2863.
XX
XX
AC Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCTGCTCAGCTCCCAATTA 2212
Db 25 TTCTCTGCTCAGCTCCCGATTA 1

RESULT 607
ABL51377/c
ID ABL51377 standard; DNA; 25 BP.
XX
XX
AC ABL51377;
XX
DT 28-JUN-2002 (first entry)
XX
DE Mutant DSPP gene detection related 5' PCR primer D482932.
XX
KW Mutant DSPP gene detection; chromosome 4q21; dentin sialophosphoprotein;
KW hereditary opalescent dentin; periodontal; gene therapy; mineralisation;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2092 TTTTCTTGAGCCGAGCTTTGCTC 2116
Db 25 TTAATTTTGAGACAGAGTTTGCTC 1

RESULT 608
ADB04671
ID ADB04671 standard; DNA; 25 BP.
XX
XX
AC ADB04671;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5657.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2180 TCCACACATTCTCCTCCCTCAGCT 2204
Db 1 TCACACATTCTCCTCCTTCAGTCT 25

RESULT 609
ADB04676
ID ADB04676 standard; DNA; 25 BP.
XX
XX
AC ADB04676;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5662.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

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Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCTCCCAA 2209
DB 1 CCATTCTCTGCTCAGCTCCCGA 25

RESULT 610
ADB04670
ID ADB04670 standard; DNA; 25 BP.
XX
AC ADB04670;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5656.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MD24; MD27; MDZ12; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2179 TTCGCACCATTCCTCTGCTCAGCC 2203
DB 1 TTCACACCATTCCTCTGCTTCAGTC 25

RESULT 611
ADB04745
ID ADB04745 standard; DNA; 25 BP.
XX
AC ADB04745;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5731.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MD24; MD27; MDZ12; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2254 TTGTACTTTTGTAGTACAGCGGTT 2278
DB 1 TTGTATTTTGTAGTACAGCGGGT 25

RESULT 612
ADB04579
ID ADB04579 standard; DNA; 25 BP.
XX
AC ADB04579;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5565.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MD24; MD27; MDZ12; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTAGACCGAGTCT 2111
DB 1 TTTTATTTTGTAGACAGAGTCT 25
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RESULT 613
ADB04665
ID ADB04665 standard; DNA; 25 BP.
XX
AC ADB04665;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5651.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MD24; MD27; MDZ12; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2174 CCGGGTTTCGACCATTCCTCTGCT 2198
DB 1 CTGGGTTTCACCATTCCTCTGCTT 25

RESULT 614
ADB04578
ID ADB04578 standard; DNA; 25 BP.
XX
AC ADB04578;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5564.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MD24; MD27; MDZ12; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2086 TTATTATTTTGTAGACCGAGTC 2110
DB 1 TTTTATTTTGTAGACAGAGTC 25

RESULT 615
ADB04746
ID ADB04746 standard; DNA; 25 BP.
XX
AC ADB04746;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5732.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MD24; MD27; MDZ12; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2255 TGTACTTTTGTAGACAGCGGTTT 2279
DB 1 TGTATTTTGTAGACAGCGGGT 25

RESULT 616
ADB04672
ID ADB04672 standard; DNA; 25 BP.
XX
AC ADB04672;
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[illegible]

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Db      1 GTGCTGGGATTANAGGTGTGAACAC 26

RESULT 623
AAH91096/c
ID   AAH91096 standard; DNA; 26 BP.
AC     AAH91096;
XX
XX
DT   09-OCT-2001 (first entry)
DE   Human inflammatory bowel disease associated polymorphic site #171.
KW   Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW   single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match      0.9%; Score 20.2; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2345 GTGCTGGGATTACAGGCATGAGCCAC 2370
Db      26 GTGCTGGGATTGCANGTGTGAGCCAC 1

RESULT 624
AD112547/c
ID   AD112547 standard; DNA; 26 BP.
AC     AD112547;
XX
XX
DT   22-APR-2004 (first entry)
DE   Mutant human BRCA1 genomic DNA resulting from deletion 4 SegID 30.
KW   ds; cancer; human; tumour suppressor;
KW   breast cancer susceptibility gene 1; BRCA1; repetitive Alu;

Query Match      0.9%; Score 20.2; DB 1; Length 26;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2144 GATCTTGCTCACTCAAGCTCTGC 2168
Db      25 GATCTTGCTCACTCAAGACCTCTGC 1

RESULT 625
AAT73703/c
ID   AAT73703 standard; DNA; 20 BP.
AC     AAT73703;
XX
XX
DT   27-FEB-1998 (first entry)
DE   PCR primer SRI used to prepare probes for diagnosing Alzheimer's.
KW   PCR primer SRI; Alzheimer's disease; probe; diagnosis; fluorescence;
KW   yeast artificial chromosome library; YAC; chromosome 14; presenile; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2122 CCCAGGCTGGAGTGCAGTGG 2141
Db      20 CCCAGGCTGGAGTGCAGTGG 1

RESULT 626
AAV85762/c
ID   AAV85762 standard; DNA; 20 BP.
XX

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AC     AAV85762;
XX
XX
DT   10-FEB-1999 (first entry)
DE   LRP5 exon primer 57-4 1r.
XX
XX
KW   LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KW   insulin dependent diabetes mellitus; autoimmune disease;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2344 AGTGCTGGGATTACAGGCAT 2363
Db      20 AGTGCTGGGATTACAGGCAT 1

RESULT 627
AAV85840/c
ID   AAV85840 standard; DNA; 20 BP.
AC     AAV85840;
XX
XX
DT   10-FEB-1999 (first entry)
DE   LRP5 SNP primer 57-4 1r.
XX
XX
KW   LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KW   insulin dependent diabetes mellitus; autoimmune disease;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2344 AGTGCTGGGATTACAGGCAT 2363
Db      20 AGTGCTGGGATTACAGGCAT 1

RESULT 628
AAZ37506/c
ID   AAZ37506 standard; DNA; 20 BP.
AC     AAZ37506;
XX
XX
DT   07-JAN-2000 (first entry)
DE   Human mdm2 phosphorothioate oligodeoxynucleotide #36.
KW   Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW   antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29 GCCTGTGTGGCCCTGTGTGT 48
Db      20 GCCTGTGTGGCCCTGTGTGT 1

RESULT 629
AAZ37519/c
ID   AAZ37519 standard; DNA; 20 BP.
AC     AAZ37519;
XX
XX
DT   07-JAN-2000 (first entry)
DE   Human mdm2 phosphorothioate oligodeoxynucleotide #49.
KW   Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;

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KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 TGGCCCGAGAGTGGAAATGA 193  
ID AAZ37547/c  
XX  
AC AAZ37547;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #77.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 GTAACCACTTCACAGATTCC 370  
ID AAZ37566/c  
XX  
AC AAZ37566;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #96.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 GCCAAGCTTCTCTGTGAAAG 594  
ID AAZ37584/c  
XX  
AC AAZ37584;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #114.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1046 TAGTGTAGAAATTTGAAGTTG 1065  
ID AAZ37632/c  
XX  
AC AAZ37632;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #162.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 GAATTCGGCTTCCTGAAGATA 1311  
ID AAZ37639/c  
XX  
AC AAZ37639;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #127.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 AGACCATCTACCTCATCTAG 793  
ID AAZ37639/c  
XX  
AC AAZ37639;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #127.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Db 20 AGACCATCTACCTCATCTAG 1  
RESULT 633  
AAZ37597/c  
ID AAZ37597 standard; DNA; 20 BP.  
XX  
AC AAZ37597;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #127.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TGTGTGAAAGAGCAGTAG 946  
ID AAZ37608/c  
XX  
AC AAZ37608;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #138.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1046 TAGTGTAGAAATTTGAAGTTG 1065  
ID AAZ37632/c  
XX  
AC AAZ37632;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #162.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 GAATTCGGCTTCCTGAAGATA 1311  
ID AAZ37639/c  
XX  
AC AAZ37639;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #127.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 AGACCATCTACCTCATCTAG 793  
ID AAZ37639/c  
XX  
AC AAZ37639;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #127.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

XX AAZ37639;  
AC  
XX  
DT 07-JAN-2000 (first entry)  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #169.  
XX  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KW antisenase; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1368 GCTGAAGAGGGCTTTGATGT 1387  
Db 20 GCTGAAGAGGGCTTTGATGT 1  
RESULT 637  
AAZ37643/c  
ID AAZ37643 standard; DNA; 20 BP.  
XX  
AC AAZ37643;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #173.  
XX  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KW antisenase; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1434 GTTGAGGAAATGATGATAA 1453  
Db 20 GTTGAGGAAATGATGATAA 1  
RESULT 638  
AAZ37651/c  
ID AAZ37651 standard; DNA; 20 BP.  
XX  
AC AAZ37651;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #181.  
XX  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KW antisenase; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1506 ACTTCTAGTAGCATTATTTA 1525  
Db 20 ACTTCTAGTAGCATTATTTA 1  
RESULT 639  
AAZ37654/c  
ID AAZ37654 standard; DNA; 20 BP.  
XX  
AC AAZ37654;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #184.

KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KW antisenase; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1533 CAAGAAGATGTGAAGAGTT 1552  
Db 20 CAAGAAGATGTGAAGAGTT 1  
RESULT 640  
AAZ37664/c  
ID AAZ37664 standard; DNA; 20 BP.  
XX  
AC AAZ37664;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #194.  
XX  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KW antisenase; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1657 GCATTGTCCATGGCAAAACA 1676  
Db 20 GCATTGTCCATGGCAAAACA 1  
RESULT 641  
AAZ37677/c  
ID AAZ37677 standard; DNA; 20 BP.  
XX  
AC AAZ37677;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #207.  
XX  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KW antisenase; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1798 TATAAGAGAATTATATATT 1817  
Db 20 TATAAGAGAATTATATATT 1  
RESULT 642  
AAZ37693/c  
ID AAZ37693 standard; DNA; 20 BP.  
XX  
AC AAZ37693;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #223.  
XX  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KW antisenase; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1913 AGTATAATTGACCTACTTTG 1932
DB 20 AGTATAATTGACCTACTTTG 1

RESULT 643
AAZ37701/c
ID AAZ37701 standard; DNA; 20 BP.
XX AC
XX AC
XX AAZ37701;
XX 07-JAN-2000 (first entry)
DT DT
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #231.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1982 ATCCTTTACACCACTCCTTA 2001
DB 20 ATCCTTTACACCACTCCTTA 1

RESULT 644
AAZ37715/c
ID AAZ37715 standard; DNA; 20 BP.
XX AC
XX AC
XX AAZ37715;
XX 07-JAN-2000 (first entry)
DT DT
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #245.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2140 GGGTGATCTTGGCTCACTGC 2159
DB 20 GGGTGATCTTGGCTCACTGC 1

RESULT 645
AAZ37717/c
ID AAZ37717 standard; DNA; 20 BP.
XX AC
XX AC
XX AAZ37717;
XX 07-JAN-2000 (first entry)
DT DT
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #247.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TCACTGCAAGCTCTGCCCTC 2172
DB 20 TCACTGCAAGCTCTGCCCTC 1

RESULT 646
AAZ37487/c
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ID AAZ37487 standard; DNA; 20 BP.
XX AC
XX AAZ37487;
XX 07-JAN-2000 (first entry)
DT DT
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #17.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 TAGTTGACCTGCTATAAGA 1804
DB 20 TAGTTGACCTGCTATAAGA 1

RESULT 647
AAZ37495/c
ID AAZ37495 standard; DNA; 20 BP.
XX AC
XX AC
XX AAZ37495;
XX 07-JAN-2000 (first entry)
DT DT
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #25.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGGAAGA 56
DB 20 GGCCCTGTGTGCGGAAGA 1

RESULT 648
AAZ37507/c
ID AAZ37507 standard; DNA; 20 BP.
XX AC
XX AC
XX AAZ37507;
XX 07-JAN-2000 (first entry)
DT DT
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #37.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TGTGGCCCTGTGTGCGGAA 53
DB 20 TGTGGCCCTGTGTGCGGAA 1

RESULT 649
AAZ37526/c
ID AAZ37526 standard; DNA; 20 BP.
XX AC
XX AC
XX AAZ37526;
XX 07-JAN-2000 (first entry)
DT DT
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #56.
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XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 ATGTGAGGACGAGGCAAT 313
DB 20 ATGTGAGGACGAGGCAAT 1

RESULT 650
AAZ37536/c
ID AAZ37536 standard; DNA; 20 BP.
XX
AC AAZ37536;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #66.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 AGGCAATGTGCAATACCA 325
DB 20 AGGCAATGTGCAATACCA 1

RESULT 651
AAZ37539/c
ID AAZ37539 standard; DNA; 20 BP.
XX
AC AAZ37539;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #69.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAAATGTGCAATACCAAT 328
DB 20 CAAATGTGCAATACCAAT 1

RESULT 652
AAZ37540/c
ID AAZ37540 standard; DNA; 20 BP.
XX
AC AAZ37540;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #70.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1.
QY 310 AAATGTGCAATACCAATG 329
DB 20 AAATGTGCAATACCAATG 1

RESULT 653
AAZ37558/c
ID AAZ37558 standard; DNA; 20 BP.
XX
AC AAZ37558;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #88.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 503 ACGATTATATGATGAGAAGC 522
DB 20 ACGATTATATGATGAGAAGC 1

RESULT 654
AAZ37559/c
ID AAZ37559 standard; DNA; 20 BP.
XX
AC AAZ37559;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #89.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGAGAAGCAACAATATTG 534
DB 20 TGAGAAGCAACAATATTG 1

RESULT 655
AAZ37569/c
ID AAZ37569 standard; DNA; 20 BP.
XX
AC AAZ37569;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #99.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 AGGAAATATATACCATGAT 619
DB 20 AGGAAATATATACCATGAT 1

RESULT 656
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AAZ37614/c
ID  AAZ37614 standard; DNA; 20 BP.
XX
AC  AAZ37614;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #144.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1092 CTTAGTGAAGAGGACAGA 1111
    |||||
DB  20 CTTAGTGAAGAGGACAGA 1

RESULT 657
AAZ37616/c
ID  AAZ37616 standard; DNA; 20 BP.
XX
AC  AAZ37616;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #146.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1105 GACAAGAACTCTCAGATGAA 1124
    |||||
DB  20 GACAAGAACTCTCAGATGAA 1

RESULT 658
AAZ37617/c
ID  AAZ37617 standard; DNA; 20 BP.
XX
AC  AAZ37617;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #147.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1115 CTCAGATGAAGATGATGAGG 1134
    |||||
DB  20 CTCAGATGAAGATGATGAGG 1

RESULT 659
AAZ37670/c
ID  AAZ37670 standard; DNA; 20 BP.
XX
AC  AAZ37670;
XX
DT  07-JAN-2000 (first entry)
XX
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DE  Human mdm2 phosphorothioate oligodeoxynucleotide #200.
XX
AC  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1710 AAGCTAAAGAAAAGGAATAA 1729
    |||||
DB  20 AAGCTAAAGAAAAGGAATAA 1

RESULT 660
AAZ37675/c
ID  AAZ37675 standard; DNA; 20 BP.
XX
AC  AAZ37675;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #205.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1757 TCAATGATGTGCTAACTT 1776
    |||||
DB  20 TCAATGATGTGCTAACTT 1

RESULT 661
AAZ37685/c
ID  AAZ37685 standard; DNA; 20 BP.
XX
AC  AAZ37685;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #215.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1855 TTTATTACATATATCAAAG 1874
    |||||
DB  20 TTTATTACATATATCAAAG 1

RESULT 662
AAZ37721/c
ID  AAZ37721 standard; DNA; 20 BP.
XX
AC  AAZ37721;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #251.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2198 TCAGCCTCCCAATTAGCTTG 2217
Db 20 TCAGCCTCCCAATTAGCTTG 1
RESULT 663
AAZ37729/c
ID AAZ37729 standard; DNA; 20 BP.
XX
AC AAZ37729;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #259.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTCACCGTTAGCCA 2293
Db 20 GGGTTTCACCGTTAGCCA 1
RESULT 664
AAZ37483/c
ID AAZ37483 standard; DNA; 20 BP.
XX
AC AAZ37483;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #13.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1047 AGTGAGAAATTGAAGTTGA 1066
Db 20 AGTGAGAAATTGAAGTTGA 1
RESULT 665
AAZ37492/c
ID AAZ37492 standard; DNA; 20 BP.
XX
AC AAZ37492;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #22.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2256 GTACTTTTACTAGACACAGG 2275
Db 20 GTACTTTTACTAGACACAGG 1
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RESULT 666
AAZ37509/c
ID AAZ37509 standard; DNA; 20 BP.
XX
AC AAZ37509;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #39.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 50 GGAAGATGGAGCAAGAAGC 69
Db 20 GGAAGATGGAGCAAGAAGC 1
RESULT 667
AAZ37515/c
ID AAZ37515 standard; DNA; 20 BP.
XX
AC AAZ37515;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #45.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 GCAGCCAGGAGCACCGTCCC 139
Db 20 GCAGCCAGGAGCACCGTCCC 1
RESULT 668
AAZ37615/c
ID AAZ37615 standard; DNA; 20 BP.
XX
AC AAZ37615;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #145.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1100 AGAAGACCAAGAACTCTCAG 1119
Db 20 AGAAGACCAAGAACTCTCAG 1
RESULT 669
AAZ37669/c
ID AAZ37669 standard; DNA; 20 BP.
XX
AC AAZ37669;
XX
DT 07-JAN-2000 (first entry)
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XX Human mdm2 phosphorothioate oligodeoxynucleotide #199.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAGAGCTAAAGAAA 1721
DB 20 GTGCAAGAGAGCTAAAGAAA 1

RESULT 670
AAZ37672/c
ID AAZ37672 standard; DNA; 20 BP.
XX
AC AAZ37672;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #202.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 ATAAGCCCTGCCAGTATGT 1745
DB 20 ATAAGCCCTGCCAGTATGT 1

RESULT 671
AAZ37702/c
ID AAZ37702 standard; DNA; 20 BP.
XX
AC AAZ37702;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #232.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1990 CACCAACTCTTAATTTTAAA 2009
DB 20 CACCAACTCTTAATTTTAAA 1

RESULT 672
AAZ37707/c
ID AAZ37707 standard; DNA; 20 BP.
XX
AC AAZ37707;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #237.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2051 TTTTCTTAATATGTATATG 2070
DB 20 TTTTCTTAATATGTATATG 1

RESULT 673
AAZ37510/c
ID AAZ37510 standard; DNA; 20 BP.
XX
AC AAZ37510;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #40.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CAAGAAGCCGAGCCCGAGGG 81
DB 20 CAAGAAGCCGAGCCCGAGGG 1

RESULT 674
AAZ37511/c
ID AAZ37511 standard; DNA; 20 BP.
XX
AC AAZ37511;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #41.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGAGCCCGAGGGCGGCCGC 89
DB 20 CGAGCCCGAGGGCGGCCGC 1

RESULT 675
AAZ37529/c
ID AAZ37529 standard; DNA; 20 BP.
XX
AC AAZ37529;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #59.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TGAGGAGCAGGCAATGTGC 317
DB 20 TGAGGAGCAGGCAATGTGC 1

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RESULT 676
AAZ37581/c
ID AAZ37581 standard; DNA; 20 BP.
XX
AC AAZ37581;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #111.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

QY 740 GGAAGAGAAACCTTCATCTT 759
DB 20 GGAAGAGAAACCTTCATCTT 1

RESULT 677
AAZ37583/c
ID AAZ37583 standard; DNA; 20 BP.
XX
AC AAZ37583;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #113.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

QY 761 ACATTTGGTTCTAGACCAT 780
DB 20 ACATTTGGTTCTAGACCAT 1

RESULT 678
AAZ37598/c
ID AAZ37598 standard; DNA; 20 BP.
XX
AC AAZ37598;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #128.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

QY 936 AGAAGCAGTAGCAGTGAATC 955
DB 20 AGAAGCAGTAGCAGTGAATC 1

RESULT 679
AAZ37603/c
ID AAZ37603 standard; DNA; 20 BP.
XX
AC AAZ37603;
XX

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DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #133.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 996 AGTGAACATTCAGGTGATTG 1015
DB 20 AGTGAACATTCAGGTGATTG 1

RESULT 680
AAZ37604/c
ID AAZ37604 standard; DNA; 20 BP.
XX
AC AAZ37604;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #134.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1006 CAGGTGATTCGTTGGATCAG 1025
DB 20 CAGGTGATTCGTTGGATCAG 1

RESULT 681
AAZ37622/c
ID AAZ37622 standard; DNA; 20 BP.
XX
AC AAZ37622;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #152.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1170 GATACAGATTCATTTCGAAGA 1189
DB 20 GATACAGATTCATTTCGAAGA 1

RESULT 682
AAZ37623/c
ID AAZ37623 standard; DNA; 20 BP.
XX
AC AAZ37623;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #153.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1184 TGAAGAGATCCTGAAATTT 1203
Db      ||||| ||||| ||||| ||||| |||||
      20 TGAAGAAGATCCTGAAATTT 1

RESULT 683
AAZ37647/c
ID AAZ37647 standard; DNA; 20 BP.
XX
AC AAZ37647;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #177.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1466 TTCACAATCACAGAAAGTG 1485
Db      ||||| ||||| ||||| ||||| |||||
      20 TTCACAATCACAGAAAGTG 1

RESULT 684
AAZ37650/c
ID AAZ37650 standard; DNA; 20 BP.
XX
AC AAZ37650;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #180.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GCCATCAACTTCTAGTAGCA 1518
Db      ||||| ||||| ||||| ||||| |||||
      20 GCCATCAACTTCTAGTAGCA 1

RESULT 685
AAZ37653/c
ID AAZ37653 standard; DNA; 20 BP.
XX
AC AAZ37653;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #183.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 TTTATAGCAGCCAGAGAT 1541
Db      ||||| ||||| ||||| ||||| |||||
      20 TTTATAGCAGCCAGAGAT 1
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RESULT 686
AAZ37662/c
ID AAZ37662 standard; DNA; 20 BP.
XX
AC AAZ37662;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #192.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1624 GTGTGATTTGTCAAGGTGCA 1643
Db      ||||| ||||| ||||| ||||| |||||
      20 GTGTGATTTGTCAAGGTGCA 1

RESULT 687
AAZ37668/c
ID AAZ37668 standard; DNA; 20 BP.
XX
AC AAZ37668;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #198.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 CCTGCTTTACATGTGCAAG 1709
Db      ||||| ||||| ||||| ||||| |||||
      20 CCTGCTTTACATGTGCAAG 1

RESULT 688
AAZ37671/c
ID AAZ37671 standard; DNA; 20 BP.
XX
AC AAZ37671;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #201.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 AAAGGAATAAGCCCTGCCCA 1739
Db      ||||| ||||| ||||| ||||| |||||
      20 AAAGGAATAAGCCCTGCCCA 1

RESULT 689
AAZ37694/c
ID AAZ37694 standard; DNA; 20 BP.
XX
AC AAZ37694;
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XX 07-JAN-2000 (first entry)  
DT Human mdm2 phosphorothioate oligodeoxynucleotide #224.  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
DE antisense; modulation; oligonucleotide; expression; inhibition;  
KW  
XX  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1920 TTGACCTACTTTGGTAGTGG 1939  
DB 20 TTGACCTACTTTGGTAGTGG 1  
RESULT 690  
AAZ37695/c  
ID AAZ37695 standard; DNA; 20 BP.  
XX  
XX AAZ37695;  
AC  
XX 07-JAN-2000 (first entry)  
DT Human mdm2 phosphorothioate oligodeoxynucleotide #225.  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
DE antisense; modulation; oligonucleotide; expression; inhibition;  
KW  
XX  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1933 GTAGTGGAAATGTGAATACT 1952  
DB 20 GTAGTGGAAATGTGAATACT 1  
RESULT 691  
AAZ37719/c  
ID AAZ37719 standard; DNA; 20 BP.  
XX  
XX AAZ37719;  
AC  
XX 07-JAN-2000 (first entry)  
DT Human mdm2 phosphorothioate oligodeoxynucleotide #249.  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
DE antisense; modulation; oligonucleotide; expression; inhibition;  
KW  
XX  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2185 CCATTCTCTGCTCAGCCT 2204  
DB 20 CCATTCTCTGCTCAGCCT 1  
RESULT 692  
AAZ37723/c  
ID AAZ37723 standard; DNA; 20 BP.  
XX  
XX AAZ37723;  
AC  
XX 07-JAN-2000 (first entry)  
DT Human mdm2 phosphorothioate oligodeoxynucleotide #253.  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
DE antisense; modulation; oligonucleotide; expression; inhibition;  
KW

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2210 TTAGCTTGGCCTACAGTCAT 2229  
DB 20 TTAGCTTGGCCTACAGTCAT 1  
RESULT 693  
AAZ37477/c  
ID AAZ37477 standard; DNA; 20 BP.  
XX  
XX AAZ37477;  
AC  
XX 07-JAN-2000 (first entry)  
DT Human mdm2 phosphorothioate oligodeoxynucleotide #7.  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
DE antisense; modulation; oligonucleotide; expression; inhibition;  
KW  
XX  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 181 GAGAGTGGAAATGATCCCGA 200  
DB 20 GAGAGTGGAAATGATCCCGA 1  
RESULT 694  
AAZ37512/c  
ID AAZ37512 standard; DNA; 20 BP.  
XX  
XX AAZ37512;  
AC  
XX 07-JAN-2000 (first entry)  
DT Human mdm2 phosphorothioate oligodeoxynucleotide #42.  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
DE antisense; modulation; oligonucleotide; expression; inhibition;  
KW  
XX  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 98 TGACCGAGATCCTGCTGCTT 117  
DB 20 TGACCGAGATCCTGCTGCTT 1  
RESULT 695  
AAZ37516/c  
ID AAZ37516 standard; DNA; 20 BP.  
XX  
XX AAZ37516;  
AC  
XX 07-JAN-2000 (first entry)  
DT Human mdm2 phosphorothioate oligodeoxynucleotide #46.  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
DE antisense; modulation; oligonucleotide; expression; inhibition;  
KW  
XX  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 150 AGTGCCTACGAGCGCCAGT 169  
DB 150 AGTGCCTACGAGCGCCAGT 169

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Db      20 AGTGGGTACGAGCGCCAGT 1
RESULT 696
AAZ37570/c
ID  AAZ37570 standard; DNA; 20 BP.
AC  AAZ37570;
XX
XX  07-JAN-2000 (first entry)
DT
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #100.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      609 TATACCATGATCTACAGGAA 628
      |||||
Db      20 TATACCATGATCTACAGGAA 1

RESULT 697
AAZ37586/c
ID  AAZ37586 standard; DNA; 20 BP.
AC  AAZ37586;
XX
XX  07-JAN-2000 (first entry)
DT
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #116.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      798 AGAGCAATTAGTGACAGAGA 817
      |||||
Db      20 AGAGCAATTAGTGACAGAGA 1

RESULT 698
AAZ37592/c
ID  AAZ37592 standard; DNA; 20 BP.
AC  AAZ37592;
XX
XX  07-JAN-2000 (first entry)
DT
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #122.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      867 TCTGATAGTATTTCCCTTTC 886
      |||||
Db      20 TCTGATAGTATTTCCCTTTC 1

RESULT 699
AAZ37610/c
ID  AAZ37610 standard; DNA; 20 BP.
XX
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AC  AAZ37610;
XX
XX  07-JAN-2000 (first entry)
DT
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #140.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1059 GAAGTTGAATCTCTCGACTC 1078
      |||||
Db      20 GAAGTTGAATCTCTCGACTC 1

RESULT 700
AAZ37648/c
ID  AAZ37648 standard; DNA; 20 BP.
AC  AAZ37648;
XX
XX  07-JAN-2000 (first entry)
DT
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #178.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1481 AAGTGAAGACTATTCTCAGC 1500
      |||||
Db      20 AAGTGAAGACTATTCTCAGC 1

RESULT 701
AAZ37652/c
ID  AAZ37652 standard; DNA; 20 BP.
AC  AAZ37652;
XX
XX  07-JAN-2000 (first entry)
DT
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #182.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1517 CATTATTATAGCAGCCAG 1536
      |||||
Db      20 CATTATTATAGCAGCCAG 1

RESULT 702
AAZ37657/c
ID  AAZ37657 standard; DNA; 20 BP.
AC  AAZ37657;
XX
XX  07-JAN-2000 (first entry)
DT
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #187.
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
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KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 GAAGAAACCCCAAGACAAGA 1579
DB 20 GAAGAAACCCCAAGACAAGA 1

RESULT 703
AAZ37682/c
ID AAZ37682 standard; DNA; 20 BP.
XX
AC AAZ37682;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #212.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1832 CTAGGAATTAGACAACCTG 1851
DB 20 CTAGGAATTAGACAACCTG 1

RESULT 704
AAZ37713/c
ID AAZ37713 standard; DNA; 20 BP.
XX
AC AAZ37713;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #243.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2123 CCAGCTGGAGTGCAGTGGG 2142
DB 20 CCAGCTGGAGTGCAGTGGG 1

RESULT 705
AAZ37731/c
ID AAZ37731 standard; DNA; 20 BP.
XX
AC AAZ37731;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #261.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGGTCTCGATCTC 2309
DB 20 GCCAGGATGGTCTCGATCTC 1

KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCCAAGCGCGAAACCCCG 292
DB 20 CTCCAAGCGCGAAACCCCG 1

RESULT 707
AAZ37517/c
ID AAZ37517 standard; DNA; 20 BP.
XX
AC AAZ37517;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #47.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 CGAGCGCCCGAGTCCCTGGC 177
DB 20 CGAGCGCCCGAGTCCCTGGC 1

RESULT 708
AAZ37530/c
ID AAZ37530 standard; DNA; 20 BP.
XX
AC AAZ37530;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #60.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 GAGGAGCAGCGAAATGTGCA 318
DB 20 GAGGAGCAGCGAAATGTGCA 1

RESULT 709
AAZ37534/c
ID AAZ37534 standard; DNA; 20 BP.
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XX AAZ37534;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #64.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisease; modulation; oligonucleotide; expression; inhibition;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAAAATGTGCAATACC 323
DB 20 GCAGGCAAAATGTGCAATACC 1

RESULT 710
AAZ37546/c
ID AAZ37546 standard; DNA; 20 BP.
XX
XX AAZ37546;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #76.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisease; modulation; oligonucleotide; expression; inhibition;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 TACCTACTGATGTGCTGTA 353
DB 20 TACCTACTGATGTGCTGTA 1

RESULT 711
AAZ37552/c
ID AAZ37552 standard; DNA; 20 BP.
XX
XX AAZ37552;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #82.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisease; modulation; oligonucleotide; expression; inhibition;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGCCATTGCTTTTGAAGTTA 422
DB 20 AGCCATTGCTTTTGAAGTTA 1

RESULT 712
AAZ37556/c
ID AAZ37556 standard; DNA; 20 BP.
XX
XX AAZ37556;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #86.
XX

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KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 ATATTATGACTAAACGATTGA 509
DB 20 ATATTATGACTAAACGATTGA 1

RESULT 713
AAZ37573/c
ID AAZ37573 standard; DNA; 20 BP.
XX
XX AAZ37573;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #103.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisease; modulation; oligonucleotide; expression; inhibition;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 646 AGCAGGAATCATCGGACTCA 665
DB 20 AGCAGGAATCATCGGACTCA 1

RESULT 714
AAZ37620/c
ID AAZ37620 standard; DNA; 20 BP.
XX
XX AAZ37620;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #150.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisease; modulation; oligonucleotide; expression; inhibition;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 GTGTATCAGCGGGGAGAG 1168
DB 20 GTGTATCAGCGGGGAGAG 1

RESULT 715
AAZ37649/c
ID AAZ37649 standard; DNA; 20 BP.
XX
XX AAZ37649;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #179.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisease; modulation; oligonucleotide; expression; inhibition;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1489 ACTATTCTCAGCCATCAACT 1508
Db 20 ACTATTCTCAGCCATCAACT 1

RESULT 716
AAZ37663/c
ID AAZ37663 standard; DNA; 20 BP.
AC AAZ37663;
XX
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #193.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AAAATGGTTGCATTGTCCAT 1667
Db 20 AAAATGGTTGCATTGTCCAT 1

RESULT 717
AAZ37703/c
ID AAZ37703 standard; DNA; 20 BP.
AC AAZ37703;
XX
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #233.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 TCCTAAATTTAAATAATTTC 2016
Db 20 TCCTAAATTTAAATAATTTC 1

RESULT 718
AAZ37722/c
ID AAZ37722 standard; DNA; 20 BP.
AC AAZ37722;
XX
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #252.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 CCTCCCAATTAGCTTGGCCT 2221
Db 20 CCTCCCAATTAGCTTGGCCT 1

RESULT 719
AAZ37738/c

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ID AAZ37738 standard; DNA; 20 BP.
XX
AC AAZ37738;
XX
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #268.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCAC 2370
Db 20 GGATTACAGGCATGAGCCAC 1

RESULT 720
AAZ37481/c
ID AAZ37481 standard; DNA; 20 BP.
AC AAZ37481;
XX
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #11.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACTACTGATGCTGCT 350
Db 20 CTGTACTACTGATGCTGCT 1

RESULT 721
AAZ37484/c
ID AAZ37484 standard; DNA; 20 BP.
AC AAZ37484;
XX
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #14.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTCTGATTGTAAA 1400
Db 20 TTGATGTTCTCTGATTGTAAA 1

RESULT 722
AAZ37488/c
ID AAZ37488 standard; DNA; 20 BP.
AC AAZ37488;
XX
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #18.

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XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1818 CTAACCTATATACCCCTAGGA 1837
DB 20 CTAACCTATATACCCCTAGGA 1

RESULT 723
AAZ37538/c
ID AAZ37538 standard; DNA; 20 BP.
XX
XX AAZ37538;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #68.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 GCAAAATGTGCAATACCAACA 327
DB 20 GCAAAATGTGCAATACCAACA 1

RESULT 724
AAZ37550/c
ID AAZ37550 standard; DNA; 20 BP.
XX
XX AAZ37550;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #80.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 GACCCCTGGTTAGACCAAGC 405
DB 20 GACCCCTGGTTAGACCAAGC 1

RESULT 725
AAZ37553/c
ID AAZ37553 standard; DNA; 20 BP.
XX
XX AAZ37553;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #83.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 422 ATTAAAGTCTGTTGGTGAC 441
DB 20 ATTAAAGTCTGTTGGTGAC 1

RESULT 726
AAZ37579/c
ID AAZ37579 standard; DNA; 20 BP.
XX
XX AAZ37579;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #109.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 718 AGGACCTTGTCACAGAGCTT 737
DB 20 AGGACCTTGTCACAGAGCTT 1

RESULT 727
AAZ37582/c
ID AAZ37582 standard; DNA; 20 BP.
XX
XX AAZ37582;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #112.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 TTCATCTTCACATTTGGTTT 771
DB 20 TTCATCTTCACATTTGGTTT 1

RESULT 728
AAZ37606/c
ID AAZ37606 standard; DNA; 20 BP.
XX
XX AAZ37606;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #136.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1023 CAGGATTCAGTTTCAGATCA 1042
DB 20 CAGGATTCAGTTTCAGATCA 1

RESULT 729

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AAZ37609/c
ID AAZ37609 standard; DNA; 20 BP.
XX
AC AAZ37609;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #139.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 TAGAATTTGAAGTTGAATCT 1070
DB 20 TAGAATTTGAAGTTGAATCT 1

RESULT 730
AAZ37612/c
ID AAZ37612 standard; DNA; 20 BP.
XX
AC AAZ37612;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #142.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1077 TCAGAAGATTATAGCCTTAG 1096
DB 20 TCAGAAGATTATAGCCTTAG 1

RESULT 731
AAZ37635/c
ID AAZ37635 standard; DNA; 20 BP.
XX
AC AAZ37635;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #165.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1325 AGGGGAATCTCTGAGAAAG 1344
DB 20 AGGGGAATCTCTGAGAAAG 1

RESULT 732
AAZ37640/c
ID AAZ37640 standard; DNA; 20 BP.
XX
AC AAZ37640;
XX
DT 07-JAN-2000 (first entry)
XX

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DE Human mdm2 phosphorothioate oligodeoxynucleotide #170.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1401 AAAACTATAGTGAATGATTC 1420
DB 20 AAACTATAGTGAATGATTC 1

RESULT 733
AAZ37642/c
ID AAZ37642 standard; DNA; 20 BP.
XX
AC AAZ37642;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #172.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1421 CAGAGAGTCATGTGTTGAGG 1440
DB 20 CAGAGAGTCATGTGTTGAGG 1

RESULT 734
AAZ37645/c
ID AAZ37645 standard; DNA; 20 BP.
XX
AC AAZ37645;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #175.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATAAAATTACACAGCTTC 1468
DB 20 GATAAAATTACACAGCTTC 1

RESULT 735
AAZ37674/c
ID AAZ37674 standard; DNA; 20 BP.
XX
AC AAZ37674;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #204.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1745 TAGACCAACCAATTCAAATGA 1764
DB 20 TAGACCAACCAATTCAAATGA 1
RESULT 736
AAZ37681/c
ID AAZ37681 standard; DNA; 20 BP.
XX AC AAZ37681;
XX AC AAZ37681;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #211.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1823 TATATAACCCCTAGGAATTGA 1842
DB 20 TATATAACCCCTAGGAATTGA 1
RESULT 737
AAZ37699/c
ID AAZ37699 standard; DNA; 20 BP.
XX AC AAZ37699;
XX AC AAZ37699;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #229.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1969 GAATATGTAGCTCATCTTT 1988
DB 20 GAATATGTAGCTCATCTTT 1
RESULT 738
AAZ37709/c
ID AAZ37709 standard; DNA; 20 BP.
XX AC AAZ37709;
XX AC AAZ37709;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #239.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2072 CATTAAATGTAACCTATTGA 2091
DB 20 CATTAAATGTAACCTATTGA 1
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RESULT 739
AAZ37716/c
ID AAZ37716 standard; DNA; 20 BP.
XX AC AAZ37716;
XX AC AAZ37716;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #246.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2146 TCTTGGCTCACTGCAAGCTC 2165
DB 20 TCTTGGCTCACTGCAAGCTC 1
RESULT 740
AAZ37727/c
ID AAZ37727 standard; DNA; 20 BP.
XX AC AAZ37727;
XX AC AAZ37727;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #257.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2253 TTTGTACTTTTAGTAGAGAC 2272
DB 20 TTTGTACTTTTAGTAGAGAC 1
RESULT 741
AAZ37476/c
ID AAZ37476 standard; DNA; 20 BP.
XX AC AAZ37476;
XX AC AAZ37476;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #6.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 147 ATTAGTGCCTACGAGCGCCC 166
DB 20 ATTAGTGCCTACGAGCGCCC 1
RESULT 742
AAZ37485/c
ID AAZ37485 standard; DNA; 20 BP.
XX AC AAZ37485;
XX AC AAZ37485;
XX DT 07-JAN-2000 (first entry)
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XX Human mdm2 phosphorothioate oligodeoxynucleotide #15.
DE
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTACATGTGCAAGAAGCT 1714
DB 20 TTTACATGTGCAAGAAGCT 1

RESULT 743
AAZ37489/c
ID AAZ37489 standard; DNA; 20 BP.
XX
AC AAZ37489;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #19.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGGATAGTGATATT 1953
DB 20 TAGTGGATAGTGATATT 1

RESULT 744
AAZ37491/c
ID AAZ37491 standard; DNA; 20 BP.
XX
AC AAZ37491;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #21.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2224 AGTCATCTGCCACACACCT 2243
DB 20 AGTCATCTGCCACACACCT 1

RESULT 745
AAZ37508/c
ID AAZ37508 standard; DNA; 20 BP.
XX
AC AAZ37508;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #38.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GTGTGTCGGAAGATGGAGC 62
DB 20 GTGTGTCGGAAGATGGAGC 1

RESULT 746
AAZ37522/c
ID AAZ37522 standard; DNA; 20 BP.
XX
AC AAZ37522;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #52.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CTTCCGCACTAGTCAGTCCC 236
DB 20 CTTCCGCACTAGTCAGTCCC 1

RESULT 747
AAZ37533/c
ID AAZ37533 standard; DNA; 20 BP.
XX
AC AAZ37533;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #63.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GAGCAGGCAAAATGTGCAATA 321
DB 20 GAGCAGGCAAAATGTGCAATA 1

RESULT 748
AAZ37571/c
ID AAZ37571 standard; DNA; 20 BP.
XX
AC AAZ37571;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #101.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 TCTACAGGAACCTTGGTAGTA 638
DB 20 TCTACAGGAACCTTGGTAGTA 1

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RESULT 749
AAZ37572/c
ID AAZ37572 standard; DNA; 20 BP.
XX
XX
AC AAZ37572;
XX
DT 07-JAN-2000. (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #102.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 634 TAGTAGTCAATCAGCAGGAA 653
Db 20 TAGTAGTCAATCAGCAGGAA 1

RESULT 750
AAZ37574/c
ID AAZ37574 standard; DNA; 20 BP.
XX
XX
AC AAZ37574;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #104.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 ATCGGACTCAGTACATCTG 675
Db 20 ATCGGACTCAGTACATCTG 1

RESULT 751
AAZ37607/c
ID AAZ37607 standard; DNA; 20 BP.
XX
XX
AC AAZ37607;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #137.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1034 TTCAGATCAGTTAGTGTAG 1053
Db 20 TTCAGATCAGTTAGTGTAG 1

RESULT 752
AAZ37611/c
ID AAZ37611 standard; DNA; 20 BP.
XX
XX
AC AAZ37611;
XX

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DT 07-JAN-2000 (first entry)
XX
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #141.
XX
XX
AC AAZ37619;
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1068 TCTCTCGACTCAGAGATTA 1087
Db 20 TCTCTCGACTCAGAGATTA 1

RESULT 753
AAZ37619/c
ID AAZ37619 standard; DNA; 20 BP.
XX
XX
AC AAZ37619;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #149.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1135 TATATCAAGTTACTGTGTAT 1154
Db 20 TATATCAAGTTACTGTGTAT 1

RESULT 754
AAZ37630/c
ID AAZ37630 standard; DNA; 20 BP.
XX
XX
AC AAZ37630;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #160.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 TGTGGGCCCTTCGTGAGAA 1294
Db 20 TGTGGGCCCTTCGTGAGAA 1

RESULT 755
AAZ37633/c
ID AAZ37633 standard; DNA; 20 BP.
XX
XX
AC AAZ37633;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #163.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1301 TCCTGAAGATAAAGGGAAG 1320
DB 20 TCCTGAAGATAAAGGGAAG 1

RESULT 756
AAZ37656/c
ID AAZ37656 standard; DNA; 20 BP.
XX
AC AAZ37656;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #186.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GTTTGAAGGGAAGAAACCC 1569
DB 20 GTTTGAAGGGAAGAAACCC 1

RESULT 757
AAZ37658/c
ID AAZ37658 standard; DNA; 20 BP.
XX
AC AAZ37658;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #189.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAAGACAAGAGAGAG 1585
DB 20 ACCCAAGACAAGAGAGAG 1

RESULT 758
AAZ37660/c
ID AAZ37660 standard; DNA; 20 BP.
XX
AC AAZ37660;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #190.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 CTTAATGCCATTGAACCTTG 1624
DB 20 CTTAATGCCATTGAACCTTG 1
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RESULT 759
AAZ37678/c
ID AAZ37678 standard; DNA; 20 BP.
XX
AC AAZ37678;
XX
DT 07-JAN-2000 (first entry)
XX
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Human mdm2 phosphorothioate oligodeoxynucleotide #208.

Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1804 AGAATTATATATTTCTAACT 1823
DB 20 AGAATTATATATTTCTAACT 1
```

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RESULT 760
AAZ37720/c
ID AAZ37720 standard; DNA; 20 BP.
XX
AC AAZ37720;
XX
DT 07-JAN-2000 (first entry)
XX
```

Human mdm2 phosphorothioate oligodeoxynucleotide #250.

Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 2191 TCCTGCTCAGCCTCCCAAT 2210
DB 20 TCCTGCTCAGCCTCCCAAT 1
```

```
RESULT 761
AAZ37479/c
ID AAZ37479 standard; DNA; 20 BP.
XX
AC AAZ37479;
XX
DT 07-JAN-2000 (first entry)
XX
```

Human mdm2 phosphorothioate oligodeoxynucleotide #9.

Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 295 TGCTGAGGAGCAGGCAATG 314
DB 20 TGCTGAGGAGCAGGCAATG 1
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RESULT 762
AAZ37482/c
ID AAZ37482 standard; DNA; 20 BP.
XX
AC AAZ37482;
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XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #12.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 617 GATCTACAGGAAGCTGTAG 636
DB 20 GATCTACAGGAAGCTGTAG 1
RESULT 763
AAZ37505/c
ID AAZ37505 standard; DNA; 20 BP.
XX
AC AAZ37505;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #35.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 GCTTCTGGGGCCTGTGGC 39
DB 20 GCTTCTGGGGCCTGTGGC 1
RESULT 764
AAZ37527/c
ID AAZ37527 standard; DNA; 20 BP.
XX
AC AAZ37527;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #57.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 GGTGAGGAGCAGGCAATGT 315
DB 20 GGTGAGGAGCAGGCAATGT 1
RESULT 765
AAZ37528/c
ID AAZ37528 standard; DNA; 20 BP.
XX
AC AAZ37528;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #58.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW

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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 297 GTGAGGAGCAGGCAATGTG 316
DB 20 GTGAGGAGCAGGCAATGTG 1
RESULT 766
AAZ37537/c
ID AAZ37537 standard; DNA; 20 BP.
XX
AC AAZ37537;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #67.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 307 GGCATATGTGCAATACCAAC 326
DB 20 GGCATATGTGCAATACCAAC 1
RESULT 767
AAZ37551/c
ID AAZ37551 standard; DNA; 20 BP.
XX
AC AAZ37551;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #81.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GGTAGACCAAGCCATTGC 411
DB 20 GGTAGACCAAGCCATTGC 1
RESULT 768
AAZ37596/c
ID AAZ37596 standard; DNA; 20 BP.
XX
AC AAZ37596;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #126.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 915 ATAAGGGAGATATGTTGTA 934
DB 20 ATAAGGGAGATATGTTGTA 1

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Db      20 ATAGGAGATATGTTGTGA 1

RESULT 769
AAZ37599/c
ID  AAZ37599 standard; DNA; 20 BP.
XX
XX
AC  AAZ37599;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #129.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW  antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      949 GTGAATCTACAGGACGCCA 968
Db      20 GTGAATCTACAGGACGCCA 1

RESULT 770
AAZ37624/c
ID  AAZ37624 standard; DNA; 20 BP.
XX
XX
AC  AAZ37624;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #154.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW  antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1196 TGAATTTTCCTAGCTGACT 1215
Db      20 TGAATTTTCCTAGCTGACT 1

RESULT 771
AAZ37636/c
ID  AAZ37636 standard; DNA; 20 BP.
XX
XX
AC  AAZ37636;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #166.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW  antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1333 TCTCTGAGAAAGCCAAACTG 1352
Db      20 TCTCTGAGAAAGCCAAACTG 1

RESULT 772
AAZ37661/c
ID  AAZ37661 standard; DNA; 20 BP.
XX
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AC  AAZ37661;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #191.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW  antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1617 GAACCTTGCTGATTTGTCA 1636
Db      20 GAACCTTGCTGATTTGTCA 1

RESULT 773
AAZ37680/c
ID  AAZ37680 standard; DNA; 20 BP.
XX
XX
AC  AAZ37680;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #210.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW  antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1816 TTCTAACTATATAACCCCTAG 1835
Db      20 TTCTAACTATATAACCCCTAG 1

RESULT 774
AAZ37696/c
ID  AAZ37696 standard; DNA; 20 BP.
XX
XX
AC  AAZ37696;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #226.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW  antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1940 AATAGTGAATACTTACTATA 1959
Db      20 AATAGTGAATACTTACTATA 1

RESULT 775
AAZ37710/c
ID  AAZ37710 standard; DNA; 20 BP.
XX
XX
AC  AAZ37710;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #240.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
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KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTTGCTGTATC 2122
DB 20 ACCGAGTCTTGCTGTATC 1
|||||

RESULT 776
AAZ37714/c
ID AAZ37714 standard; DNA; 20 BP.
XX
AC AAZ37714;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #244.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2133 GTCCAGTGGGTGATCTGGC 2152
DB 20 GTCCAGTGGGTGATCTGGC 1
|||||

RESULT 777
AAZ37726/c
ID AAZ37726 standard; DNA; 20 BP.
XX
AC AAZ37726;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #256.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2232 GCCACACACCTGGCTAATT 2251
DB 20 GCCACACACCTGGCTAATT 1
|||||

RESULT 778
AAZ37475/c
ID AAZ37475 standard; DNA; 20 BP.
XX
AC AAZ37475;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #5.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCCTGCTG 114
|||||

KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CTCTGACCGAGATCCTGCTG 1
|||||

RESULT 779
AAZ37480/c
ID AAZ37480 standard; DNA; 20 BP.
XX
AC AAZ37480;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #10.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AGCAGCGCAATGTGCAATAC 322
DB 20 AGCAGCGCAATGTGCAATAC 1
|||||

RESULT 780
AAZ37524/c
ID AAZ37524 standard; DNA; 20 BP.
XX
AC AAZ37524;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #54.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 CCGGATGGTGAGGAGCAGG 308
DB 20 CCGGATGGTGAGGAGCAGG 1
|||||

RESULT 781
AAZ37542/c
ID AAZ37542 standard; DNA; 20 BP.
XX
AC AAZ37542;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #72.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTC 331
DB 20 ATGTGCAATACCAACATGTC 1
|||||

RESULT 782
AAZ37545/c
ID AAZ37545 standard; DNA; 20 BP.
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XX AAZ37545;
AC
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #75.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 CAACATGCTGTACTACTG 342
Db 20 CAACATGCTGTACTACTG 1

RESULT 783
AAZ37565/c
ID AAZ37565 standard; DNA; 20 BP.
XX
AC AAZ37565;
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #95.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 GTTGGCGTGCCAGCTTCT 585
Db 20 GTTGGCGTGCCAGCTTCT 1

RESULT 784
AAZ37577/c
ID AAZ37577 standard; DNA; 20 BP.
XX
AC AAZ37577;
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #107.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 GTCACCTTGAAGTGGGAGT 710
Db 20 GTCACCTTGAAGTGGGAGT 1

RESULT 785
AAZ37587/c
ID AAZ37587 standard; DNA; 20 BP.
XX
AC AAZ37587;
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #117.
XX

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KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 GAGACAGAGAAAATTCAGA 829
Db 20 GAGACAGAGAAAATTCAGA 1

RESULT 786
AAZ37621/c
ID AAZ37621 standard; DNA; 20 BP.
XX
AC AAZ37621;
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #151.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1161 GGGGAGAGTGATACAGATTC 1180
Db 20 GGGGAGAGTGATACAGATTC 1

RESULT 787
AAZ37627/c
ID AAZ37627 standard; DNA; 20 BP.
XX
AC AAZ37627;
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #157.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1226 CACTTCATGCAATGAAATGA 1245
Db 20 CACTTCATGCAATGAAATGA 1

RESULT 788
AAZ37676/c
ID AAZ37676 standard; DNA; 20 BP.
XX
AC AAZ37676;
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #206.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1787 GTTGACCTGTCTATAAGAGA 1806  
 Db 20 GTTGACCTGTCTATAAGAGA 1

## RESULT 789

AAZ37679/c

ID AAZ37679 standard; DNA; 20 BP.

XX

AC AAZ37679;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #209.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 TTATATATTTCTTAACATATAT 1827

Db 20 TTATATATTTCTTAACATATAT 1

## RESULT 790

AAZ37706/c

ID AAZ37706 standard; DNA; 20 BP.

XX

AC AAZ37706;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #236.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 TCTGTCTTAAATGAGAAGTA 2039

Db 20 TCTGTCTTAAATGAGAAGTA 1

## RESULT 791

AAZ37734/c

ID AAZ37734 standard; DNA; 20 BP.

XX

AC AAZ37734;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #264.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCCT 2338

Db 20 TGATCCGCCACCTCGGCCT 1

## RESULT 792

AAZ37523/c

ID AAZ37523 standard; DNA; 20 BP.

XX

AC AAZ37523;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #53.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGGAAACTGGGAGTCTTGA 261

Db 20 AGGAAACTGGGAGTCTTGA 1

## RESULT 793

AAZ37525/c

ID AAZ37525 standard; DNA; 20 BP.

XX

AC AAZ37525;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #55.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GATGGTGAGGAGCAGGCAAA 312

Db 20 GATGGTGAGGAGCAGGCAAA 1

## RESULT 794

AAZ37549/c

ID AAZ37549 standard; DNA; 20 BP.

XX

AC AAZ37549;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #79.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 GCTTCGGAACAAGAGACCCT 391

Db 20 GCTTCGGAACAAGAGACCCT 1

## RESULT 795

AAZ37568/c

ID AAZ37568 standard; DNA; 20 BP.

XX

AC AAZ37568;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #98.

```
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
QY Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 593 AGAGCACAGGAAATATATATA 612
DB 20 AGAGCACAGGAAATATATATA 1

RESULT 796
AAZ37585/c
ID AAZ37585 standard; DNA; 20 BP.
XX AC AAZ37585;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #115.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
QY Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 CATCTAGAGGAGCAATT 806
DB 20 CATCTAGAGGAGCAATT 1

RESULT 797
AAZ37588/c
ID AAZ37588 standard; DNA; 20 BP.
XX AC AAZ37588;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #118.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
QY Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 824 TTCAGATGAATATCTGCTG 843
DB 20 TTCAGATGAATATCTGCTG 1

RESULT 798
AAZ37589/c
ID AAZ37589 standard; DNA; 20 BP.
XX AC AAZ37589;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #119.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
QY Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 833 ATTATCTGGTGAACGACAAA 852
DB 20 ATTATCTGGTGAACGACAAA 1

RESULT 799
AAZ37602/c
ID AAZ37602 standard; DNA; 20 BP.
XX AC AAZ37602;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #132.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
QY Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 TGATGCTGGTGAAGTGAAC 1002
DB 20 TGATGCTGGTGAAGTGAAC 1

RESULT 800
AAZ37637/c
ID AAZ37637 standard; DNA; 20 BP.
XX AC AAZ37637;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #167.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
QY Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1346 CAAACTGGAAACTCAACAC 1365
DB 20 CAAACTGGAAACTCAACAC 1

RESULT 801
AAZ37638/c
ID AAZ37638 standard; DNA; 20 BP.
XX AC AAZ37638;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #168.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
QY Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1358 CTCACACACAGCTGAAGAGG 1377
DB 20 CTCACACACAGCTGAAGAGG 1

RESULT 802
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AAZ37659/c  
ID AAZ37659 standard; DNA; 20 BP.  
XX  
AC AAZ37659;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #189.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1580 AGAGAGTGTGGATCTAGTT 1599  
Db |||||||||||||||||||  
20 AGAGAGTGTGGATCTAGTT 1

RESULT 803  
AAZ37665/c  
ID AAZ37665 standard; DNA; 20 BP.  
XX  
AC AAZ37665;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #195.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1667 TGGCAAAACAGGACATCTTA 1686  
Db |||||||||||||||||||  
20 TGGCAAAACAGGACATCTTA 1

RESULT 804  
AAZ37673/c  
ID AAZ37673 standard; DNA; 20 BP.  
XX  
AC AAZ37673;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #203.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1736 CCCAGTATGTAGACAACAA 1755  
Db |||||||||||||||||||  
20 CCCAGTATGTAGACAACAA 1

RESULT 805  
AAZ37690/c  
ID AAZ37690 standard; DNA; 20 BP.  
XX  
AC AAZ37690;  
XX  
DT 07-JAN-2000 (first entry)  
XX

DE Human mdm2 phosphorothioate oligodeoxynucleotide #220.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1898 AGATTTCTCTCTTTAGTAT 1917  
Db |||||||||||||||||||  
20 AGATTTCTCTCTTTAGTAT 1

RESULT 806  
AAZ37705/c  
ID AAZ37705 standard; DNA; 20 BP.  
XX  
AC AAZ37705;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #235.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2015 TCTACTCTGTCTTAAATGAG 2034  
Db |||||||||||||||||||  
20 TCTACTCTGTCTTAAATGAG 1

RESULT 807  
AAZ37733/c  
ID AAZ37733 standard; DNA; 20 BP.  
XX  
AC AAZ37733;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #263.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2307 CTCCTGACCTCGTGATCCGC 2326  
Db |||||||||||||||||||  
20 CTCCTGACCTCGTGATCCGC 1

RESULT 808  
AAZ37560/c  
ID AAZ37560 standard; DNA; 20 BP.  
XX  
AC AAZ37560;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #90.  
XX  
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
antisense; modulation; oligonucleotide; expression; inhibition;  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 525 CAACATATTGTATATGTTTC 544
DB 20 CAACATATTGTATATGTTTC 1

RESULT 809
AAZ37593/c
ID AAZ37593 standard; DNA; 20 BP.
XX
AC AAZ37593;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #123.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 880 CCTTTTCCTTTGATGAAAGC 899
DB 20 CCTTTTCCTTTGATGAAAGC 1

RESULT 810
AAZ37601/c
ID AAZ37601 standard; DNA; 20 BP.
XX
AC AAZ37601;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #131.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 971 GAATCCGGATCTTGATGCTG 990
DB 20 GAATCCGGATCTTGATGCTG 1

RESULT 811
AAZ37666/c
ID AAZ37666 standard; DNA; 20 BP.
XX
AC AAZ37666;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #196.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1675 CAGGACATCTTATGGCCTGC 1694
DB 20 CAGGACATCTTATGGCCTGC 1

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RESULT 812
AAZ37667/c
ID AAZ37667 standard; DNA; 20 BP.
XX
AC AAZ37667;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #197.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1684 TTATGGCCTGCTTTACATGT 1703
DB 20 TTATGGCCTGCTTTACATGT 1

RESULT 813
AAZ37683/c
ID AAZ37683 standard; DNA; 20 BP.
XX
AC AAZ37683;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #213.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1840 TTAGACAACCTGAAATTTAT 1859
DB 20 TTAGACAACCTGAAATTTAT 1

RESULT 814
AAZ37691/c
ID AAZ37691 standard; DNA; 20 BP.
XX
AC AAZ37691;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #221.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1905 TTCTCTTTAGTATAATTGAC 1924
DB 20 TTCTCTTTAGTATAATTGAC 1

RESULT 815
AAZ37724/c
ID AAZ37724 standard; DNA; 20 BP.
XX
AC AAZ37724;
XX
DT 07-JAN-2000 (first entry)

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XX Human mdm2 phosphorothioate oligodeoxynucleotide #254.
DE
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2213 GCTTGGCCTACAGTCATCTG 2232
DB 20 GCTTGGCCTACAGTCATCTG 1
RESULT 816
AAZ37736/c
ID AAZ37736 standard; DNA; 20 BP.
XX
AC AAZ37736;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #266.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2334 GGCCTCCCAAGTGTCTGGG 2353
DB 20 GGCCTCCCAAGTGTCTGGG 1
RESULT 817
AAZ37490/c
ID AAZ37490 standard; DNA; 20 BP.
XX
AC AAZ37490;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #20.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2132 AGTCAGTGGGTGATCTTG 2151
DB 20 AGTCAGTGGGTGATCTTG 1
RESULT 818
AAZ37541/c
ID AAZ37541 standard; DNA; 20 BP.
XX
AC AAZ37541;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #71.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
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```
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 311 AATGTGCAATACCAACATGT 330
DB 20 AATGTGCAATACCAACATGT 1
RESULT 819
AAZ37544/c
ID AAZ37544 standard; DNA; 20 BP.
XX
AC AAZ37544;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #74.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 314 GTGCAATACCAACATGTCTG 333
DB 20 GTGCAATACCAACATGTCTG 1
RESULT 820
AAZ37548/c
ID AAZ37548 standard; DNA; 20 BP.
XX
AC AAZ37548;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #78.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 361 CACAGATTCAGCTTCGGAA 380
DB 20 CACAGATTCAGCTTCGGAA 1
RESULT 821
AAZ37576/c
ID AAZ37576 standard; DNA; 20 BP.
XX
AC AAZ37576;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #106.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 682 AGAACAGGTGTCACTTGAA 701
DB 20 AGAACAGGTGTCACTTGAA 1
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RESULT 822
AAZ37580/c
ID AAZ37580 standard; DNA; 20 BP.
XX
AC AAZ37580;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #110.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
  Query Match 0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1311 AAGGGGAAAGATAAAGGGGA 1330
DB 20 AAGGGGAAAGATAAAGGGGA 1
  RESULT 826
  AAZ37687/c
  ID AAZ37687 standard; DNA; 20 BP.
  XX
  AC AAZ37687;
  XX
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #217.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match 0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1872 AAGTGAGAAAATCCCTCAAT 1891
DB 20 AAGTGAGAAAATCCCTCAAT 1
  RESULT 827
  AAZ37689/c
  ID AAZ37689 standard; DNA; 20 BP.
  XX
  AC AAZ37689;
  XX
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #219.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match 0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1889 AATTCACATAGATTCTTCT 1908
DB 20 AATTCACATAGATTCTTCT 1
  RESULT 828
  AAZ37704/c
  ID AAZ37704 standard; DNA; 20 BP.
  XX
  AC AAZ37704;
  XX
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #234.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #164.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
  Query Match 0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1311 AAGGGGAAAGATAAAGGGGA 1330
DB 20 AAGGGGAAAGATAAAGGGGA 1
  RESULT 826
  AAZ37687/c
  ID AAZ37687 standard; DNA; 20 BP.
  XX
  AC AAZ37687;
  XX
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #217.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match 0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1872 AAGTGAGAAAATCCCTCAAT 1891
DB 20 AAGTGAGAAAATCCCTCAAT 1
  RESULT 827
  AAZ37689/c
  ID AAZ37689 standard; DNA; 20 BP.
  XX
  AC AAZ37689;
  XX
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #219.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match 0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1889 AATTCACATAGATTCTTCT 1908
DB 20 AATTCACATAGATTCTTCT 1
  RESULT 828
  AAZ37704/c
  ID AAZ37704 standard; DNA; 20 BP.
  XX
  AC AAZ37704;
  XX
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #234.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #110.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match 0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 727 TACAAGAGCTTCAGGAAGAG 746
DB 20 TACAAGAGCTTCAGGAAGAG 1
  RESULT 823
  AAZ37600/c
  ID AAZ37600 standard; DNA; 20 BP.
  XX
  AC AAZ37600;
  XX
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #130.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match 0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 964 CGCCATCGAATCCGGATCTT 983
DB 20 CGCCATCGAATCCGGATCTT 1
  RESULT 824
  AAZ37625/c
  ID AAZ37625 standard; DNA; 20 BP.
  XX
  AC AAZ37625;
  XX
  DT 07-JAN-2000 (first entry)
  DE Human mdm2 phosphorothioate oligodeoxynucleotide #155.
  XX
  KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match 0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1207 TAGCTGACTATTGGAATGC 1226
DB 20 TAGCTGACTATTGGAATGC 1
  RESULT 825
  AAZ37634/c
  ID AAZ37634 standard; DNA; 20 BP.
  XX
  AC AAZ37634;
  XX

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2004 TTTAAATAAATTTCTACTCTG 2023
Db 20 TTTAAATAAATTTCTACTCTG 1

RESULT 829
AAZ37712/c
ID AAZ37712 standard; DNA; 20 BP.
XX
AC AAZ37712;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #242.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2116 CTGTTACCCAGGCTGGAGTG 2135
Db 20 CTGTTACCCAGGCTGGAGTG 1

RESULT 830
AAZ37486/c
ID AAZ37486 standard; DNA; 20 BP.
XX
AC AAZ37486;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #16.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1776 TATTTCCCTAGTTGACCTG 1795
Db 20 TATTTCCCTAGTTGACCTG 1

RESULT 831
AAZ37513/c
ID AAZ37513 standard; DNA; 20 BP.
XX
AC AAZ37513;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #43.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 GATCCTGCTGCTTCGAGC 124
Db 20 GATCCTGCTGCTTCGAGC 1

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RESULT 832
AAZ37535/c
ID AAZ37535 standard; DNA; 20 BP.
XX
AC AAZ37535;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #65.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 305 CAGGCAAAATGTGCAATACCA 324
Db 20 CAGGCAAAATGTGCAATACCA 1

RESULT 833
AAZ37554/c
ID AAZ37554 standard; DNA; 20 BP.
XX
AC AAZ37554;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #84.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 ACTTATCTACTATGAAGAGGT 469
Db 20 ACTTATCTACTATGAAGAGGT 1

RESULT 834
AAZ37575/c
ID AAZ37575 standard; DNA; 20 BP.
XX
AC AAZ37575;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #105.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 669 ACATCTGTGAGTGAGAACAG 688
Db 20 ACATCTGTGAGTGAGAACAG 1

RESULT 835
AAZ37591/c
ID AAZ37591 standard; DNA; 20 BP.
XX
AC AAZ37591;

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XX 07-JAN-2000 (first entry)
DT Human mdm2 phosphorothioate oligodeoxynucleotide #121.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACGCCACAAATCTGATAGTA 876
DB 20 ACGCCACAAATCTGATAGTA 1

RESULT 836
AAZ37595/c
ID AAZ37595 standard; DNA; 20 BP.
XX
XX AAZ37595;
AC
XX 07-JAN-2000 (first entry)
DT Human mdm2 phosphorothioate oligodeoxynucleotide #125.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 CTCGTGTGTATTAAGGGAG 923
DB 20 CTCGTGTGTATTAAGGGAG 1

RESULT 837
AAZ37605/c
ID AAZ37605 standard; DNA; 20 BP.
XX
XX AAZ37605;
AC
XX 07-JAN-2000 (first entry)
DT Human mdm2 phosphorothioate oligodeoxynucleotide #135.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 TTGGATCAGGATTCAGTTTC 1036
DB 20 TTGGATCAGGATTCAGTTTC 1

RESULT 838
AAZ37629/c
ID AAZ37629 standard; DNA; 20 BP.
XX
XX AAZ37629;
AC
XX 07-JAN-2000 (first entry)
DT Human mdm2 phosphorothioate oligodeoxynucleotide #159.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 CAACAGATGTTGGCCCTTC 1287
DB 20 CAACAGATGTTGGCCCTTC 1

RESULT 839
AAZ37631/c
ID AAZ37631 standard; DNA; 20 BP.
XX
XX AAZ37631;
AC
XX 07-JAN-2000 (first entry)
DT Human mdm2 phosphorothioate oligodeoxynucleotide #161.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1283 CCTTCGTGAGATTGGCTTC 1302
DB 20 CCTTCGTGAGATTGGCTTC 1

RESULT 840
AAZ37641/c
ID AAZ37641 standard; DNA; 20 BP.
XX
XX AAZ37641;
AC
XX 07-JAN-2000 (first entry)
DT Human mdm2 phosphorothioate oligodeoxynucleotide #171.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GAATGATTCAGAGATCAT 1431
DB 20 GAATGATTCAGAGATCAT 1

RESULT 841
AAZ37684/c
ID AAZ37684 standard; DNA; 20 BP.
XX
XX AAZ37684;
AC
XX 07-JAN-2000 (first entry)
DT Human mdm2 phosphorothioate oligodeoxynucleotide #214.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1850 TGAATTTTATTCATATAT 1869
DB 20 TGAATTTTATTCATATAT 1

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KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGGAAGA 56
ID AAZ37503 standard; DNA; 20 BP.
XX AAZ37503;
AC AAZ37503;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #33.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCAGCTTGGTGCTT 23
ID AAZ37514 standard; DNA; 20 BP.
XX AAZ37514;
AC AAZ37514;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #44.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TGCTTTCGACGCGAGCA 132
ID AAZ37518 standard; DNA; 20 BP.
XX AAZ37518;
AC AAZ37518;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #48.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCAGTGCCCTGGCCGGAGA 184
ID AAZ37532 standard; DNA; 20 BP.
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DB 20 CCAGTGCCCTGGCCGGAGA 1
RESULT 852
AAZ37520/c
ID AAZ37520 standard; DNA; 20 BP.
XX AAZ37520;
AC AAZ37520;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #50.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 GCCCAGGCGTGCTGCTTCC 221
ID AAZ37521 standard; DNA; 20 BP.
XX AAZ37521;
AC AAZ37521;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #51.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GCGCTGCTGCTTCCGAGTA 227
ID AAZ37531 standard; DNA; 20 BP.
XX AAZ37531;
AC AAZ37531;
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #61.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 AGGAGCAGGCAATGTGCAA 319
ID AAZ37532/c
XX AAZ37532 standard; DNA; 20 BP.
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XX AC AA237532;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #62.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GGAGCAGGCAAAATGTGCAAT 320
DB 20 GGAGCAGGCAAAATGTGCAAT 1

RESULT 856
AAZ37543/c
ID AAZ37543 standard; DNA; 20 BP.
XX AC AA237543;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #73.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 TGTGCAATACCAATGCTCT 332
DB 20 TGTGCAATACCAATGCTCT 1

RESULT 857
AAZ37555/c
ID AAZ37555 standard; DNA; 20 BP.
XX AC AA237555;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #85.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 TATCTTGGCCAGTATATTAT 496
DB 20 TATCTTGGCCAGTATATTAT 1

RESULT 858
AAZ37557/c
ID AAZ37557 standard; DNA; 20 BP.
XX AC AA237557;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #87.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

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KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGACTAAACGATTATATGAT 515
DB 20 TGACTAAACGATTATATGAT 1

RESULT 859
AAZ37562/c
ID AAZ37562 standard; DNA; 20 BP.
XX AC AA237562;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #92.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 538 ATTGTTCAAATGATCTTCTA 557
DB 20 ATTGTTCAAATGATCTTCTA 1

RESULT 860
AAZ37564/c
ID AAZ37564 standard; DNA; 20 BP.
XX AC AA237564;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #94.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 GAGATTTGTTGCGGTGCCA 578
DB 20 GAGATTTGTTGCGGTGCCA 1

RESULT 861
AAZ37567/c
ID AAZ37567 standard; DNA; 20 BP.
XX AC AA237567;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #97.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 587 TGTGAAGAGCAGAGAAA 606  
 DB 20 TGTGAAGAGCAGAGAAA 1

RESULT 862  
 AAZ37613/c  
 ID AAZ37613 standard; DNA; 20 BP.  
 XX  
 AC AAZ37613;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #143.  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 ATTATAGCCTTAGTGAAGAA 1103  
 DB 20 ATTATAGCCTTAGTGAAGAA 1

RESULT 863  
 AAZ37626/c  
 ID AAZ37626 standard; DNA; 20 BP.  
 XX  
 AC AAZ37626;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #156.  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GAAATGCACCTTCATGCAATG 1239  
 DB 20 GAAATGCACCTTCATGCAATG 1

RESULT 864  
 AAZ37628/c  
 ID AAZ37628 standard; DNA; 20 BP.  
 XX  
 AC AAZ37628;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #158.  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1257 CCATCATTGCAACAGATG 1276  
 DB 20 CCATCATTGCAACAGATG 1

RESULT 865  
 AAZ37644/c

ID AAZ37644 standard; DNA; 20 BP.  
 XX AAZ37644;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #174.  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1439 GGAAATGATGATAAAATTA 1458  
 DB 20 GGAAATGATGATAAAATTA 1

RESULT 866  
 AAZ37646/c  
 ID AAZ37646 standard; DNA; 20 BP.  
 XX  
 AC AAZ37646;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #176.  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1456 TTACACAAGCTTCACAATCA 1475  
 DB 20 TTACACAAGCTTCACAATCA 1

RESULT 867  
 AAZ37698/c  
 ID AAZ37698 standard; DNA; 20 BP.  
 XX  
 AC AAZ37698;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #228.  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1956 TATAATTTGACTTGAATATG 1975  
 DB 20 TATAATTTGACTTGAATATG 1

RESULT 868  
 AAZ37711/c  
 ID AAZ37711 standard; DNA; 20 BP.  
 XX  
 AC AAZ37711;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #241.

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XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTTACCCAGGCTG 2130
DB 20 TTGCTCTGTTACCCAGGCTG 1

RESULT 869
AAZ37718/c
ID AAZ37718 standard; DNA; 20 BP.
XX
AC AAZ37718;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #248.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2176 GGGTTGCGCACCATTCCTCG 2195
DB 20 GGGTTGCGCACCATTCCTCG 1

RESULT 870
AAZ37725/c
ID AAZ37725 standard; DNA; 20 BP.
XX
AC AAZ37725;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #255.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2218 GCCTACAGTCATCTGCCACC 2237
DB 20 GCCTACAGTCATCTGCCACC 1

RESULT 871
AAZ37732/c
ID AAZ37732 standard; DNA; 20 BP.
XX
AC AAZ37732;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #262.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2298 GGTCTCGATCTCTGACCTC 2317
DB 20 GGTCTCGATCTCTGACCTC 1

RESULT 872
AAZ37504/c
ID AAZ37504 standard; DNA; 20 BP.
XX
AC AAZ37504;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #34.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TTGGCTGCTTCTGGGCGCTG 33
DB 20 TTGGCTGCTTCTGGGCGCTG 1

RESULT 873
AAZ37561/c
ID AAZ37561 standard; DNA; 20 BP.
XX
AC AAZ37561;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #91.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 531 ATTGTATATTTCTCAATGA 550
DB 20 ATTGTATATTTCTCAATGA 1

RESULT 874
AAZ37563/c
ID AAZ37563 standard; DNA; 20 BP.
XX
AC AAZ37563;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #93.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 GATCTTCTAGGAGATTGTT 568
DB 20 GATCTTCTAGGAGATTGTT 1

RESULT 875

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AAZ37578/c
ID AAZ37578 standard; DNA; 20 BP.
XX
AC AAZ37578;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #108.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 704 TGGGAGTGATCAAAAGGACC 723
DB 20 TGGGAGTGATCAAAAGGACC 1
RESULT 876
AAZ37590/c
ID AAZ37590 standard; DNA; 20 BP.
XX
AC AAZ37590;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #120.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 844 AACGACAAAGAAAGCCAC 863
DB 20 AACGACAAAGAAAGCCAC 1
RESULT 877
AAZ37594/c
ID AAZ37594 standard; DNA; 20 BP.
XX
AC AAZ37594;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #124.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 895 AAAGCCTGGCTGTGTGTA 914
DB 20 AAAGCCTGGCTGTGTGTA 1
RESULT 878
AAZ37618/c
ID AAZ37618 standard; DNA; 20 BP.
XX
AC AAZ37618;
XX
DT 07-JAN-2000 (first entry)
XX

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DE Human mdm2 phosphorothioate oligodeoxynucleotide #148.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1124 AGATGATGAGGTATATCAAG 1143
DB 20 AGATGATGAGGTATATCAAG 1
RESULT 879
AAZ37655/c
ID AAZ37655 standard; DNA; 20 BP.
XX
AC AAZ37655;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #185.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1541 TGTGAAAGAGTTTGAAGGG 1560
DB 20 TGTGAAAGAGTTTGAAGGG 1
RESULT 880
AAZ37688/c
ID AAZ37688 standard; DNA; 20 BP.
XX
AC AAZ37688;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #218.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1883 TGCCTCAATTTCACATAGATT 1902
DB 20 TGCCTCAATTTCACATAGATT 1
RESULT 881
AAZ37692/c
ID AAZ37692 standard; DNA; 20 BP.
XX
AC AAZ37692;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #222.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX Antisense oligonucleotide S5-6 directed against MDM2 encoding RNA.  
DE  
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;  
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 GTGATCAAAAGGACCTTGTA 728  
DB 1 GTGATCAAAAGGACCTTGTA 20

RESULT 889  
AAAX35113  
ID AAX35113 standard; DNA; 20 BP.  
XX  
AC AAX35113;  
XX  
DT 01-JUL-1999 (first entry)  
XX  
DE Antisense oligonucleotide S7-2 directed against MDM2 encoding RNA.  
XX  
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;  
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 ATTGAGGTGATTGGTGGAT 1022  
DB 1 ATTGAGGTGATTGGTGGAT 20

RESULT 890  
AAAX35132/c  
ID AAX35132 standard; DNA; 20 BP.  
XX  
AC AAX35132;  
XX  
DT 01-JUL-1999 (first entry)  
XX  
DE Antisense oligonucleotide AS5-6 directed against MDM2 encoding RNA.  
XX  
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;  
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 GTGATCAAAAGGACCTTGTA 728  
DB 20 GTGATCAAAAGGACCTTGTA 1

RESULT 891  
AAAX35100  
ID AAX35100 standard; DNA; 20 BP.  
XX  
AC AAX35100;  
XX  
DT 01-JUL-1999 (first entry)  
XX  
DE Antisense oligonucleotide S2 directed against MDM2 encoding RNA.  
XX  
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;  
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 CCAGCTTCGGAACAAGAGAC 388  
DB 1 CCAGCTTCGGAACAAGAGAC 20

RESULT 892  
AAAX35101  
ID AAX35101 standard; DNA; 20 BP.  
XX  
AC AAX35101;  
XX  
DT 01-JUL-1999 (first entry)  
XX  
DE Antisense oligonucleotide S3 directed against MDM2 encoding RNA.  
XX  
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;  
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 TCTACCTCATCTAGAGGAG 799  
DB 1 TCTACCTCATCTAGAGGAG 20

RESULT 893  
AAAX35103  
ID AAX35103 standard; DNA; 20 BP.  
XX  
AC AAX35103;  
XX  
DT 01-JUL-1999 (first entry)  
XX  
DE Antisense oligonucleotide S8 directed against MDM2 encoding RNA.  
XX  
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;  
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249  
DB 1 TCATGCAATGAATGAATCC 20

RESULT 894  
AAAX35137/c  
ID AAX35137 standard; DNA; 20 BP.  
XX  
AC AAX35137;  
XX  
DT 01-JUL-1999 (first entry)  
XX  
DE Antisense oligonucleotide AS7-4 directed against MDM2 encoding RNA.  
XX  
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;  
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATTGAGTTTCAGATCAGTTT 1046  
DB 20 ATTGAGTTTCAGATCAGTTT 1



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RESULT 895
AAX35139/c
ID AAX35139 standard; DNA; 20 BP.
XX
XX
AC AAX35139;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide ASS-2H directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTCAGAACAGGTGTCA 694
Db 20 GTGAGTCAGAACAGGTGTCA 1

RESULT 896
AAX35122/c
ID AAX35122 standard; DNA; 20 BP.
XX
XX
AC AAX35122;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 ACCTCACAGATTCAGCTTC 376
Db 20 ACCTCACAGATTCAGCTTC 1

RESULT 897
AAX35134/c
ID AAX35134 standard; DNA; 20 BP.
XX
XX
AC AAX35134;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7-1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 998 TGAACATTCAGGTGATTGGT 1017
Db 20 TGAACATTCAGGTGATTGGT 1

RESULT 898
AAX35094
ID AAX35094 standard; DNA; 20 BP.
XX
XX
AC AAX35094;
XX

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DT 01-JUL-1999 (first entry)
XX
XX Antisense oligonucleotide S4 directed against MDM2 encoding RNA.
XX
XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TTGGCCAGTATATTATGACT 500
Db 1 TTGGCCAGTATATTATGACT 20

RESULT 899
AAX35099
ID AAX35099 standard; DNA; 20 BP.
XX
XX
AC AAX35099;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 ACCTCACAGATTCAGCTTC 376
Db 1 ACCTCACAGATTCAGCTTC 20

RESULT 900
AAX35116
ID AAX35116 standard; DNA; 20 BP.
XX
XX
AC AAX35116;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S7-5 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTTAGTGTAGAATT 1057
Db 1 GATCAGTTTAGTGTAGAATT 20

RESULT 901
AAX35121/c
ID AAX35121 standard; DNA; 20 BP.
XX
XX
AC AAX35121;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 TGGATCAGGATTCAGTTTCA 1037
Db      20 TGGATCAGGATTCAGTTTCA 1

RESULT 902
AAX35126/c
ID AAX35126 standard; DNA; 20 BP.
XX
AC AAX35126;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide AS8 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249
Db      20 TCATGCAATGAATGAATCC 1

RESULT 903
AAX35096
ID AAX35096 standard; DNA; 20 BP.
XX
AC AAX35096;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide S7 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 TGGATCAGGATTCAGTTTCA 1037
Db      1 TGGATCAGGATTCAGTTTCA 20

RESULT 904
AAX35127/c
ID AAX35127 standard; DNA; 20 BP.
XX
AC AAX35127;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide AS5-1 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAACAG 688
Db      20 ACATCTGTGAGTGAACAG 1
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RESULT 905
AAX35111
ID AAX35111 standard; DNA; 20 BP.
XX
AC AAX35111;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide SS-7 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 AAGGACCTTGTACAGAGCT 736
Db      1 AAGGACCTTGTACAGAGCT 20

RESULT 906
AAX35123/c
ID AAX35123 standard; DNA; 20 BP.
XX
AC AAX35123;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide AS2 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 CCAGCTTCGGAACAAGAGAC 388
Db      20 CCAGCTTCGGAACAAGAGAC 1

RESULT 907
AAX35095
ID AAX35095 standard; DNA; 20 BP.
XX
AC AAX35095;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide S5 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 695 CCTTGAAGGTGGAGTGATC 714
Db      1 CCTTGAAGGTGGAGTGATC 20

RESULT 908
AAX35119/c
ID AAX35119 standard; DNA; 20 BP.
XX
AC AAX35119;
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XX 01-JUL-1999 (first entry)
XX Antisense oligonucleotide AS4 directed against MDM2 encoding RNA.
XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
XX inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TTGCCAGTATATTATGACT 500
DB 20 TTGCCAGTATATTATGACT 1

RESULT 909
AAX35138/c
ID AAX35138 standard; DNA; 20 BP.
XX
XX AAX35138;
XX
DT 01-JUL-1999 (first entry)
XX
XX Antisense oligonucleotide AS7-5 directed against MDM2 encoding RNA.
DE MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTTACTGTAGATT 1057
DB 20 GATCAGTTTACTGTAGATT 1

RESULT 910
AAX35102
ID AAX35102 standard; DNA; 20 BP.
XX
XX AAX35102;
XX
DT 01-JUL-1999 (first entry)
XX
XX Antisense oligonucleotide S6 directed against MDM2 encoding RNA.
DE MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 TCCTTAGCTGACTATTGGAA 1222
DB 1 TCCTTAGCTGACTATTGGAA 20

RESULT 911
AAX35106
ID AAX35106 standard; DNA; 20 BP.
XX
XX AAX35106;
XX
DT 01-JUL-1999 (first entry)
XX
XX Antisense oligonucleotide S5-2 directed against MDM2 encoding RNA.
DE MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
DB 1 GTGAGTGAGAACAGGTGTCA 20

RESULT 912
AAX35112
ID AAX35112 standard; DNA; 20 BP.
XX
XX AAX35112;
XX
DT 01-JUL-1999 (first entry)
XX
XX Antisense oligonucleotide S7-1 directed against MDM2 encoding RNA.
DE MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 998 TGAACATTTCAGGTGATTGGT 1017
DB 1 TGAACATTTCAGGTGATTGGT 20

RESULT 913
AAX35131/c
ID AAX35131 standard; DNA; 20 BP.
XX
XX AAX35131;
XX
DT 01-JUL-1999 (first entry)
XX
XX Antisense oligonucleotide AS5-5 directed against MDM2 encoding RNA.
DE MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723
DB 20 TGGGAGTGATCAAAAGGACC 1

RESULT 914
AAX35115
ID AAX35115 standard; DNA; 20 BP.
XX
XX AAX35115;
XX
DT 01-JUL-1999 (first entry)
XX
XX Antisense oligonucleotide S7-4 directed against MDM2 encoding RNA.
DE MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATTCACTTTTCAGATCATGTTT 1046
DB 1 ATTCACTTTTCAGATCATGTTT 1046

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Db      1 ATTCAGTTTCAGATCAGTTT 20

RESULT 915
AAX35107
ID AAX35107 standard; DNA; 20 BP.
XX
AC AAX35107;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      680 TGAGAACAGGTGTCTACCTTG 699
Db      1 TGAGAACAGGTGTCTACCTTG 20

RESULT 916
AAX35124/c
ID AAX35124 standard; DNA; 20 BP.
XX
AC AAX35124;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      780 TCTACCTCATCTAGAGGAG 799
Db      20 TCTACCTCATCTAGAGGAG 1

RESULT 917
AAX35133/c
ID AAX35133 standard; DNA; 20 BP.
XX
AC AAX35133;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS5-7 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      717 AAGGACCTTGTCAGAGCT 736
Db      20 AAGGACCTTGTCAGAGCT 1

RESULT 918
AAX35109
ID AAX35109 standard; DNA; 20 BP.
XX
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```
AC AAX35109;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-5 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      704 TGGGAGTGATCAAAAGGACC 723
Db      1 TGGGAGTGATCAAAAGGACC 20

RESULT 919
AAX35105
ID AAX35105 standard; DNA; 20 BP.
XX
AC AAX35105;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      669 ACATCTGTGAGTGAGAACAG 688
Db      1 ACATCTGTGAGTGAGAACAG 20

RESULT 920
AAX35108
ID AAX35108 standard; DNA; 20 BP.
XX
AC AAX35108;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-4 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      685 ACAGGTGTCACTTGAAGGT 704
Db      1 ACAGGTGTCACTTGAAGGT 20

RESULT 921
AAX35128/c
ID AAX35128 standard; DNA; 20 BP.
XX
AC AAX35128;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS5-2 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
```

```
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACACAGGTGTCA 694
DB 20 GTGAGTGAGAACACAGGTGTCA 1
|||||
DB 20 TAGTAGAGACAGGGTTTCAC 1
|||||

RESULT 922
AAAX35129/c
ID AAX35129 standard; DNA; 20 BP.
XX
AC AAX35129;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS5-3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGAACAGGTGTCACTTG 699
DB 20 TGAGAACAGGTGTCACTTG 1
|||||

RESULT 923
AAAX35135/c
ID AAX35135 standard; DNA; 20 BP.
XX
AC AAX35135;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7-2 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 ATTCAGGTGATTGGTTGGAT 1022
DB 20 ATTCAGGTGATTGGTTGGAT 1
|||||

RESULT 924
AAZ43583/c
ID AAZ43583 standard; DNA; 20 BP.
XX
AC AAZ43583;
XX
DT 21-FEB-2000 (first entry)
XX
DE Alzheimer's disease detecting primer #10.
XX
KW Alzheimer's disease; primer; dihydrolipoamidodisuccinyl transferase;
KW mitochondria; alpha-ketoglutarate dehydrogenase; detection; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCAC 2282
DB 20 TAGTAGAGACAGGGTTTCAC 1
|||||

KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACACAGGTGTCA 694
DB 20 GTGAGTGAGAACACAGGTGTCA 1
|||||
DB 20 TAGTAGAGACAGGGTTTCAC 1
|||||

RESULT 925
AAAY96410/c
ID AAA96410 standard; DNA; 20 BP.
XX
AC AAA96410;
XX
DT 08-FEB-2001 (first entry)
XX
DE Primer used to amplify a sara43/44 polymorphic microsatellite repeat.
XX
KW Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;
KW ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRL; lupus;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
DB 20 CCCAGGCTGGAGTGCAGTGG 1
|||||

RESULT 926
AAZ89373
ID AAZ89373 standard; DNA; 20 BP.
XX
AC AAZ89373;
XX
DT 15-JUN-2000 (first entry)
XX
DE Human mdm-2 PCR primer MDM2PR1.
XX
KW Human; mdm-2; PCR primer; reaction container; quantitation; diagnosis;
KW food analysis; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1531 GCCAAGAAGATGTGAAGAG 1550
DB 1 GCCAAGAAGATGTGAAGAG 20
|||||

RESULT 927
AAA28013
ID AAA28013 standard; DNA; 20 BP.
XX
AC AAA28013;
XX
DT 29-AUG-2000 (first entry)
XX
DE Uncoupling protein isoform UCP5SI nucleotide sequence PCR primer.
XX
KW Uncoupling protein 5; UCP5; metabolism; chromosome 10q23-25; H+ leak;
KW metabolic rate; obesity; stroke; trauma; burn trauma; sepsis; infection;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2349 TGGATTACAGGCATGAGCC 2368
DB 1 TGGATTACAGGCATGAGCC 20
|||||

RESULT 928
AAA14945/c
ID AAA14945 standard; DNA; 20 BP.
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XX AAA14945;
AC
XX
DT 08-AUG-2000 (first entry)
DE PCR primer SR1 used to amplify the repeated DNA sequences Alu.
XX Chromosomal labelling; chromosomal band; IRS-PCR; Alu; LINE; karyotype;
XX interspersed repeat sequence-polymerase chain reaction; probe;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCAGGCTGGAGTGCAGTGG 2141
Db 20 CCCAGGCTGGAGTGCAGTGG 1

RESULT 929
AAA97667/c
ID AAA97667 standard; DNA; 20 BP.
XX
AC AAA97667;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2 PCR primer 4.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 676 TGAGTGAGACACAGGTGCAC 695
Db 20 TGAGTGAGACACAGGTGCAC 1

RESULT 930
AAA97654/c
ID AAA97654 standard; DNA; 20 BP.
XX
AC AAA97654;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2-targeted pseudocyclic oligonucleotide 12.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
Db 20 GTGAGTGAGAACAGGTGTCA 1

RESULT 931
AAA97657/c
ID AAA97657 standard; DNA; 20 BP.
XX
AC AAA97657;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2-targeted pseudocyclic oligonucleotide 1.
XX

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KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
Db 20 GTGAGTGAGAACAGGTGTCA 1

RESULT 932
AAA97656/c
ID AAA97656 standard; DNA; 20 BP.
XX
AC AAA97656;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2-targeted pseudocyclic oligonucleotide 14.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
Db 20 GTGAGTGAGAACAGGTGTCA 1

RESULT 933
AAA97665/c
ID AAA97665 standard; DNA; 20 BP.
XX
AC AAA97665;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2 PCR primer 2.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
Db 20 GTGAGTGAGAACAGGTGTCA 1

RESULT 934
AAA97669/c
ID AAA97669 standard; DNA; 20 BP.
XX
AC AAA97669;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2 PCR primer 6.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
Db 20 GTGAGTGAGAACAGGTGTCA 1

RESULT 934
AAA97669/c
ID AAA97669 standard; DNA; 20 BP.
XX
AC AAA97669;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2 PCR primer 6.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 672 TCTGTGAGTGAGAACAGGTG 691  
 Db 20 TCTGTGAGTGAGAACAGGTG 1

RESULT 935  
 AAA97655/c  
 ID AAA97655 standard; DNA; 20 BP.  
 XX  
 AC  
 AC AAA97655;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Human MDM2-targeted pseudocyclic oligonucleotide 13.  
 KW Pseudocyclic oligonucleotide; functional segment; protective segment;  
 KW nucleic acid detection; mRNA cleavage; antisense therapy;  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTC 694  
 Db 20 GTGAGTGAGAACAGGTGTC 1

RESULT 936  
 AAA97666/c  
 ID AAA97666 standard; DNA; 20 BP.  
 XX  
 AC  
 AC AAA97666;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Human MDM2 PCR primer 3.  
 KW Pseudocyclic oligonucleotide; functional segment; protective segment;  
 KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 GAGTGAGAACAGGTGTACC 696  
 Db 20 GAGTGAGAACAGGTGTACC 1

RESULT 937  
 AAA97668/c  
 ID AAA97668 standard; DNA; 20 BP.  
 XX  
 AC  
 AC AAA97668;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Human MDM2 PCR primer 5.  
 KW Pseudocyclic oligonucleotide; functional segment; protective segment;  
 KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 674 TGTGAGTGAGAACAGGTGTC 693  
 Db 20 TGTGAGTGAGAACAGGTGTC 1

RESULT 938  
 AAD14808

ID AAD14808 standard; DNA; 20 BP.  
 XX  
 AC  
 AC AAD14808;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Human glycogen synthase kinase 3 alpha antisense oligo ISIS #116649.  
 KW Human; glycogen synthase kinase 3 alpha; antidiabetic; cytostatic;  
 KW antisense therapy; diabetes; hyperproliferative disorder; inflammation;  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAAGTGCTGGGATTAC 2357  
 Db 1 TCCCAAAGTGCTGGGATTAC 20

RESULT 939  
 AAK95176/c  
 ID AAK95176 standard; DNA; 20 BP.  
 XX  
 AC  
 AC AAK95176;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human cDNA clone-specific primer, SEQ ID NO: 4421.  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTGCTGGGATTACAGG 2360  
 Db 20 CAAAGTGCTGGGATTACAGG 1

RESULT 940  
 AAF23807/c  
 ID AAF23807 standard; DNA; 20 BP.  
 XX  
 AC  
 AC AAF23807;  
 XX  
 DT 22-MAR-2001 (first entry)  
 XX  
 DE Oligo #7 used to produce ligand-conjugated oligomeric compounds.  
 KW Ligand-conjugated oligomeric compound; aryl propionic acid;  
 KW nucleic acid delivery; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTCATGTGCAAGAAGCT 1714  
 Db 20 TTTCATGTGCAAGAAGCT 1

RESULT 941  
 AAF80627/c  
 ID AAF80627 standard; DNA; 20 BP.  
 XX  
 AC  
 AC AAF80627;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligonucleotide #1.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
KW  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTG 20  
Db 20 GCACCGCGGAGCTTGGCTG 1

RESULT 942

AAF80629/c

ID AAF80629 standard; DNA; 20 BP.

XX

AC AAF80629;

XX

DT 02-MAY-2001 (first entry)

XX

DE Human mdm2 phosphorothioate oligonucleotide #3.

XX

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCTCTGCTG 114  
Db 20 CTCTGACCGAGATCTCTGCTG 1

RESULT 943

AAF80643/c

ID AAF80643 standard; DNA; 20 BP.

XX

AC AAF80643;

XX

DT 02-MAY-2001 (first entry)

XX

DE Human mdm2 phosphorothioate oligonucleotide #17.

XX

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGGAAATAGTAATACTT 1953  
Db 20 TAGTGGAAATAGTAATACTT 1

RESULT 944

AAF80681/c

ID AAF80681 standard; DNA; 20 BP.

XX

AC AAF80681;

XX

DT 02-MAY-2001 (first entry)

XX

DE Human mdm2 phosphorothioate oligonucleotide #55.

XX

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GGTGAGGAGCAGCAATGT 315  
Db 20 GGTGAGGAGCAGCAATGT 1

RESULT 945

AAF80687/c

ID AAF80687 standard; DNA; 20 BP.

XX

AC AAF80687;

XX

DT 02-MAY-2001 (first entry)

XX

DE Human mdm2 phosphorothioate oligonucleotide #61.

XX

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GAGCAGGCAATGTGCAATA 321  
Db 20 GAGCAGGCAATGTGCAATA 1

RESULT 946

AAF80688/c

ID AAF80688 standard; DNA; 20 BP.

XX

AC AAF80688;

XX

DT 02-MAY-2001 (first entry)

XX

DE Human mdm2 phosphorothioate oligonucleotide #62.

XX

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAATGTGCAATACC 323  
Db 20 GCAGGCAATGTGCAATACC 1

RESULT 947

AAF80700/c

ID AAF80700 standard; DNA; 20 BP.

XX

AC AAF80700;

XX

DT 02-MAY-2001 (first entry)

XX

DE Human mdm2 phosphorothioate oligonucleotide #74.

XX

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 TACCTACTGATGTGCTGTA 353  
Db 20 TACCTACTGATGTGCTGTA 1

RESULT 948



```
AAF80705/c
ID AAF80705 standard; DNA; 20 BP.
XX
AC AAF80705;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #79.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 GGTTAGACCAAGCCATTGC 411
Db ||||| ||||| ||||| ||||| |||||
20 GGTTAGACCAAGCCATTGC 1

RESULT 949
AAF80710/c
ID AAF80710 standard; DNA; 20 BP.
XX
AC AAF80710;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #84.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 ATATTATGACTAAACGATTA 509
Db ||||| ||||| ||||| ||||| |||||
20 ATATTATGACTAAACGATTA 1

RESULT 950
AAF80720/c
ID AAF80720 standard; DNA; 20 BP.
XX
AC AAF80720;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #94.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 GCCAAGCTTCTCTGTGAAG 594
Db ||||| ||||| ||||| ||||| |||||
20 GCCAAGCTTCTCTGTGAAG 1

RESULT 951
AAF80727/c
ID AAF80727 standard; DNA; 20 BP.
XX
AC AAF80727;
XX
DT 02-MAY-2001 (first entry)
XX

DE Human mdm2 phosphorothioate oligonucleotide #101.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 646 AGCAGGAATCATCGGACTCA 665
Db ||||| ||||| ||||| ||||| |||||
20 AGCAGGAATCATCGGACTCA 1

RESULT 952
AAF80728/c
ID AAF80728 standard; DNA; 20 BP.
XX
AC AAF80728;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #102.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 ATCGGACTCAGGTACATCTG 675
Db ||||| ||||| ||||| ||||| |||||
20 ATCGGACTCAGGTACATCTG 1

RESULT 953
AAF80733/c
ID AAF80733 standard; DNA; 20 BP.
XX
AC AAF80733;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #107.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 718 AGGACCTTGTACAAGAGCTT 737
Db ||||| ||||| ||||| ||||| |||||
20 AGGACCTTGTACAAGAGCTT 1

RESULT 954
AAF80795/c
ID AAF80795 standard; DNA; 20 BP.
XX
AC AAF80795;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #169.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GAATGATCCAGAGATCAT 1431
DB 20 GAATGATCCAGAGATCAT 1

RESULT 955
AAF80798/c
ID AAF80798 standard; DNA; 20 BP.
XX
AC AAF80798;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #172.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1439 GGAAATGATGATAAAATTA 1458
DB 20 GGAAATGATGATAAAATTA 1

RESULT 956
AAF80888/c
ID AAF80888 standard; DNA; 20 BP.
XX
AC AAF80888;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #262.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCT 2338
DB 20 TGATCCGCCACCTCGGCT 1

RESULT 957
AAF80641/c
ID AAF80641 standard; DNA; 20 BP.
XX
AC AAF80641;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #15.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 TAGTTGACCTGTCTATAGA 1804
DB 20 TAGTTGACCTGTCTATAGA 1

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RESULT 958
AAF80689/c
ID AAF80689 standard; DNA; 20 BP.
XX
AC AAF80689;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #63.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGCAATGTGCAATACCA 324
DB 20 CAGGCAATGTGCAATACCA 1

RESULT 959
AAF80718/c
ID AAF80718 standard; DNA; 20 BP.
XX
AC AAF80718;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #92.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 GAGATTGTTGGCGTGCCA 578
DB 20 GAGATTGTTGGCGTGCCA 1

RESULT 960
AAF80735/c
ID AAF80735 standard; DNA; 20 BP.
XX
AC AAF80735;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #109.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 740 GGAAGAGAAACCTTCATCTT 759
DB 20 GGAAGAGAAACCTTCATCTT 1

RESULT 961
AAF80778/c
ID AAF80778 standard; DNA; 20 BP.
XX
AC AAF80778;
XX
DT 02-MAY-2001 (first entry)

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XX Human mdm2 phosphorothioate oligonucleotide #152.  
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1196 TGAATTTCTTAGCTGACT 1215  
 DB 20 TGAATTTCTTAGCTGACT 1

RESULT 962  
 AAF80784/c  
 ID AAF80784 standard; DNA; 20 BP.  
 XX AC AAF80784;  
 XX

DT 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #158.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1275 TGTGGGCCCTTCGTGAGAA 1294  
 DB 20 TGTGGGCCCTTCGTGAGAA 1

RESULT 963  
 AAF80788/c  
 ID AAF80788 standard; DNA; 20 BP.  
 XX AC AAF80788;  
 XX

DT 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #162.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1311 AAAGGGAAGATAAAGGGGA 1330  
 DB 20 AAAGGGAAGATAAAGGGGA 1

RESULT 964  
 AAF80789/c  
 ID AAF80789 standard; DNA; 20 BP.  
 XX AC AAF80789;  
 XX

DT 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #163.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1325 AGGGGAATCTCTGAGAAAG 1344  
 DB 20 AGGGGAATCTCTGAGAAAG 1

RESULT 965  
 AAF80791/c  
 ID AAF80791 standard; DNA; 20 BP.  
 XX AC AAF80791;  
 XX

DT 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #165.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1346 CAAACTGGAAACTCAACAC 1365  
 DB 20 CAAACTGGAAACTCAACAC 1

RESULT 966  
 AAF80801/c  
 ID AAF80801 standard; DNA; 20 BP.  
 XX AC AAF80801;  
 XX

DT 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #175.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1466 TTCACAATCACAAAGATG 1485  
 DB 20 TTCACAATCACAAAGATG 1

RESULT 967  
 AAF80817/c  
 ID AAF80817 standard; DNA; 20 BP.  
 XX AC AAF80817;  
 XX

DT 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #191.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1648 AAAATGTTGCATTTGCCAT 1667  
 DB 20 AAAATGTTGCATTTGCCAT 1

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RESULT 968
AAF80826/c
ID AAF80826 standard; DNA; 20 BP.
XX
XX AAF80826;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #200.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 ATAAGCCCTGCCAGTATGT 1745
DB 20 ATAAGCCCTGCCAGTATGT 1
XX

RESULT 969
AAF80836/c
ID AAF80836 standard; DNA; 20 BP.
XX
XX AAF80836;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #210.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 ATAAGCCCTGCCAGTATGT 1745
DB 20 ATAAGCCCTGCCAGTATGT 1
XX

RESULT 970
AAF80839/c
ID AAF80839 standard; DNA; 20 BP.
XX
XX AAF80839;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #213.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1832 CTAGGAATTTAGACAACTG 1851
DB 20 CTAGGAATTTAGACAACTG 1
XX

RESULT 970
AAF80839/c
ID AAF80839 standard; DNA; 20 BP.
XX
XX AAF80839;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #213.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1855 TTTATTTCATATATCAAG 1874
DB 20 TTTATTTCATATATCAAG 1
XX

RESULT 971
AAF80842/c
ID AAF80842 standard; DNA; 20 BP.
XX
XX AAF80842;
XX
XX

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DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #216.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1883 TGCCTCAATTCACATAGATT 1902
DB 20 TGCCTCAATTCACATAGATT 1
XX

RESULT 972
AAF80845/c
ID AAF80845 standard; DNA; 20 BP.
XX
XX AAF80845;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #219.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1905 TTCTCTTTAGTATAATTGAC 1924
DB 20 TTCTCTTTAGTATAATTGAC 1
XX

RESULT 973
AAF80848/c
ID AAF80848 standard; DNA; 20 BP.
XX
XX AAF80848;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #222.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1920 TTGACCTACTTGGTAGTGG 1939
DB 20 TTGACCTACTTGGTAGTGG 1
XX

RESULT 974
AAF80860/c
ID AAF80860 standard; DNA; 20 BP.
XX
XX AAF80860;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #234.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 TCTGCTTAAATGAGAAGTA 2039
DB 20 TCTGCTTAAATGAGAAGTA 1

RESULT 975
AAF80892/c
ID AAF80892 standard; DNA; 20 BP.
XX
AC AAF80892;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #266.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCAC 2370
DB 20 GGATTACAGGCATGAGCCAC 1

RESULT 976
AAF80638/c
ID AAF80638 standard; DNA; 20 BP.
XX
AC AAF80638;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #12.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTGATTGTA 1400
DB 20 TTGATGTTCTGATTGTA 1

RESULT 977
AAF80674/c
ID AAF80674 standard; DNA; 20 BP.
XX
AC AAF80674;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #48.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 GCCCAGGGCGTGTGCTTCC 221
DB 20 GCCCAGGGCGTGTGCTTCC 1

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 978
AAF80745/c
ID AAF80745 standard; DNA; 20 BP.
XX
AC AAF80745;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #119.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACGCCACAAATCTGATAGTA 876
DB 20 ACGCCACAAATCTGATAGTA 1

RESULT 979
AAF80755/c
ID AAF80755 standard; DNA; 20 BP.
XX
AC AAF80755;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #129.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 971 GAATCCGGATCTTGATGCTG 990
DB 20 GAATCCGGATCTTGATGCTG 1

RESULT 980
AAF80763/c
ID AAF80763 standard; DNA; 20 BP.
XX
AC AAF80763;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #137.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 TAGAATTTGAAGTTGAATCT 1070
DB 20 TAGAATTTGAAGTTGAATCT 1

RESULT 981
AAF80767/c
ID AAF80767 standard; DNA; 20 BP.
XX
AC AAF80767;

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XX 02-MAY-2001 (first entry)
DT Human mdm2 phosphorothioate oligonucleotide #141.
DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 ATTATAGCCTTAGTGAAGAA 1103
DB 20 ATTATAGCCTTAGTGAAGAA 1

RESULT 982
AAF80785/c
ID AAF80785 standard; DNA; 20 BP.
XX
AC AAF80785;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #159.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1283 CCTTCGTGAGAAATGGCTTC 1302
DB 20 CCTTCGTGAGAAATGGCTTC 1

RESULT 983
AAF80820/c
ID AAF80820 standard; DNA; 20 BP.
XX
AC AAF80820;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #194.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1675 CAGGACATCTTATGGCCTGC 1694
DB 20 CAGGACATCTTATGGCCTGC 1

RESULT 984
AAF80840/c
ID AAF80840 standard; DNA; 20 BP.
XX
AC AAF80840;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #214.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
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```
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TATATCAAAAGTGAGAAAATG 1884
DB 20 TATATCAAAAGTGAGAAAATG 1

RESULT 985
AAF80850/c
ID AAF80850 standard; DNA; 20 BP.
XX
AC AAF80850;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #224.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
```

```
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1940 AATAGTGAATACTTACTATA 1959
DB 20 AATAGTGAATACTTACTATA 1

RESULT 986
AAF80859/c
ID AAF80859 standard; DNA; 20 BP.
XX
AC AAF80859;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #233.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
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```
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2015 TCTACTCTGCTTAAATGAG 2034
DB 20 TCTACTCTGCTTAAATGAG 1

RESULT 987
AAF80861/c
ID AAF80861 standard; DNA; 20 BP.
XX
AC AAF80861;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #235.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
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```
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2051 TTTTCTTAAATATGTATATG 2070
DB 20 TTTTCTTAAATATGTATATG 1
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Db      20 TTTTCTTAATAATATGATATG 1

RESULT 988
AAF80883/c
ID   AAF80883 standard; DNA; 20 BP.
XX
XX
AC   AAF80883;
XX
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #257.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2274 GGGTTTCACCGTGTAGCCA 2293
      |||||
      20 GGGTTTCACCGTGTAGCCA 1

Db

RESULT 989
AAF80889/c
ID   AAF80889 standard; DNA; 20 BP.
XX
XX
AC   AAF80889;
XX
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #263.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2325 GCCCACCTCGGCTCCCAA 2344
      |||||
      20 GCCCACCTCGGCTCCCAA 1

Db

RESULT 990
AAF80634/c
ID   AAF80634 standard; DNA; 20 BP.
XX
XX
AC   AAF80634;
XX
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #8.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      303 AGCAGGCAATGTGCAATAC 322
      |||||
      20 AGCAGGCAATGTGCAATAC 1

Db

RESULT 991
AAF80646/c
ID   AAF80646 standard; DNA; 20 BP.
XX
XX

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AC   AAF80646;
XX
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #20.
XX
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2256 GTACTTTTAGTAGACAGG 2275
      |||||
      20 GTACTTTTAGTAGACAGG 1

Db

RESULT 992
AAF80671/c
ID   AAF80671 standard; DNA; 20 BP.
XX
XX
AC   AAF80671;
XX
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #45.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      158 CGAGCGCCCGAGTGCCCTGGC 177
      |||||
      20 CGAGCGCCCGAGTGCCCTGGC 1

Db

RESULT 993
AAF80715/c
ID   AAF80715 standard; DNA; 20 BP.
XX
XX
AC   AAF80715;
XX
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #89.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      531 ATTGTATATTGTCAAATGA 550
      |||||
      20 ATTGTATATTGTCAAATGA 1

Db

RESULT 994
AAF80719/c
ID   AAF80719 standard; DNA; 20 BP.
XX
XX
AC   AAF80719;
XX
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #93.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 GTTGGCGTGCACAGCTTCT 585
DB 20 GTTGGCGTGCACAGCTTCT 1

RESULT 995
AAF80725/c
ID AAF80725 standard; DNA; 20 BP.
XX
AC AAF80725;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #99.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 TCTACAGAACTTGGTAGTA 638
DB 20 TCTACAGAACTTGGTAGTA 1

RESULT 996
AAF80742/c
ID AAF80742 standard; DNA; 20 BP.
XX
AC AAF80742;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #116.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 824 TTCAGATCAATTATCTGGTG 843
DB 20 TTCAGATCAATTATCTGGTG 1

RESULT 997
AAF80756/c
ID AAF80756 standard; DNA; 20 BP.
XX
AC AAF80756;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #130.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 TGATGCTGGTGAAGTGAAC 1002
DB 20 TGATGCTGGTGAAGTGAAC 1

RESULT 998
AAF80765/c
ID AAF80765 standard; DNA; 20 BP.
XX
AC AAF80765;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #139.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1068 TCTCTGACTCAGAAGATTA 1087
DB 20 TCTCTGACTCAGAAGATTA 1

RESULT 999
AAF80779/c
ID AAF80779 standard; DNA; 20 BP.
XX
AC AAF80779;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #153.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 TAGCTGACTATTGGAATGC 1226
DB 20 TAGCTGACTATTGGAATGC 1

RESULT 1000
AAF80803/c
ID AAF80803 standard; DNA; 20 BP.
XX
AC AAF80803;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #177.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1489 ACTATTCTCAGCCATCAACT 1508
DB 20 ACTATTCTCAGCCATCAACT 1

RESULT 1001
AAF80810/c
ID AAF80810 standard; DNA; 20 BP.
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XX AAF80810;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #184.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1550 GTTTGAAGGGAAGAACCC 1569
| | | | | | | | | | | | | | | | | |
Db 20 GTTTGAAGGGAAGAACCC 1

RESULT 1002
AAF80812/c
ID AAF80812 standard; DNA; 20 BP.
XX
XX AC AAF80812;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #186.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1566 ACCCAAGACAAAGAGAG 1585
| | | | | | | | | | | | | | | | | |
Db 20 ACCCAAGACAAAGAGAG 1

RESULT 1003
AAF80828/c
ID AAF80828 standard; DNA; 20 BP.
XX
XX AC AAF80828;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #202.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1745 TAGACACCAATTCAAATGA 1764
| | | | | | | | | | | | | | | | | |
Db 20 TAGACACCAATTCAAATGA 1

RESULT 1004
AAF80831/c
ID AAF80831 standard; DNA; 20 BP.
XX
XX AC AAF80831;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #205.
XX
XX

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KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1798 TATAAGAGAATTATATTT 1817
| | | | | | | | | | | | | | | | | |
Db 20 TATAAGAGAATTATATTT 1

RESULT 1005
AAF80834/c
ID AAF80834 standard; DNA; 20 BP.
XX
XX AC AAF80834;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #208.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1816 TTCTAACTATATAACCCCTAG 1835
| | | | | | | | | | | | | | | | | |
Db 20 TTCTAACTATATAACCCCTAG 1

RESULT 1006
AAF80846/c
ID AAF80846 standard; DNA; 20 BP.
XX
XX AC AAF80846;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #220.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1908 TCCTTAGTATATTGACCTA 1927
| | | | | | | | | | | | | | | | | |
Db 20 TCCTTAGTATATTGACCTA 1

RESULT 1007
AAF80866/c
ID AAF80866 standard; DNA; 20 BP.
XX
XX AC AAF80866;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #240.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2116 CTGTTACCCAGGCTGGAGTG 2135
Db 20 CTGTTACCCAGGCTGGAGTG 1

RESULT 1008
AAF80878/c
ID AAF80878 standard; DNA; 20 BP.
XX
AC AAF80878;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #252.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2213 GCTTGCCTACAGTCATCTG 2232
Db 20 GCTTGCCTACAGTCATCTG 1

RESULT 1009
AAF80633/c
ID AAF80633 standard; DNA; 20 BP.
XX
AC AAF80633;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #7.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2295 TGGTGAGGAGCAGGCAAAATG 314
Db 20 TGGTGAGGAGCAGGCAAAATG 1

RESULT 1010
AAF80639/c
ID AAF80639 standard; DNA; 20 BP.
XX
AC AAF80639;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #13.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTACATGTGCAAGAAAGCT 1714
Db 20 TTTACATGTGCAAGAAAGCT 1

RESULT 1011
AAF80676/c
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ID AAF80676 standard; DNA; 20 BP.
XX
AC AAF80676;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #50.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CTTCCGCGAGTAGTCAGTCCC 236
Db 20 CTTCCGCGAGTAGTCAGTCCC 1

RESULT 1012
AAF80694/c
ID AAF80694 standard; DNA; 20 BP.
XX
AC AAF80694;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #68.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 AAATGTGCAATACCAACATG 329
Db 20 AAATGTGCAATACCAACATG 1

RESULT 1013
AAF80695/c
ID AAF80695 standard; DNA; 20 BP.
XX
AC AAF80695;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #69.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 AATGTGCAATACCAACATGT 330
Db 20 AATGTGCAATACCAACATGT 1

RESULT 1014
AAF80708/c
ID AAF80708 standard; DNA; 20 BP.
XX
AC AAF80708;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #82.
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XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 ACTTATCTATGAAAGAGGT 469
Db 20 ACTTATCTATGAAAGAGGT 1

RESULT 1015
AAF80743/c
ID AAF80743 standard; DNA; 20 BP.
XX
AC AAF80743;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #117.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 833 ATTATCTGGTGAACGACAAA 852
Db 20 ATTATCTGGTGAACGACAAA 1

RESULT 1016
AAF80751/c
ID AAF80751 standard; DNA; 20 BP.
XX
AC AAF80751;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #125.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 927 TGTGTGAAGACAGCTAG 946
Db 20 TGTGTGAAGACAGCTAG 1

RESULT 1017
AAF80752/c
ID AAF80752 standard; DNA; 20 BP.
XX
AC AAF80752;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #126.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 936 AGAAGCAGTAGCAGTGAATC 955
Db 20 AGAAGCAGTAGCAGTGAATC 1

RESULT 1018
AAF80781/c
ID AAF80781 standard; DNA; 20 BP.
XX
AC AAF80781;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #155.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1226 CACTTCATGCAATGAAATGA 1245
Db 20 CACTTCATGCAATGAAATGA 1

RESULT 1019
AAF80815/c
ID AAF80815 standard; DNA; 20 BP.
XX
AC AAF80815;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #189.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1617 GAACCTTGCTGATTTGTCA 1636
Db 20 GAACCTTGCTGATTTGTCA 1

RESULT 1020
AAF80822/c
ID AAF80822 standard; DNA; 20 BP.
XX
AC AAF80822;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #196.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 CCTGCTTTACATGTGCAAG 1709
Db 20 CCTGCTTTACATGTGCAAG 1

RESULT 1021

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AAF80824/c
ID AAF80824 standard; DNA; 20 BP.
AC AAF80824;
XX
XX 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #198.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1710 AAGCTAAAGAAAGGAATAA 1729
Db 20 AAGCTAAAGAAAGGAATAA 1
XX
RESULT 1022
AAF80825/c
ID AAF80825 standard; DNA; 20 BP.
XX
XX AAF80825;
XX
XX 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #199.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1720 AAAGGAATAAGCCTGCCCA 1739
Db 20 AAAGGAATAAGCCTGCCCA 1
XX
RESULT 1023
AAF80841/c
ID AAF80841 standard; DNA; 20 BP.
XX
XX AAF80841;
XX
XX 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #215.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1872 AAGTGAGAAATGCCTCAAT 1891
Db 20 AAGTGAGAAATGCCTCAAT 1
XX
RESULT 1024
AAF80844/c
ID AAF80844 standard; DNA; 20 BP.
XX
XX AAF80844;
XX
XX 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #218.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1898 AGATTCTTCTCTTTAGTAT 1917
Db 20 AGATTCTTCTCTTTAGTAT 1
XX
RESULT 1025
AAF80854/c
ID AAF80854 standard; DNA; 20 BP.
XX
XX AAF80854;
XX
XX 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #228.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1973 ATGTAGTCTATCCTTTACAC 1992
Db 20 ATGTAGTCTATCCTTTACAC 1
XX
RESULT 1026
AAF80857/c
ID AAF80857 standard; DNA; 20 BP.
XX
XX AAF80857;
XX
XX 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #231.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1997 TCCTAATTTTAAATAATTTC 2016
Db 20 TCCTAATTTTAAATAATTTC 1
XX
RESULT 1027
AAF80667/c
ID AAF80667 standard; DNA; 20 BP.
XX
XX AAF80667;
XX
XX 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #41.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 GATCCTGCTGCTTTCCGAGC 124
Db 20 GATCCTGCTGCTTTCCGAGC 1

RESULT 1028
AAF80670/c
ID AAF80670 standard; DNA; 20 BP.
XX AC
XX AC AAF80670;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #44.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 AGTCGTACGAGCCGCCAGT 169
Db 20 AGTCGTACGAGCCGCCAGT 1

RESULT 1029
AAF80672/c
ID AAF80672 standard; DNA; 20 BP.
XX AC
XX AC AAF80672;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #46.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 CCAGTGCCCTGCGCCGAGA 184
Db 20 CCAGTGCCCTGCGCCGAGA 1

RESULT 1030
AAF80675/c
ID AAF80675 standard; DNA; 20 BP.
XX AC
XX AC AAF80675;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #49.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 GGCCTGCTGCTTCGCGAGTA 227
Db 20 GGCCTGCTGCTTCGCGAGTA 1

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RESULT 1031
AAF80682/c
ID AAF80682 standard; DNA; 20 BP.
XX AC
XX AC AAF80682;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #56.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 297 GTGAGGAGCAGGCAATGTG 316
Db 20 GTGAGGAGCAGGCAATGTG 1

RESULT 1032
AAF80683/c
ID AAF80683 standard; DNA; 20 BP.
XX AC
XX AC AAF80683;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #57.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 298 TGAGGAGCAGGCAATGTGC 317
Db 20 TGAGGAGCAGGCAATGTGC 1

RESULT 1033
AAF80704/c
ID AAF80704 standard; DNA; 20 BP.
XX AC
XX AC AAF80704;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #78.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 GACCTGCTTAGACCAAGC 405
Db 20 GACCTGCTTAGACCAAGC 1

RESULT 1034
AAF80706/c
ID AAF80706 standard; DNA; 20 BP.
XX AC
XX AC AAF80706;
XX DT 02-MAY-2001 (first entry)

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XX Human mdm2 phosphorothioate oligonucleotide #80.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW
XX
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGCCATTCCTTTTGAAGTTA 422
DB 20 AGCCATTCCTTTTGAAGTTA 1

RESULT 1035
AAF80734/c
ID AAF80734 standard; DNA; 20 BP.
XX
AC AAF80734;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #108.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 TACAAGAGCTTCAGAGAG 746
DB 20 TACAAGAGCTTCAGAGAG 1

RESULT 1036
AAF80736/c
ID AAF80736 standard; DNA; 20 BP.
XX
AC AAF80736;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #110.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 TTCATCTTCACATTTGGTTT 771
DB 20 TTCATCTTCACATTTGGTTT 1

RESULT 1037
AAF80741/c
ID AAF80741 standard; DNA; 20 BP.
XX
AC AAF80741;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #115.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 GAGACAGAGAAAATTCAGA 829
DB 20 GAGACAGAGAAAATTCAGA 1

RESULT 1038
AAF80747/c
ID AAF80747 standard; DNA; 20 BP.
XX
AC AAF80747;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #121.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 CCCTTTCCTTTGATGAAAGC 899
DB 20 CCCTTTCCTTTGATGAAAGC 1

RESULT 1039
AAF80772/c
ID AAF80772 standard; DNA; 20 BP.
XX
AC AAF80772;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #146.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 AGATGATGAGGTATATCAAG 1143
DB 20 AGATGATGAGGTATATCAAG 1

RESULT 1040
AAF80797/c
ID AAF80797 standard; DNA; 20 BP.
XX
AC AAF80797;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #171.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1434 GTTGAGGAAAATGATGATAA 1453
DB 20 GTTGAGGAAAATGATGATAA 1

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RESULT 1041
AAF80811/c
ID AAF80811 standard; DNA; 20 BP.
XX
XX AAF80811;
AC
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #185.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 GAAGAAACCCCAAGCAAGA 1579
Db 20 GAAGAAACCCCAAGCAAGA 1

RESULT 1042
AAF80814/c
ID AAF80814 standard; DNA; 20 BP.
XX
XX AAF80814;
AC
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #188.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 CTTAATGCCATTGAACCTTG 1624
Db 20 CTTAATGCCATTGAACCTTG 1

RESULT 1043
AAF80816/c
ID AAF80816 standard; DNA; 20 BP.
XX
XX AAF80816;
AC
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #190.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1624 GTGTGATTGTCAAGGTGCA 1643
Db 20 GTGTGATTGTCAAGGTGCA 1

RESULT 1044
AAF80853/c
ID AAF80853 standard; DNA; 20 BP.
XX
XX AAF80853;
AC
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #6.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #227.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1969 GAATATGTAGCTCATCCTTT 1988
Db 20 GAATATGTAGCTCATCCTTT 1

RESULT 1045
AAF80869/c
ID AAF80869 standard; DNA; 20 BP.
XX
XX AAF80869;
AC
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #243.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2140 GGGTGATCTGGCTCACTGC 2159
Db 20 GGGTGATCTGGCTCACTGC 1

RESULT 1046
AAF80875/c
ID AAF80875 standard; DNA; 20 BP.
XX
XX AAF80875;
AC
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #249.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2198 TCAGCCTCCCAATTAGCTTG 2217
Db 20 TCAGCCTCCCAATTAGCTTG 1

RESULT 1047
AAF80632/c
ID AAF80632 standard; DNA; 20 BP.
XX
XX AAF80632;
AC
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #6.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCCAAGCGCGAAACCCCG 292
Db 20 CTCCAAGCGCGAAACCCCG 1

RESULT 1048
AAF80637/c
ID AAF80637 standard; DNA; 20 BP.
XX
AC AAF80637;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #11.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1047 AGTGTAGAAATTGAAGTTGA 1066
Db 20 AGTGTAGAAATTGAAGTTGA 1

RESULT 1049
AAF80657/c
ID AAF80657 standard; DNA; 20 BP.
XX
AC AAF80657;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #31.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCGAGCTTGGCTGCTT 23
Db 20 CCGCGCGAGCTTGGCTGCTT 1

RESULT 1050
AAF80679/c
ID AAF80679 standard; DNA; 20 BP.
XX
AC AAF80679;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #53.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GATGCTGAGGACGAGCAAA 312
Db 20 GATGCTGAGGACGAGCAAA 1
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RESULT 1051
AAF80686/c
ID AAF80686 standard; DNA; 20 BP.
XX
AC AAF80686;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #60.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GGAGCAGGCAAAATGTGCAAT 320
Db 20 GGAGCAGGCAAAATGTGCAAT 1

RESULT 1052
AAF80732/c
ID AAF80732 standard; DNA; 20 BP.
XX
AC AAF80732;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #106.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723
Db 20 TGGGAGTGATCAAAAGGACC 1

RESULT 1053
AAF80739/c
ID AAF80739 standard; DNA; 20 BP.
XX
AC AAF80739;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #113.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 CATCTAGAAGGAGAGCAATT 806
Db 20 CATCTAGAAGGAGAGCAATT 1

RESULT 1054
AAF80761/c
ID AAF80761 standard; DNA; 20 BP.
XX
AC AAF80761;
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XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #135.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX KW
XX QY 1034 TTCAGATCAGTTTAGTGTAG 1053
    DB 20 TTCAGATCAGTTTAGTGTAG 1
    RESULT 1055
    AAF80764/c
    ID AAF80764 standard; DNA; 20 BP.
    XX AC AAF80764;
    XX DT 02-MAY-2001 (first entry)
    XX DE Human mdm2 phosphorothioate oligonucleotide #138.
    XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
    XX KW
    XX QY 1059 GAAGTTGAATCTCTCGACTC 1078
    DB 20 GAAGTTGAATCTCTCGACTC 1
    RESULT 1056
    AAF80809/c
    ID AAF80809 standard; DNA; 20 BP.
    XX AC AAF80809;
    XX DT 02-MAY-2001 (first entry)
    XX DE Human mdm2 phosphorothioate oligonucleotide #183.
    XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
    XX KW
    XX QY 1541 TGTGAAAGAGTTTGAAAGGG 1560
    DB 20 TGTGAAAGAGTTTGAAAGGG 1
    RESULT 1057
    AAF80849/c
    ID AAF80849 standard; DNA; 20 BP.
    XX AC AAF80849;
    XX DT 02-MAY-2001 (first entry)
    XX DE Human mdm2 phosphorothioate oligonucleotide #223.
    XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
    XX KW
    XX QY 1033 GTAGTGAATAGTGAATACT 1952
    DB 20 GTAGTGAATAGTGAATACT 1
    RESULT 1058
    AAF80879/c
    ID AAF80879 standard; DNA; 20 BP.
    XX AC AAF80879;
    XX DT 02-MAY-2001 (first entry)
    XX DE Human mdm2 phosphorothioate oligonucleotide #253.
    XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
    XX KW
    XX QY 2218 GCCTACAGTCATCTGCCACC 2237
    DB 20 GCCTACAGTCATCTGCCACC 1
    RESULT 1059
    AAF80658/c
    ID AAF80658 standard; DNA; 20 BP.
    XX AC AAF80658;
    XX DT 02-MAY-2001 (first entry)
    XX DE Human mdm2 phosphorothioate oligonucleotide #32.
    XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
    XX KW
    XX QY 14 TTGGCTGCTTCTGGGGCCTG 33
    DB 20 TTGGCTGCTTCTGGGGCCTG 1
    RESULT 1060
    AAF80660/c
    ID AAF80660 standard; DNA; 20 BP.
    XX AC AAF80660;
    XX DT 02-MAY-2001 (first entry)
    XX DE Human mdm2 phosphorothioate oligonucleotide #34.
    XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
    XX KW
    XX QY 29 GCCTGTGTGGCCCTGTGTGT 48
    DB 20 GCCTGTGTGGCCCTGTGTGT 48
    Query Match 0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  
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Db      20 GCCTGTGTGGCCCTGTGTGT 1

RESULT 1061
AAF80668/c
ID AAF80668 standard; DNA; 20 BP.
XX
XX
AC AAF80668;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #42.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      113 TGCCTTCCGACGAGGACCA 132
Db      20 TGCCTTCCGACGAGGACCA 1

RESULT 1062
AAF80678/c
ID AAF80678 standard; DNA; 20 BP.
XX
XX
AC AAF80678;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #52.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 CCCGATGGTGAGGAGCAGG 308
Db      20 CCCGATGGTGAGGAGCAGG 1

RESULT 1063
AAF80709/c
ID AAF80709 standard; DNA; 20 BP.
XX
XX
AC AAF80709;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #83.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      477 TATCTTGGCCAGTATATTAT 496
Db      20 TATCTTGGCCAGTATATTAT 1

RESULT 1064
AAF80714/c
ID AAF80714 standard; DNA; 20 BP.
XX
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```
AC AAF80714;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #88.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      525 CAACATATTGTATATTGTTTC 544
Db      20 CAACATATTGTATATTGTTTC 1

RESULT 1065
AAF80723/c
ID AAF80723 standard; DNA; 20 BP.
XX
XX
AC AAF80723;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #97.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      600 AGGAAATATATACCATGAT 619
Db      20 AGGAAATATATACCATGAT 1

RESULT 1066
AAF80724/c
ID AAF80724 standard; DNA; 20 BP.
XX
XX
AC AAF80724;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #98.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      609 TATACCATGATCTACAGGAA 628
Db      20 TATACCATGATCTACAGGAA 1

RESULT 1067
AAF80750/c
ID AAF80750 standard; DNA; 20 BP.
XX
XX
AC AAF80750;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #124.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
```

XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 ATAAGGGAGATATGTTGTGA 934  
|||||  
DB 20 ATAAGGGAGATATGTTGTGA 1

RESULT 1068

AAF80768/c  
ID AAF80768 standard; DNA; 20 BP.

XX  
AC AAF80768;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #142.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 CTTAGTCAAGAGGACAAAGA 1111  
|||||  
DB 20 CTTAGTCAAGAGGACAAAGA 1

RESULT 1069

AAF80771/c  
ID AAF80771 standard; DNA; 20 BP.

XX  
AC AAF80771;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #145.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 CTCAGATGAAGATGATGAGG 1134  
|||||  
DB 20 CTCAGATGAAGATGATGAGG 1

RESULT 1070

AAF80813/c  
ID AAF80813 standard; DNA; 20 BP.

XX  
AC AAF80813;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #187.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 AGAGAGTGTGGAATCTAGTT 1599

DB 20 AGAGAGTGTGGAATCTAGTT 1  
|||||

RESULT 1071

AAF80874/c  
ID AAF80874 standard; DNA; 20 BP.

XX  
AC AAF80874;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #248.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 TCCTGCCTCAGCTCCCAAT 2210  
|||||  
DB 20 TCCTGCCTCAGCTCCCAAT 1

RESULT 1072

AAF80881/c  
ID AAF80881 standard; DNA; 20 BP.

XX  
AC AAF80881;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #255.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2253 TTTGTACTTTTAGTAGAGAC 2272  
|||||  
DB 20 TTTGTACTTTTAGTAGAGAC 1

RESULT 1073

AAF80885/c  
ID AAF80885 standard; DNA; 20 BP.

XX  
AC AAF80885;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #259.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGCTCTCGATCTC 2309  
|||||  
DB 20 GCCAGGATGCTCTCGATCTC 1

RESULT 1074

AAF80887/c  
ID AAF80887 standard; DNA; 20 BP.

```

XX AAF80887;
AC
XX
DT 02-MAY-2001 (first entry)
DE
XX Human mdm2 phosphorothioate oligonucleotide #261.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCCGC 2326
Db 20 CTCCTGACCTCGTGATCCGC 1

RESULT 1075
AAF80663/c
ID AAF80663 standard; DNA; 20 BP.
XX
AC AAF80663;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #37.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GGAAGAATGGAGCAAGAGC 69
Db 20 GGAAGAATGGAGCAAGAGC 1

RESULT 1076
AAF80665/c
ID AAF80665 standard; DNA; 20 BP.
XX
AC AAF80665;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #39.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGAGCCCGAGGGCGCGCGC 89
Db 20 CGAGCCCGAGGGCGCGCGC 1

RESULT 1077
AAF80669/c
ID AAF80669 standard; DNA; 20 BP.
XX
AC AAF80669;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #43.
XX

```

```

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 GCAGCCGAGGACCGTCCC 139
Db 20 GCAGCCGAGGACCGTCCC 1

RESULT 1078
AAF80717/c
ID AAF80717 standard; DNA; 20 BP.
XX
AC AAF80717;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #91.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 GATCTTCTAGGAGATTGTT 568
Db 20 GATCTTCTAGGAGATTGTT 1

RESULT 1079
AAF80738/c
ID AAF80738 standard; DNA; 20 BP.
XX
AC AAF80738;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #112.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 AGACCATCTACCTCATCTAG 793
Db 20 AGACCATCTACCTCATCTAG 1

RESULT 1080
AAF80754/c
ID AAF80754 standard; DNA; 20 BP.
XX
AC AAF80754;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #128.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 AGACCATCTACCTCATCTAG 793
Db 20 AGACCATCTACCTCATCTAG 1

RESULT 1080
AAF80754/c
ID AAF80754 standard; DNA; 20 BP.
XX
AC AAF80754;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #128.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 964 CGCCATCGAATCCGATCTT 983  
 DB 20 CGCCATCGAATCCGATCTT 1

## RESULT 1081

AAF80775/c

ID AAF80775 standard; DNA; 20 BP.

XX AC AAF80775;

XX 02-MAY-2001 (first entry)

DT Human mdm2 phosphorothioate oligonucleotide #149.

DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX Query Match 0.8%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1161 GGGGAGAGTGATACAGATTC 1180

DB 20 GGGGAGAGTGATACAGATTC 1

## RESULT 1082

AAF80780/c

ID AAF80780 standard; DNA; 20 BP.

XX AC AAF80780;

XX 02-MAY-2001 (first entry)

DT Human mdm2 phosphorothioate oligonucleotide #154.

DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX Query Match 0.8%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GAAATGCATTCATGCAATG 1239

DB 20 GAAATGCATTCATGCAATG 1

## RESULT 1083

AAF80806/c

ID AAF80806 standard; DNA; 20 BP.

XX AC AAF80806;

XX 02-MAY-2001 (first entry)

DT Human mdm2 phosphorothioate oligonucleotide #180.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX Query Match 0.8%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 CATTATTATAGCAGCCAAG 1536

DB 20 CATTATTATAGCAGCCAAG 1

## RESULT 1084

AAF80829/c

ID AAF80829 standard; DNA; 20 BP.

XX AC AAF80829;

XX 02-MAY-2001 (first entry)

DT Human mdm2 phosphorothioate oligonucleotide #203.

DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX Query Match 0.8%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1757 TCAAATGATTGTGCTAACTT 1776

DB 20 TCAAATGATTGTGCTAACTT 1

## RESULT 1085

AAF80851/c

ID AAF80851 standard; DNA; 20 BP.

XX AC AAF80851;

XX 02-MAY-2001 (first entry)

DT Human mdm2 phosphorothioate oligonucleotide #225.

DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX Query Match 0.8%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1948 ATACTTACTATAATTGACT 1967

DB 20 ATACTTACTATAATTGACT 1

## RESULT 1086

AAF80864/c

ID AAF80864 standard; DNA; 20 BP.

XX AC AAF80864;

XX 02-MAY-2001 (first entry)

DT Human mdm2 phosphorothioate oligonucleotide #238.

DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX Query Match 0.8%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTTGTCTCTTAC 2122

DB 20 ACCGAGTCTTGTCTCTTAC 1

## RESULT 1087

AAF80867/c

ID AAF80867 standard; DNA; 20 BP.

XX AC AAF80867;

XX 02-MAY-2001 (first entry)

DT Human mdm2 phosphorothioate oligonucleotide #241.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
KW  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2123 CCAGGCTGGAGTGCAGTGG 2142  
DB 20 CCAGGCTGGAGTGCAGTGG 1

RESULT 1088  
AAF80677/c  
ID AAF80677 standard; DNA; 20 BP.  
XX  
AC AAF80677;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligonucleotide #51.  
XX  
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGGAACTGGGAGTCTTGA 261  
DB 20 AGGAACTGGGAGTCTTGA 1

RESULT 1089  
AAF80707/c  
ID AAF80707 standard; DNA; 20 BP.  
XX  
AC AAF80707;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligonucleotide #81.  
XX  
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 ATTAAGTCTGTGTGCAC 441  
DB 20 ATTAAGTCTGTGTGCAC 1

RESULT 1090  
AAF80722/c  
ID AAF80722 standard; DNA; 20 BP.  
XX  
AC AAF80722;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligonucleotide #96.  
XX  
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 593 AGAGCACAGGAAATATATA 612  
DB 20 AGAGCACAGGAAATATATA 1

RESULT 1091  
AAF80731/c  
ID AAF80731 standard; DNA; 20 BP.  
XX  
AC AAF80731;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligonucleotide #105.  
XX  
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 GTCACCTTGAAGTGGGAGT 710  
DB 20 GTCACCTTGAAGTGGGAGT 1

RESULT 1092  
AAF80737/c  
ID AAF80737 standard; DNA; 20 BP.  
XX  
AC AAF80737;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligonucleotide #111.  
XX  
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 761 ACATTGGTTTCTAGACCAT 780  
DB 20 ACATTGGTTTCTAGACCAT 1

RESULT 1093  
AAF80757/c  
ID AAF80757 standard; DNA; 20 BP.  
XX  
AC AAF80757;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligonucleotide #131.  
XX  
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 996 AGTGAACATTCAGGTGATTG 1015  
DB 20 AGTGAACATTCAGGTGATTG 1

RESULT 1094

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AAF80777/c
ID  AAF80777 standard; DNA; 20 BP.
XX
AC  AAF80777;
XX
DT  02-MAY-2001 (first entry)
XX
DE  Human mdm2 phosphorothioate oligonucleotide #151.
XX
KW  Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1184 TGAAGAAGATCCTGAAATTT 1203
Db  20 TGAAGAAGATCCTGAAATTT 1

RESULT 1095
AAF80782/c
ID  AAF80782 standard; DNA; 20 BP.
XX
AC  AAF80782;
XX
DT  02-MAY-2001 (first entry)
XX
DE  Human mdm2 phosphorothioate oligonucleotide #156.
XX
KW  Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1257 CCATCACAATGCAACAGATG 1276
Db  20 CCATCACAATGCAACAGATG 1

RESULT 1096
AAF80790/c
ID  AAF80790 standard; DNA; 20 BP.
XX
AC  AAF80790;
XX
DT  02-MAY-2001 (first entry)
XX
DE  Human mdm2 phosphorothioate oligonucleotide #164.
XX
KW  Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1333 TCTCTGAGAAAGCCAAACTG 1352
Db  20 TCTCTGAGAAAGCCAAACTG 1

RESULT 1097
AAF80821/c
ID  AAF80821 standard; DNA; 20 BP.
XX
AC  AAF80821;
XX
DT  02-MAY-2001 (first entry)
XX

DE  Human mdm2 phosphorothioate oligonucleotide #195.
XX
KW  Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1684 TTATGGCCTGCTTTACATGT 1703
Db  20 TTATGGCCTGCTTTACATGT 1

RESULT 1098
AAF80838/c
ID  AAF80838 standard; DNA; 20 BP.
XX
AC  AAF80838;
XX
DT  02-MAY-2001 (first entry)
XX
DE  Human mdm2 phosphorothioate oligonucleotide #212.
XX
KW  Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1850 TGAATTTATTTCACATATAT 1869
Db  20 TGAATTTATTTCACATATAT 1

RESULT 1099
AAF80843/c
ID  AAF80843 standard; DNA; 20 BP.
XX
AC  AAF80843;
XX
DT  02-MAY-2001 (first entry)
XX
DE  Human mdm2 phosphorothioate oligonucleotide #217.
XX
KW  Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1889 AATTCACATAGATTTCTTCT 1908
Db  20 AATTCACATAGATTTCTTCT 1

RESULT 1100
AAF80872/c
ID  AAF80872 standard; DNA; 20 BP.
XX
AC  AAF80872;
XX
DT  02-MAY-2001 (first entry)
XX
DE  Human mdm2 phosphorothioate oligonucleotide #246.
XX
KW  Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2176 GGGTTGCGACCAATTCCTG 2195
Db 20 GGGTTGCGACCAATTCCTG 1

RESULT 1101
AAF80876/c
ID AAF80876 standard; DNA; 20 BP.
XX
AC AAF80876;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #250.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2202 CCTCCCAATTAGCTTGGCCT 2221
Db 20 CCTCCCAATTAGCTTGGCCT 1

RESULT 1102
AAF80882/c
ID AAF80882 standard; DNA; 20 BP.
XX
AC AAF80882;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #256.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2265 GTAGAGACAGGGTTTCACCG 2284
Db 20 GTAGAGACAGGGTTTCACCG 1

RESULT 1103
AAF80691/c
ID AAF80691 standard; DNA; 20 BP.
XX
AC AAF80691;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #65.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 307 GGCAATGTGCAATACCAAC 326
Db 20 GGCAATGTGCAATACCAAC 1
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RESULT 1104
AAF80692/c
ID AAF80692 standard; DNA; 20 BP.
XX
AC AAF80692;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #66.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 308 GCAAATGTGCAATACCAACA 327
Db 20 GCAAATGTGCAATACCAACA 1

RESULT 1105
AAF80730/c
ID AAF80730 standard; DNA; 20 BP.
XX
AC AAF80730;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #104.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 682 AGAACAGGTGTACCTTGAA 701
Db 20 AGAACAGGTGTACCTTGAA 1

RESULT 1106
AAF80759/c
ID AAF80759 standard; DNA; 20 BP.
XX
AC AAF80759;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #133.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1017 TTGGATCAGGATTCAGTTTC 1036
Db 20 TTGGATCAGGATTCAGTTTC 1

RESULT 1107
AAF80766/c
ID AAF80766 standard; DNA; 20 BP.
XX
AC AAF80766;
XX
DT 02-MAY-2001 (first entry)
```



XX Human mdm2 phosphorothioate oligonucleotide #140.  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1077 TCAGAAGATTATAGCCTTAG 1096  
 |||||  
 Db 20 TCAGAAGATTATAGCCTTAG 1

RESULT 1108  
 AAF80792/c  
 ID AAF80792 standard; DNA; 20 BP.

XX AAF80792;  
 XX 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #166.  
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1358 CTCAACACACAGCTGAAGAGG 1377  
 |||||  
 Db 20 CTCAACACACAGCTGAAGAGG 1

RESULT 1109  
 AAF80796/c  
 ID AAF80796 standard; DNA; 20 BP.

XX AAF80796;  
 XX 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #170.  
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1421 CAGAGACTCATGTGTTGAGG 1440  
 |||||  
 Db 20 CAGAGACTCATGTGTTGAGG 1

RESULT 1110  
 AAF80818/c  
 ID AAF80818 standard; DNA; 20 BP.

XX AAF80818;  
 XX 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #192.  
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1657 GCATTGTCCATGCGAAAACA 1676  
 |||||  
 Db 20 GCATTGTCCATGCGAAAACA 1

RESULT 1111  
 AAF80835/c  
 ID AAF80835 standard; DNA; 20 BP.

XX AAF80835;  
 XX 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #209.  
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1823 TATATAACCCCTAGGAATTTA 1842  
 |||||  
 Db 20 TATATAACCCCTAGGAATTTA 1

RESULT 1112  
 AAF80858/c  
 ID AAF80858 standard; DNA; 20 BP.

XX AAF80858;  
 XX 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #232.  
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2004 TTTAAATAATTTCTACTCTG 2023  
 |||||  
 Db 20 TTTAAATAATTTCTACTCTG 1

RESULT 1113  
 AAF80865/c  
 ID AAF80865 standard; DNA; 20 BP.

XX AAF80865;  
 XX 02-MAY-2001 (first entry)  
 XX Human mdm2 phosphorothioate oligonucleotide #239.  
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2111 TTGCTCTGTATCCAGGCTG 2130  
 |||||  
 Db 20 TTGCTCTGTATCCAGGCTG 1

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RESULT 1114
AAF80870/c
ID AAF80870 standard; DNA; 20 BP.
XX
XX AAF80870;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #244.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 2146 TCTTGGCTCACTGCAAGCTC 2165
DB 20 TCTTGGCTCACTGCAAGCTC 1

RESULT 1115
AAF80891/c
ID AAF80891 standard; DNA; 20 BP.
XX
XX AAF80891;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #265.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 2341 CAAAGTGCTGGGATTACAGG 2360
DB 20 CAAAGTGCTGGGATTACAGG 1

RESULT 1116
AAF80630/c
ID AAF80630 standard; DNA; 20 BP.
XX
XX AAF80630;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #4.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 147 ATTAGTGGCTAGGAGCGCC 166
DB 20 ATTAGTGGCTAGGAGCGCC 1

RESULT 1117
AAF80631/c
ID AAF80631 standard; DNA; 20 BP.
XX
XX AAF80631;
XX

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DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #5.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 181 GAGAGTGGGAATGATCCCCGA 200
DB 20 GAGAGTGGGAATGATCCCCGA 1

RESULT 1118
AAF80661/c
ID AAF80661 standard; DNA; 20 BP.
XX
XX AAF80661;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #35.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 34 TGTGGCCCTGTGTGCGAA 53
DB 20 TGTGGCCCTGTGTGCGAA 1

RESULT 1119
AAF80662/c
ID AAF80662 standard; DNA; 20 BP.
XX
XX AAF80662;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #36.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 43 GTGTGTCGGAAGATGGAGC 62
DB 20 GTGTGTCGGAAGATGGAGC 1

RESULT 1120
AAF80684/c
ID AAF80684 standard; DNA; 20 BP.
XX
XX AAF80684;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #58.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 GAGGAGCAGGCAATGTGCA 318
Db 20 GAGGAGCAGGCAATGTGCA 1

RESULT 1121
AAF80685/c
ID AAF80685 standard; DNA; 20 BP.
XX
AC AAF80685;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #59.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 AGGAGCAGGCAATGTGCA 319
Db 20 AGGAGCAGGCAATGTGCA 1

RESULT 1122
AAF80726/c
ID AAF80726 standard; DNA; 20 BP.
XX
AC AAF80726;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #100.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 634 TAGTAGTCAATCAGCAGAA 653
Db 20 TAGTAGTCAATCAGCAGAA 1

RESULT 1123
AAF80749/c
ID AAF80749 standard; DNA; 20 BP.
XX
AC AAF80749;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #123.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 CTCTGTGTGTAATAAGGAG 923
Db 20 CTCTGTGTGTAATAAGGAG 1

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1124
AAF80753/c
ID AAF80753 standard; DNA; 20 BP.
XX
AC AAF80753;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #127.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 949 GTGAATCTACAGGACGCCA 968
Db 20 GTGAATCTACAGGACGCCA 1

RESULT 1125
AAF80783/c
ID AAF80783 standard; DNA; 20 BP.
XX
AC AAF80783;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #157.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 CAACAGATGTTGGCCCTTC 1287
Db 20 CAACAGATGTTGGCCCTTC 1

RESULT 1126
AAF80793/c
ID AAF80793 standard; DNA; 20 BP.
XX
AC AAF80793;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #167.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 GCTGAAGAGGGCTTTGATGT 1387
Db 20 GCTGAAGAGGGCTTTGATGT 1

RESULT 1127
AAF80799/c
ID AAF80799 standard; DNA; 20 BP.
XX
AC AAF80799;
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XX 02-MAY-2001 (first entry)
DT Human mdm2 phosphorothioate oligonucleotide #173.
DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATAAAATTACACAGCTTC 1468
Db 20 GATAAAATTACACAGCTTC 1

RESULT 1128
AAF80832/c
ID AAF80832 standard; DNA; 20 BP.
XX
AC AAF80832;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #206.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1804 AGAATTATATATTTCTAACT 1823
Db 20 AGAATTATATATTTCTAACT 1

RESULT 1129
AAF80833/c
ID AAF80833 standard; DNA; 20 BP.
XX
AC AAF80833;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #207.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 TTATATATTTCTAACTATAT 1827
Db 20 TTATATATTTCTAACTATAT 1

RESULT 1130
AAF80847/c
ID AAF80847 standard; DNA; 20 BP.
XX
AC AAF80847;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #221.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1913 AGTATAATTGACCTACTTTG 1932
Db 20 AGTATAATTGACCTACTTTG 1

RESULT 1131
AAF80873/c
ID AAF80873 standard; DNA; 20 BP.
XX
AC AAF80873;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #247.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCCT 2204
Db 20 CCATTCTCTGCTCAGCCT 1

RESULT 1132
AAF80642/c
ID AAF80642 standard; DNA; 20 BP.
XX
AC AAF80642;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #16.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1818 CTAATATATATACCTAGGA 1837
Db 20 CTAATATATATACCTAGGA 1

RESULT 1133
AAF80664/c
ID AAF80664 standard; DNA; 20 BP.
XX
AC AAF80664;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #38.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CAAGAGCCGAGCCGAGGG 81
Db 62 CAAGAGCCGAGCCGAGGG 81
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Db      20 CAAGAGCCGAGCCCGAGGG 1

RESULT 1134
AAF80673/c
ID AAF80673 standard; DNA; 20 BP.
XX
AC AAF80673;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #47.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      174 TGGCCCGAGAGTGAATGA 193
      |||||
Db      20 TGGCCCGAGAGTGAATGA 1

RESULT 1135
AAF80697/c
ID AAF80697 standard; DNA; 20 BP.
XX
AC AAF80697;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #71.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      313 TGTGCAATACCAACATGCT 332
      |||||
Db      20 TGTGCAATACCAACATGCT 1

RESULT 1136
AAF80703/c
ID AAF80703 standard; DNA; 20 BP.
XX
AC AAF80703;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #77.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      372 GCTTCGGAAACAAGACCCT 391
      |||||
Db      20 GCTTCGGAAACAAGACCCT 1

RESULT 1137
AAF80716/c
ID AAF80716 standard; DNA; 20 BP.
XX

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AC AAF80716;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #90.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      538 ATTGTTCAAATGATCTTCTA 557
      |||||
Db      20 ATTGTTCAAATGATCTTCTA 1

RESULT 1138
AAF80746/c
ID AAF80746 standard; DNA; 20 BP.
XX
AC AAF80746;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #120.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      867 TCTGATAGTATTCCCTTTC 886
      |||||
Db      20 TCTGATAGTATTCCCTTTC 1

RESULT 1139
AAF80760/c
ID AAF80760 standard; DNA; 20 BP.
XX
AC AAF80760;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #134.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1023 CAGGATTCAGTTTCAGATCA 1042
      |||||
Db      20 CAGGATTCAGTTTCAGATCA 1

RESULT 1140
AAF80773/c
ID AAF80773 standard; DNA; 20 BP.
XX
AC AAF80773;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #147.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1135 TATATCAAGTTACTGTGTAT 1154
    |||||
Db 20 TATATCAAGTTACTGTGTAT 1

RESULT 1141
AAF80774/c
ID AAF80774 standard; DNA; 20 BP.
XX
AC AAF80774;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #148.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 GTGTATCAGCGAGGGGAGAG 1168
    |||||
Db 20 GTGTATCAGCGAGGGGAGAG 1

RESULT 1142
AAF80776/c
ID AAF80776 standard; DNA; 20 BP.
XX
AC AAF80776;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #150.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1170 GATACAGATTTCATTGGAAGA 1189
    |||||
Db 20 GATACAGATTTCATTGGAAGA 1

RESULT 1143
AAF80804/c
ID AAF80804 standard; DNA; 20 BP.
XX
AC AAF80804;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #178.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GCCATCAACTTCTAGTAGCA 1518
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Db 20 GCCATCAACTTCTAGTAGCA 1

RESULT 1144
AAF80827/c
ID AAF80827 standard; DNA; 20 BP.
XX
AC AAF80827;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #201.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 CCCAGTATGTAGACAACCAA 1755
    |||||
Db 20 CCCAGTATGTAGACAACCAA 1

RESULT 1145
AAF80830/c
ID AAF80830 standard; DNA; 20 BP.
XX
AC AAF80830;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #204.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1787 GTTGACCTGTCTATAAGAGA 1806
    |||||
Db 20 GTTGACCTGTCTATAAGAGA 1

RESULT 1146
AAF80856/c
ID AAF80856 standard; DNA; 20 BP.
XX
AC AAF80856;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #230.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1990 CACCAACTCTTAATTTTAAA 2009
    |||||
Db 20 CACCAACTCTTAATTTTAAA 1

RESULT 1147
AAF80863/c
ID AAF80863 standard; DNA; 20 BP.
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XX AAF80863;
AC
XX
DT
XX
XX 02-MAY-2001 (first entry)
XX Human mdm2 phosphorothioate oligonucleotide #237.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2072 CATTAAATGTAACCTATTATTA 2091
Db 20 CATTAAATGTAACCTATTATTA 1

RESULT 1148
AAF80890/c
ID AAF80890 standard; DNA; 20 BP.
XX
AC AAF80890;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #264.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2334 GGCCTCCCAAAGTCTGGGA 2353
Db 20 GGCCTCCCAAAGTCTGGGA 1

RESULT 1149
AAF80644/c
ID AAF80644 standard; DNA; 20 BP.
XX
AC AAF80644;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #18.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2132 AGTCAGTGGGTGATCTTGG 2151
Db 20 AGTCAGTGGGTGATCTTGG 1

RESULT 1150
AAF80645/c
ID AAF80645 standard; DNA; 20 BP.
XX
AC AAF80645;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #19.
XX

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2224 AGTCATCTGCCACCACACCT 2243
Db 20 AGTCATCTGCCACCACACCT 1

RESULT 1151
AAF80666/c
ID AAF80666 standard; DNA; 20 BP.
XX
AC AAF80666;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #40.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 TGACCGAGATCCTGTGCTT 117
Db 20 TGACCGAGATCCTGTGCTT 1

RESULT 1152
AAF80680/c
ID AAF80680 standard; DNA; 20 BP.
XX
AC AAF80680;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #54.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 ATGCTGAGGAGCAGGCAAAAT 313
Db 20 ATGCTGAGGAGCAGGCAAAAT 1

RESULT 1153
AAF80693/c
ID AAF80693 standard; DNA; 20 BP.
XX
AC AAF80693;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #67.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 309 CAAATGTGCAATACCAACAT 328
DB 20 CAAATGTGCAATACCAACAT 1

RESULT 1154
AAF80696/c
ID AAF80696 standard; DNA; 20 BP.
XX AAF80696;
AC AAF80696;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #70.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTC 331
DB 20 ATGTGCAATACCAACATGTC 1

RESULT 1155
AAF80699/c
ID AAF80699 standard; DNA; 20 BP.
XX AAF80699;
AC AAF80699;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #73.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 CAACATGCTGTACTACTG 342
DB 20 CAACATGCTGTACTACTG 1

RESULT 1156
AAF80701/c
ID AAF80701 standard; DNA; 20 BP.
XX AAF80701;
AC AAF80701;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #75.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 GTAACCACTCACAGATTCC 370
DB 20 GTAACCACTCACAGATTCC 1

RESULT 1157
AAF80713/c

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ID AAF80713 standard; DNA; 20 BP.
XX AAF80713;
AC AAF80713;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #87.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGAGAGCAACACATATTG 534
DB 20 TGAGAGCAACACATATTG 1

RESULT 1158
AAF80744/c
ID AAF80744 standard; DNA; 20 BP.
XX AAF80744;
AC AAF80744;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #118.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 AACGACAAAGAAAACGCCAC 863
DB 20 AACGACAAAGAAAACGCCAC 1

RESULT 1159
AAF80748/c
ID AAF80748 standard; DNA; 20 BP.
XX AAF80748;
AC AAF80748;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #122.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 AAAGCCTGGCTCTGTGTGTA 914
DB 20 AAAGCCTGGCTCTGTGTGTA 1

RESULT 1160
AAF80769/c
ID AAF80769 standard; DNA; 20 BP.
XX AAF80769;
AC AAF80769;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #143.

```



XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 KW  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 AGAAGGACAAGAACTCTCAG 1119  
 ID AAF80770/c  
 XX  
 AC AAF80770;  
 XX

RESULT 1161  
 AAF80770/c  
 ID AAF80770 standard; DNA; 20 BP.  
 XX  
 AC AAF80770;  
 XX

DT 02-MAY-2001 (first entry)  
 XX  
 XX Human mdm2 phosphorothioate oligonucleotide #144.  
 XX  
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 GACAAGAACTCTCAGATGAA 1124  
 ID AAF80800/c  
 XX  
 AC AAF80800;  
 XX

RESULT 1162  
 AAF80800/c  
 ID AAF80800 standard; DNA; 20 BP.  
 XX  
 AC AAF80800;  
 XX

DT 02-MAY-2001 (first entry)  
 XX  
 XX Human mdm2 phosphorothioate oligonucleotide #174.  
 XX  
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1456 TTACACAAGCTTCAATCA 1475  
 ID AAF80855/c  
 XX  
 AC AAF80855;  
 XX

RESULT 1163  
 AAF80855/c  
 ID AAF80855 standard; DNA; 20 BP.  
 XX  
 AC AAF80855;  
 XX

DT 02-MAY-2001 (first entry)  
 XX  
 XX Human mdm2 phosphorothioate oligonucleotide #229.  
 XX  
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1982 ATCCTTTACCAACTCCTA 2001  
 ID AAF80862/c  
 XX  
 AC AAF80862;  
 XX

RESULT 1164  
 AAF80862/c  
 ID AAF80862 standard; DNA; 20 BP.  
 XX  
 AC AAF80862;  
 XX

DT 02-MAY-2001 (first entry)  
 XX  
 XX Human mdm2 phosphorothioate oligonucleotide #236.  
 XX  
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2059 AATATGTATATGACATTAA 2078  
 ID AAF80871/c  
 XX  
 AC AAF80871;  
 XX

RESULT 1165  
 AAF80871/c  
 ID AAF80871 standard; DNA; 20 BP.  
 XX  
 AC AAF80871;  
 XX

DT 02-MAY-2001 (first entry)  
 XX  
 XX Human mdm2 phosphorothioate oligonucleotide #245.  
 XX  
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TCACTGCAAGCTCTGCCCTC 2172  
 ID AAF80877/c  
 XX  
 AC AAF80877;  
 XX

RESULT 1166  
 AAF80877/c  
 ID AAF80877 standard; DNA; 20 BP.  
 XX  
 AC AAF80877;  
 XX

DT 02-MAY-2001 (first entry)  
 XX  
 XX Human mdm2 phosphorothioate oligonucleotide #251.  
 XX  
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2210 TTAGCTTGGCCTACAGTCAT 2229  
 ID AAF80877/c  
 XX  
 AC AAF80877;  
 XX

RESULT 1167  
 AAF80877/c  
 ID AAF80877 standard; DNA; 20 BP.  
 XX  
 AC AAF80877;  
 XX

AAF80884/c  
 ID AAF80884 standard; DNA; 20 BP.  
 XX  
 AC AAF80884;

XX DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #258.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Query Match 0.8%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2283 CGTGTAGCCAGGATGGTCT 2302

DB 20 CGTGTAGCCAGGATGGTCT 1

RESULT 1168

AAF80628/c

ID AAF80628 standard; DNA; 20 BP.

XX AC AAF80628;

XX DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #2.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Query Match 0.8%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GCCCTGTGTGTCGGAAGA 56

DB 20 GCCCTGTGTGTCGGAAGA 1

RESULT 1169

AAF80698/c

ID AAF80698 standard; DNA; 20 BP.

XX AC AAF80698;

XX DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #72.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Query Match 0.8%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 GTGCAATACCAACATGTCTG 333

DB 20 GTGCAATACCAACATGTCTG 1

RESULT 1170

AAF80711/c

ID AAF80711 standard; DNA; 20 BP.

XX AC AAF80711;

XX DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #85.  
 XX  
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 XX

XX Query Match 0.8%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGACTAAACGATTATATGAT 515

DB 20 TGACTAAACGATTATATGAT 1

RESULT 1171

AAF80729/c

ID AAF80729 standard; DNA; 20 BP.

XX AC AAF80729;

XX DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #103.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Query Match 0.8%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGAACAG 688

DB 20 ACATCTGTGAGTGAGAACAG 1

RESULT 1172

AAF80762/c

ID AAF80762 standard; DNA; 20 BP.

XX AC AAF80762;

XX DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #136.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Query Match 0.8%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1046 TAGTGTAGAAATTGAAGTTG 1065

DB 20 TAGTGTAGAAATTGAAGTTG 1

RESULT 1173

AAF80787/c

ID AAF80787 standard; DNA; 20 BP.

XX AC AAF80787;

XX DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #161.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Query Match 0.8%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1301 TCCTGAAGATAAAGGGAAG 1320
DB 20 TCCTGAAGATAAAGGGAAG 1

RESULT 1174
AAF80794/c
ID AAF80794 standard; DNA; 20 BP.
XX AC AAF80794;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #168.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1401 AAACTATAGTGAATGATTC 1420
DB 20 AAACTATAGTGAATGATTC 1

RESULT 1175
AAF80805/c
ID AAF80805 standard; DNA; 20 BP.
XX AC AAF80805;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #179.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1506 ACTTCTAGTAGCATTATTTA 1525
DB 20 ACTTCTAGTAGCATTATTTA 1

RESULT 1176
AAF80807/c
ID AAF80807 standard; DNA; 20 BP.
XX AC AAF80807;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #181.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 TTTATAGCAGCCAGAGAT 1541
DB 20 TTTATAGCAGCCAGAGAT 1
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RESULT 1177
AAF80886/c
ID AAF80886 standard; DNA; 20 BP.
XX AC AAF80886;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #260.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCTGACCTC 2317
DB 20 GGTCTCGATCTCTGACCTC 1

RESULT 1178
AAF80635/c
ID AAF80635 standard; DNA; 20 BP.
XX AC AAF80635;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #9.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACTACTGATGGTGCT 350
DB 20 CTGTACTACTGATGGTGCT 1

RESULT 1179
AAF80636/c
ID AAF80636 standard; DNA; 20 BP.
XX AC AAF80636;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #10.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 GATCTACAGGAAGCTTGCTAG 636
DB 20 GATCTACAGGAAGCTTGCTAG 1

RESULT 1180
AAF80640/c
ID AAF80640 standard; DNA; 20 BP.
XX AC AAF80640;
XX DT 02-MAY-2001 (first entry)
```

```
XX Human mdm2 phosphorothioate oligonucleotide #14.
DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
KW
XX
Query Match
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1776 TATTTCCCTAGTTGACCTG 1795
DB 20 TATTTCCCTAGTTGACCTG 1
RESULT 1181
AAF80649/c
ID AAF80649 standard; DNA; 20 BP.
XX
AC AAF80649;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #23.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 GGCCCTGTGTTCGGAAGA 56
DB 20 GGCCCTGTGTTCGGAAGA 1
RESULT 1182
AAF80659/c
ID AAF80659 standard; DNA; 20 BP.
XX
AC AAF80659;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #33.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 GCTTCTGGGGCTGTGTGGC 39
DB 20 GCTTCTGGGGCTGTGTGGC 1
RESULT 1183
AAF80690/c
ID AAF80690 standard; DNA; 20 BP.
XX
AC AAF80690;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #64.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 587 TGTGAAGAGCACAGGAAA 606
DB 20 TGTGAAGAGCACAGGAAA 1
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 306 AGGCAAAATGTGCAATACCAA 325
DB 20 AGGCAAAATGTGCAATACCAA 1
RESULT 1184
AAF80702/c
ID AAF80702 standard; DNA; 20 BP.
XX
AC AAF80702;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #76.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 361 CACAGATTCAGCTTCGAA 380
DB 20 CACAGATTCAGCTTCGAA 1
RESULT 1185
AAF80712/c
ID AAF80712 standard; DNA; 20 BP.
XX
AC AAF80712;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #86.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 503 ACGATTATATGATGAGAAGC 522
DB 20 ACGATTATATGATGAGAAGC 1
RESULT 1186
AAF80721/c
ID AAF80721 standard; DNA; 20 BP.
XX
AC AAF80721;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #95.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 503 ACGATTATATGATGAGAAGC 522
DB 20 ACGATTATATGATGAGAAGC 1
RESULT 1186
AAF80721/c
ID AAF80721 standard; DNA; 20 BP.
XX
AC AAF80721;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #95.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 587 TGTGAAGAGCACAGGAAA 606
DB 20 TGTGAAGAGCACAGGAAA 1
```

```
RESULT 1187
AAF80740/c
ID   AAF80740 standard; DNA; 20 BP.
XX
XX
AC   AAF80740;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #114.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   798 AGAGCAATTAGTGAGACAGA 817
Db   20 AGAGCAATTAGTGAGACAGA 1

RESULT 1188
AAF80758/c
ID   AAF80758 standard; DNA; 20 BP.
XX
XX
AC   AAF80758;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #132.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1006 CAGGTGATTGGTTGGATCAG 1025
Db   20 CAGGTGATTGGTTGGATCAG 1

RESULT 1189
AAF80786/c
ID   AAF80786 standard; DNA; 20 BP.
XX
XX
AC   AAF80786;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #160.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1292 GAATTGGCTTCCTGAAGATA 1311
Db   20 GAATTGGCTTCCTGAAGATA 1

RESULT 1190
AAF80802/c
ID   AAF80802 standard; DNA; 20 BP.
XX
XX
AC   AAF80802;
XX

RESULT 1187
XX
XX
DE   Human mdm2 phosphorothioate oligonucleotide #176.
XX
XX
AC   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1481 AAGTGAAGACTATTCTCAGC 1500
Db   20 AAGTGAAGACTATTCTCAGC 1

RESULT 1191
AAF80808/c
ID   AAF80808 standard; DNA; 20 BP.
XX
XX
AC   AAF80808;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #182.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1533 CAAGAAGATGTGAAGAGTT 1552
Db   20 CAAGAAGATGTGAAGAGTT 1

RESULT 1192
AAF80819/c
ID   AAF80819 standard; DNA; 20 BP.
XX
XX
AC   AAF80819;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #193.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1667 TGGCAAAACAGGACATCTTA 1686
Db   20 TGGCAAAACAGGACATCTTA 1

RESULT 1193
AAF80823/c
ID   AAF80823 standard; DNA; 20 BP.
XX
XX
AC   AAF80823;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #197.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
```

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAAGCTAAAGAA 1721  
DB 20 GTGCAAGAAGCTAAAGAA 1

RESULT 1194  
AAF80837/c  
ID AAF80837 standard; DNA; 20 BP.

XX AAF80837;  
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #211.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1840 TTAGACACCTGAAATTTAT 1859  
DB 20 TTAGACACCTGAAATTTAT 1

RESULT 1195  
AAF80852/c  
ID AAF80852 standard; DNA; 20 BP.

XX AAF80852;  
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #226.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1956 TATATTTGACTTGAATATG 1975  
DB 20 TATATTTGACTTGAATATG 1

RESULT 1196  
AAF80868/c  
ID AAF80868 standard; DNA; 20 BP.

XX AAF80868;  
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #242.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2133 GTGCAGTGGTGATCTTGGC 2152  
DB 20 GTGCAGTGGTGATCTTGGC 1

RESULT 1197  
AAF80880/c  
ID AAF80880 standard; DNA; 20 BP.

XX AAF80880;  
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #254.  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2232 GCCACCACCTGGCTAATT 2251  
DB 20 GCCACCACCTGGCTAATT 1

RESULT 1198  
AAD07540/c  
ID AAD07540 standard; DNA; 20 BP.

XX AAD07540;  
XX

DT 10-AUG-2001 (first entry)

XX Human mdm2 antisense oligonucleotide (ISIS #16514).

XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;  
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACTACTGATGTGCT 350  
DB 20 CTGTACTACTGATGTGCT 1

RESULT 1199  
AAD07542/c  
ID AAD07542 standard; DNA; 20 BP.

XX AAD07542;  
XX

DT 10-AUG-2001 (first entry)

XX Human mdm2 antisense oligonucleotide (ISIS #16516).

XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;  
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1047 AGTGTAGAATTTGAAGTTGA 1066  
DB 20 AGTGTAGAATTTGAAGTTGA 1

RESULT 1200  
AAD07543/c  
ID AAD07543 standard; DNA; 20 BP.

XX AAD07543;  
AC AAD07543;

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XX 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16517).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTCTGATTGTA 1400
DB 20 TTGATGTTCTCTGATTGTA 1

RESULT 1201
AAD07537/c
ID AAD07537 standard; DNA; 20 BP.
XX AC
XX AAD07537;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16511).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCACGCGCGAAGAACCCCG 292
DB 20 CTCACGCGCGAAGAACCCCG 1

RESULT 1202
AAD07539/c
ID AAD07539 standard; DNA; 20 BP.
XX AC
XX AAD07539;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16513).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AGCAGGCAATGTGCAATAC 322
DB 20 AGCAGGCAATGTGCAATAC 1

RESULT 1203
AAD07549/c
ID AAD07549 standard; DNA; 20 BP.
XX AC
XX AAD07549;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16523).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2132 AGTCAGTGGTGATCTTGG 2151
DB 20 AGTCAGTGGTGATCTTGG 1

RESULT 1204
AAD07554/c
ID AAD07554 standard; DNA; 20 BP.
XX AC
XX AAD07554;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #17615).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGGAAGA 56
DB 20 GGCCCTGTGTGCGGAAGA 1

RESULT 1205
AAD07532/c
ID AAD07532 standard; DNA; 20 BP.
XX AC
XX AAD07532;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16506).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTG 20
DB 20 GCACCGCGGAGCTTGGCTG 1

RESULT 1206
AAD07533/c
ID AAD07533 standard; DNA; 20 BP.
XX AC
XX AAD07533;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16507).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGGAAGA 56
DB 20 GGCCCTGTGTGCGGAAGA 1

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Db 20 GGCCCTGTGTGTCGGAAGA 1

RESULT 1207  
AAD07541/c  
ID AAD07541 standard; DNA; 20 BP.  
XX  
AC AAD07541;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide (ISIS #16515).  
XX  
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;  
tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 GATCTACAGGACTTGGTAG 636  
|||||  
Db 20 GATCTACAGGACTTGGTAG 1

RESULT 1208  
AAD07546/c  
ID AAD07546 standard; DNA; 20 BP.  
XX  
AC AAD07546;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide (ISIS #16520).  
XX  
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;  
tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 TAGTTGACCTGTCTATAAGA 1804  
|||||  
Db 20 TAGTTGACCTGTCTATAAGA 1

RESULT 1209  
AAD07547/c  
ID AAD07547 standard; DNA; 20 BP.  
XX  
AC AAD07547;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide (ISIS #16521).  
XX  
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;  
tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1818 CTAACCTATATACCCCTAGGA 1837  
|||||  
Db 20 CTAACCTATATACCCCTAGGA 1

RESULT 1210  
AAD07535/c  
ID AAD07535 standard; DNA; 20 BP.  
XX

AC AAD07535;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide (ISIS #16509).  
XX  
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;  
tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATTAGTCGTACGAGCGCCC 166  
|||||  
Db 20 ATTAGTCGTACGAGCGCCC 1

RESULT 1211  
AAD07538/c  
ID AAD07538 standard; DNA; 20 BP.  
XX  
AC AAD07538;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide (ISIS #16512).  
XX  
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;  
tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 TGGTGAGGACGAGCAATG 314  
|||||  
Db 20 TGGTGAGGACGAGCAATG 1

RESULT 1212  
AAD07550/c  
ID AAD07550 standard; DNA; 20 BP.  
XX  
AC AAD07550;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide (ISIS #16524).  
XX  
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;  
tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2224 AGTCATCTGCCACACACCT 2243  
|||||  
Db 20 AGTCATCTGCCACACACCT 1

RESULT 1213  
AAD07545/c  
ID AAD07545 standard; DNA; 20 BP.  
XX  
AC AAD07545;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide (ISIS #16519).  
XX  
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;



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KW tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1776 TATTTCCCTAGTTGACCTG 1795
DB 20 TATTTCCCTAGTTGACCTG 1

RESULT 1214
AAD07548/c
ID AAD07548 standard; DNA; 20 BP.
XX
AC AAD07548;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16522).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGGAAATGATGAATCTT 1953
DB 20 TAGTGGAAATGATGAATCTT 1

RESULT 1215
AAD07544/c
ID AAD07544 standard; DNA; 20 BP.
XX
AC AAD07544;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16518).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTACATGTGCAAGAAGCT 1714
DB 20 TTTACATGTGCAAGAAGCT 1

RESULT 1216
AAD07534/c
ID AAD07534 standard; DNA; 20 BP.
XX
AC AAD07534;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16508).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCCTGCTG 114

KW tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1776 TATTTCCCTAGTTGACCTG 1795
DB 20 TATTTCCCTAGTTGACCTG 1

RESULT 1217
AAD07536/c
ID AAD07536 standard; DNA; 20 BP.
XX
AC AAD07536;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16510).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GAGAGTGAATGATCCCCGA 200
DB 20 GAGAGTGAATGATCCCCGA 1

RESULT 1218
AAD07551/c
ID AAD07551 standard; DNA; 20 BP.
XX
AC AAD07551;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16525).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2256 GTACTTTTGTAGTAGACAGG 2275
DB 20 GTACTTTTGTAGTAGACAGG 1

RESULT 1219
AAH21705/c
ID AAH21705 standard; DNA; 20 BP.
XX
AC AAH21705;
XX
DT 13-AUG-2001 (first entry)
XX
DE MDM-2 phosphorothioate oligonucleotide.
XX
KW Phosphorothioate; MDM-2; HIV-1; gag; pancreatic cancer; tumour;
KW Panc 1 tumour; colon cancer; prodrug; polyanion; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTCAGTGAGAACAGGTGTCA 694
DB 20 GTCAGTGAGAACAGGTGTCA 1

RESULT 1220
AAH38246
ID AAH38246 standard; DNA; 20 BP.
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XX AAH38246;
AC
XX 14-AUG-2001 (first entry)
DT
DE SNP specific lower PCR primer SEQ ID 1042.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAAGTCTGGGATTAC 2357
Db 1 TCCCAAAGTCTGGGATTAC 20

RESULT 1221
AAH38602
ID AAH38602 standard; DNA; 20 BP.
XX
XX AAH38602;
AC
XX 14-AUG-2001 (first entry)
DT
DE SNP specific lower PCR primer SEQ ID 1398.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2352 GATTACAGGCATGAGCCACC 2371
Db 1 GATTACAGGCATGAGCCACC 20

RESULT 1222
AAF28586/c
ID AAF28586 standard; DNA; 20 BP.
XX
XX AAF28586;
AC
XX 02-APR-2001 (first entry)
DT
DE Epo-R PCR primer #1.
XX
XX Human; myeloid progenitor cell; transplantation; PCR primer; c-kit;
KW CD117; IL-7Ra1pha; interleukin-7 receptor alpha; Epo-R; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTGTCTGGGATTACAGGCAT 2363
Db 20 AGTGTCTGGGATTACAGGCAT 1

RESULT 1223
AAH20702/c
ID AAH20702 standard; DNA; 20 BP.
XX
XX AAH20702;
AC
XX 13-AUG-2001 (first entry)
DT
DE Human telomeric repeat binding factor 2 oligonucleotide 111430.
XX

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KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
KW inhibitor; premature aging; hyperproliferative disorder; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTCGATCTCCT 2311
Db 20 CAGGATGGTCTCGATCTCCT 1

RESULT 1224
AAH20704/c
ID AAH20704 standard; DNA; 20 BP.
XX
XX AAH20704;
AC
XX 13-AUG-2001 (first entry)
DT
DE Human telomeric repeat binding factor 2 oligonucleotide 111432.
XX
XX Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
KW inhibitor; premature aging; hyperproliferative disorder; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGGATTACAGGCATGA 2365
Db 20 TGCTGGGATTACAGGCATGA 1

RESULT 1225
AAS29242/c
ID AAS29242 standard; DNA; 20 BP.
XX
XX AAS29242;
AC
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 16506.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCGAGCTTGCGTG 20
Db 20 GCACCGCGCGAGCTTGCGTG 1

RESULT 1226
AAS29245/c
ID AAS29245 standard; DNA; 20 BP.
XX
XX AAS29245;
AC
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 16509.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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**AAS29324/C**

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 CATTATTATTATAGCAGCCCAAG 1536  
DB 20 CATTATTATTATAGCAGCCCAAG 1

RESULT 1234  
AAS29425/c  
ID AAS29425 standard; DNA; 20 BP.

XX AC AAS29425;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31591.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GTTGAAGGGAAGAAACCC 1569  
DB 20 GTTGAAGGGAAGAAACCC 1

RESULT 1235  
AAS29440/c  
ID AAS29440 standard; DNA; 20 BP.

XX AC AAS29440;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31598.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 AAAGGAATAAGCCTGCCCCA 1739  
DB 20 AAAGGAATAAGCCTGCCCCA 1

RESULT 1236  
AAS29453/c  
ID AAS29453 standard; DNA; 20 BP.

XX AC AAS29453;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31605.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1850 TGAATTTATTTCACATATAT 1869  
DB 20 TGAATTTATTTCACATATAT 1

RESULT 1237  
AAS29458/c  
ID AAS29458 standard; DNA; 20 BP.

XX AC AAS29458;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31609.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1889 AATTCACATAGATTCTTCT 1908  
DB 20 AATTCACATAGATTCTTCT 1

RESULT 1238  
AAS29467/c  
ID AAS29467 standard; DNA; 20 BP.

XX AC AAS29467;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31777.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1956 TATAATTTGACTTGAATATG 1975  
DB 20 TATAATTTGACTTGAATATG 1

RESULT 1239  
AAS29471/c  
ID AAS29471 standard; DNA; 20 BP.

XX AC AAS29471;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31779.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1990 CACCAACTCTTAATTTTAA 2009  
DB 20 CACCAACTCTTAATTTTAA 1

RESULT 1240

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AAS29475/c
ID AAS29475 standard; DNA; 20 BP.
XX
AC AAS29475;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31780.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 TCTGCTCTTAATGAGAGTA 2039
Db 20 TCTGCTCTTAATGAGAGTA 1

RESULT 1241
AAS29487/c
ID AAS29487 standard; DNA; 20 BP.
XX
AC AAS29487;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31622.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2176 GGGTTCGCACCATCTCTCTG 2195
Db 20 GGGTTCGCACCATCTCTCTG 1

RESULT 1242
AAS29500/c
ID AAS29500 standard; DNA; 20 BP.
XX
AC AAS29500;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31788.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGGTCTCGATCTC 2309
Db 20 GCCAGGATGGTCTCGATCTC 1

RESULT 1243
AAS29274/c
ID AAS29274 standard; DNA; 20 BP.
XX
AC AAS29274;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31713.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GCTTCTGGGGCCTGTGTGGC 39
Db 20 GCTTCTGGGGCCTGTGTGGC 1

RESULT 1244
AAS29288/c
ID AAS29288 standard; DNA; 20 BP.
XX
AC AAS29288;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31720.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 TGGCCCGGAGGTGGAATGA 193
Db 20 TGGCCCGGAGGTGGAATGA 1

RESULT 1245
AAS29320/c
ID AAS29320 standard; DNA; 20 BP.
XX
AC AAS29320;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31560.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 GGTAGACCAAGCCATTGC 411
Db 20 GGTAGACCAAGCCATTGC 1

RESULT 1246
AAS29338/c
ID AAS29338 standard; DNA; 20 BP.
XX
AC AAS29338;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31733.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 AGGAAATATATACCATGAT 619  
DB 20 AGGAAATATATACCATGAT 1

RESULT 1247  
AAS29339/c  
ID AAS29339 standard; DNA; 20 BP.  
XX  
AC AAS29339;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide 31565.  
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 609 TATACATGATCTACAGGAA 628  
DB 20 TATACATGATCTACAGGAA 1

RESULT 1248  
AAS29358/c  
ID AAS29358 standard; DNA; 20 BP.  
XX  
AC AAS29358;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide 31740.  
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 ATTATCTGGTGAACGACAAA 852  
DB 20 ATTATCTGGTGAACGACAAA 1

RESULT 1249  
AAS29372/c  
ID AAS29372 standard; DNA; 20 BP.  
XX  
AC AAS29372;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide 31576.  
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 996 AGTGAACATTCAGGTGATTG 1015  
DB 20 AGTGAACATTCAGGTGATTG 1

RESULT 1250  
AAS29401/c  
ID AAS29401 standard; DNA; 20 BP.  
XX  
AC AAS29401;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide 31583.  
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 GAATTGGCTTCCTGAAGATA 1311  
DB 20 GAATTGGCTTCCTGAAGATA 1

RESULT 1251  
AAS29432/c  
ID AAS29432 standard; DNA; 20 BP.  
XX  
AC AAS29432;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide 31594.  
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AAAATGGTTGCATTGTCCAT 1667  
DB 20 AAAATGGTTGCATTGTCCAT 1

RESULT 1252  
AAS29450/c  
ID AAS29450 standard; DNA; 20 BP.  
XX  
AC AAS29450;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide 31774.  
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1823 TATATAACCCCTAGGAATTTA 1842  
DB 20 TATATAACCCCTAGGAATTTA 1

RESULT 1253  
AAS29251/c  
ID AAS29251 standard; DNA; 20 BP.  
XX  
AC AAS29251;  
XX  
DT 21-NOV-2001 (first entry)

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XX Human mdm2 antisense oligonucleotide 16515.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 GATCTACAGGAAGTGGTAG 636
DB 20 GATCTACAGGAAGTGGTAG 1

RESULT 1254
AAS29258/c
ID AAS29258 standard; DNA; 20 BP.
XX
AC AAS29258;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16522.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGGGAATAGTGAATACCTT 1953
DB 20 TAGTGGGAATAGTGAATACCTT 1

RESULT 1255
AAS29285/c
ID AAS29285 standard; DNA; 20 BP.
XX
AC AAS29285;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31555.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 AGTGCCTACGAGCGCCAGT 169
DB 20 AGTGCCTACGAGCGCCAGT 1

RESULT 1256
AAS29299/c
ID AAS29299 standard; DNA; 20 BP.
XX
AC AAS29299;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31405.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 GAGGAGCAGGCAAAATGTGCA 318
DB 20 GAGGAGCAGGCAAAATGTGCA 1

RESULT 1257
AAS29325/c
ID AAS29325 standard; DNA; 20 BP.
XX
AC AAS29325;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31424.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 ATATTATGACTAAACGATTA 509
DB 20 ATATTATGACTAAACGATTA 1

RESULT 1258
AAS29333/c
ID AAS29333 standard; DNA; 20 BP.
XX
AC AAS29333;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31426.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 GAGATTGTGTCGCGTGCCA 578
DB 20 GAGATTGTGTCGCGTGCCA 1

RESULT 1259
AAS29362/c
ID AAS29362 standard; DNA; 20 BP.
XX
AC AAS29362;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31435.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 CCCTTTCCCTTTGATGAAGC 899
DB 20 CCCTTTCCCTTTGATGAAGC 1

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RESULT 1260
AAS29383/C
ID AAS29383 standard; DNA; 20 BP.
XX
XX
AC AAS29383;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31750.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 CTTAGTGAAGAGGACAAGA 1111
DB 20 CTTAGTGAAGAGGACAAGA 1

RESULT 1261
AAS29384/C
ID AAS29384 standard; DNA; 20 BP.
XX
XX
AC AAS29384;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31579.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 AGAAGGACAAGAACTCTCAG 1119
DB 20 AGAAGGACAAGAACTCTCAG 1

RESULT 1262
AAS29393/C
ID AAS29393 standard; DNA; 20 BP.
XX
XX
AC AAS29393;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31581.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 TGAATTTCTTGTAGTGACT 1215
DB 20 TGAATTTCTTGTAGTGACT 1

RESULT 1263
AAS29418/C
ID AAS29418 standard; DNA; 20 BP.
XX
XX
AC AAS29418;
XX

DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31765.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1489 ACTATTCTCAGCCCAACT 1508
DB 20 ACTATTCTCAGCCCAACT 1

RESULT 1264
AAS29424/C
ID AAS29424 standard; DNA; 20 BP.
XX
XX
AC AAS29424;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31767.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1541 TGTGAAGAGTTTGAAGGG 1560
DB 20 TGTGAAGAGTTTGAAGGG 1

RESULT 1265
AAS29433/C
ID AAS29433 standard; DNA; 20 BP.
XX
XX
AC AAS29433;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31770.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1657 GCATTGTCCATGCAAAACA 1676
DB 20 GCATTGTCCATGCAAAACA 1

RESULT 1266
AAS29491/C
ID AAS29491 standard; DNA; 20 BP.
XX
XX
AC AAS29491;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31624.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 CCTCCCAATTAGCTTGCCCT 2221
DB 20 CCTCCCAATTAGCTTGCCCT 1

RESULT 1267
AAS29281/c
ID AAS29281 standard; DNA; 20 BP.
XX
AC AAS29281;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31554.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 TGACCCGAGATCCTGCTGCTT 117
DB 20 TGACCCGAGATCCTGCTGCTT 1

RESULT 1268
AAS29293/c
ID AAS29293 standard; DNA; 20 BP.
XX
AC AAS29293;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31557.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 CCCGGATGGTGAGGAGCAGG 308
DB 20 CCCGGATGGTGAGGAGCAGG 1

RESULT 1269
AAS29306/c
ID AAS29306 standard; DNA; 20 BP.
XX
AC AAS29306;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31413.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAAAATGTGCAATACCAAC 326
DB 20 GGCAAAATGTGCAATACCAAC 1

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 GTGCAATACCAACATGCTGTG 333
DB 20 GTGCAATACCAACATGCTGTG 1

RESULT 1271
AAS29318/c
ID AAS29318 standard; DNA; 20 BP.
XX
AC AAS29318;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31724.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 GCTTCGGAACAAGAGACCCT 391
DB 20 GCTTCGGAACAAGAGACCCT 1

RESULT 1272
AAS29331/c
ID AAS29331 standard; DNA; 20 BP.
XX
AC AAS29331;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31563.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 538 ATTGTTCAAAATGATCTTCTA 557
DB 20 ATTGTTCAAAATGATCTTCTA 1

RESULT 1273
AAS29335/c
ID AAS29335 standard; DNA; 20 BP.
XX
AC AAS29335;

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XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31564.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 575 GCCAAGCTTCTCTGTGAAG 594
Db 20 GCCAAGCTTCTCTGTGAAG 1

RESULT 1274
AAS29346/c
ID AAS29346 standard; DNA; 20 BP.
XX
XX AAS29346;
AC
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31736.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 691 GTCACCTTGAAGTGGGAGT 710
Db 20 GTCACCTTGAAGTGGGAGT 1

RESULT 1275
AAS29359/c
ID AAS29359 standard; DNA; 20 BP.
XX
XX AAS29359;
AC
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31434.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 844 AACGACAAAGAAAGCCAC 863
Db 20 AACGACAAAGAAAGCCAC 1

RESULT 1276
AAS29361/c
ID AAS29361 standard; DNA; 20 BP.
XX
XX AAS29361;
AC
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31741.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1046 TAGGTAGAAATTTGAAGTTG 1065
Db 20 TAGGTAGAAATTTGAAGTTG 1

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 867 TCTGATAGTATTTCCCTTTC 886
Db 20 TCTGATAGTATTTCCCTTTC 1

RESULT 1277
AAS29365/c
ID AAS29365 standard; DNA; 20 BP.
XX
XX AAS29365;
AC
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31436.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 915 ATAAGGAGATATGTTGTGA 934
Db 20 ATAAGGAGATATGTTGTGA 1

RESULT 1278
AAS29375/c
ID AAS29375 standard; DNA; 20 BP.
XX
XX AAS29375;
AC
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31746.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1023 CAGGATTCAGTTTCAGATCA 1042
Db 20 CAGGATTCAGTTTCAGATCA 1

RESULT 1279
AAS29377/c
ID AAS29377 standard; DNA; 20 BP.
XX
XX AAS29377;
AC
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31747.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1046 TAGGTAGAAATTTGAAGTTG 1065
Db 20 TAGGTAGAAATTTGAAGTTG 1

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Db      20 TAGGTAGAAATTGAAGTTG 1

RESULT 1280
AAS29395/c
ID AAS29395 standard; DNA; 20 BP.
XX
AC AAS29395;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31445.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1220 GAAATGCACCTTCATGCAATG 1239
      |||||
Db      20 GAAATGCACCTTCATGCAATG 1

RESULT 1281
AAS29405/c
ID AAS29405 standard; DNA; 20 BP.
XX
AC AAS29405;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31760.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1333 TCTCTGAGAAAGCAAACTG 1352
      |||||
Db      20 TCTCTGAGAAAGCAAACTG 1

RESULT 1282
AAS29406/c
ID AAS29406 standard; DNA; 20 BP.
XX
AC AAS29406;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31448.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1346 CAAACTGGAATACTCAACAC 1365
      |||||
Db      20 CAAACTGGAATACTCAACAC 1

RESULT 1283
AAS29411/c
ID AAS29411 standard; DNA; 20 BP.
XX

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AC AAS29411;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31762.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1421 CAGAGAGTCATGTGTTGAGG 1440
      |||||
Db      20 CAGAGAGTCATGTGTTGAGG 1

RESULT 1284
AAS29463/c
ID AAS29463 standard; DNA; 20 BP.
XX
AC AAS29463;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31776.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1920 TTGACCTACTTTGTTAGTGG 1939
      |||||
Db      20 TTGACCTACTTTGTTAGTGG 1

RESULT 1285
AAS29465/c
ID AAS29465 standard; DNA; 20 BP.
XX
AC AAS29465;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31612.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1940 AATAGTGAATACTTACTATA 1959
      |||||
Db      20 AATAGTGAATACTTACTATA 1

RESULT 1286
AAS29483/c
ID AAS29483 standard; DNA; 20 BP.
XX
AC AAS29483;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31782.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;

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KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2133 GTGAGTGGGTGATCTTGCC 2152
|||||
DB 20 GTGAGTGGGTGATCTTGCC 1

RESULT 1287
AAS29261/c
ID AAS29261 standard; DNA; 20 BP.
XX
AC AAS29261;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16525.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2256 GTACTTTTGTAGACAGG 2275
|||||
DB 20 GTACTTTTGTAGACAGG 1

RESULT 1288
AAS29277/c
ID AAS29277 standard; DNA; 20 BP.
XX
AC AAS29277;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31553.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GTGTGTCGGAAGATGGAGC 62
|||||
DB 20 GTGTGTCGGAAGATGGAGC 1

RESULT 1289
AAS29287/c
ID AAS29287 standard; DNA; 20 BP.
XX
AC AAS29287;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31397.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCAGTGCCCTGGCCCGGAGA 184
|||||
DB 20 CCAGTGCCCTGGCCCGGAGA 1

RESULT 1290
AAS29291/c
ID AAS29291 standard; DNA; 20 BP.
XX
AC AAS29291;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31398.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CTTCCGCGAGTAGTCAGTCCC 236
|||||
DB 20 CTTCCGCGAGTAGTCAGTCCC 1

RESULT 1291
AAS29298/c
ID AAS29298 standard; DNA; 20 BP.
XX
AC AAS29298;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31404.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TGAGGAGCAGGCAAAATGTGC 317
|||||
DB 20 TGAGGAGCAGGCAAAATGTGC 1

RESULT 1292
AAS29303/c
ID AAS29303 standard; DNA; 20 BP.
XX
AC AAS29303;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31410.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAAAATGTCAATACC 323
|||||
DB 20 GCAGGCAAAATGTCAATACC 1

RESULT 1293
AAS29307/c
ID AAS29307 standard; DNA; 20 BP.
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XX AAS29307;
AC
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31414.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 308 GCAAAATGTCATACCAACA 327
Db 20 GCAAAATGTCATACCAACA 1

RESULT 1294
AAS29315/c
ID AAS29315 standard; DNA; 20 BP.
XX
AC AAS29315;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31723.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 TACCTACTGATGGTGCTGTA 353
Db 20 TACCTACTGATGGTGCTGTA 1

RESULT 1295
AAS29316/c
ID AAS29316 standard; DNA; 20 BP.
XX
AC AAS29316;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31421.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 351 GTACACCACTCAGATTC 370
Db 20 GTACACCACTCAGATTC 1

RESULT 1296
AAS29349/c
ID AAS29349 standard; DNA; 20 BP.
XX
AC AAS29349;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31737.
XX

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KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 TACAAGAGCTTCAGGAAGAG 746
Db 20 TACAAGAGCTTCAGGAAGAG 1

RESULT 1297
AAS29388/c
ID AAS29388 standard; DNA; 20 BP.
XX
AC AAS29388;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31753.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1135 TATATCAAGTTACTGTGTAT 1154
Db 20 TATATCAAGTTACTGTGTAT 1

RESULT 1298
AAS29404/c
ID AAS29404 standard; DNA; 20 BP.
XX
AC AAS29404;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31584.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1325 AGGGGAATCTCTGAGAAAG 1344
Db 20 AGGGGAATCTCTGAGAAAG 1

RESULT 1299
AAS29422/c
ID AAS29422 standard; DNA; 20 BP.
XX
AC AAS29422;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31590.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1522 TTTATAGCAGCCAGAGAT 1541  
 DB 20 TTTATAGCAGCCAGAGAT 1

RESULT 1300  
 AAS29430/c  
 ID AAS29430 standard; DNA; 20 BP.  
 XX  
 AC AAS29430;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31455.  
 XX  
 KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1617 GAACCTTGTGATTGTCA 1636  
 DB 20 GAACCTTGTGATTGTCA 1

RESULT 1301  
 AAS29439/c  
 ID AAS29439 standard; DNA; 20 BP.  
 XX  
 AC AAS29439;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31597.  
 XX  
 KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1710 AAGCTAAAGAAAGGAATAA 1729  
 DB 20 AAGCTAAAGAAAGGAATAA 1

RESULT 1302  
 AAS29476/c  
 ID AAS29476 standard; DNA; 20 BP.  
 XX  
 AC AAS29476;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31617.  
 XX  
 KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2051 TTTCTTAAATATGATATG 2070  
 DB 20 TTTCTTAAATATGATATG 1

RESULT 1303  
 AAS29480/c

ID AAS29480 standard; DNA; 20 BP.  
 XX  
 AC AAS29480;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31467.  
 XX  
 KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTTACCCAGGCTG 2130  
 DB 20 TTGCTCTGTTACCCAGGCTG 1

RESULT 1304  
 AAS29486/c  
 ID AAS29486 standard; DNA; 20 BP.  
 XX  
 AC AAS29486;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31783.  
 XX  
 KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TCACTGCAAGCTCTGCCCTC 2172  
 DB 20 TCACTGCAAGCTCTGCCCTC 1

RESULT 1305  
 AAS29504/c  
 ID AAS29504 standard; DNA; 20 BP.  
 XX  
 AC AAS29504;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31790.  
 XX  
 KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2325 GCCCACCCTGGCCTCCCAAA 2344  
 DB 20 GCCCACCCTGGCCTCCCAAA 1

RESULT 1306  
 AAS29247/c  
 ID AAS29247 standard; DNA; 20 BP.  
 XX  
 AC AAS29247;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 16511.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 CTCCAAGCGGAAACCCCG 292  
Db 20 CTCCAAGCGGAAACCCCG 1

RESULT 1307  
AAS29252/c  
ID AAS29252 standard; DNA; 20 BP.

XX  
AC AAS29252;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 16516.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1047 AGTGAGAAATTTGAAGTTGA 1066  
Db 20 AGTGAGAAATTTGAAGTTGA 1

RESULT 1308  
AAS29264/c  
ID AAS29264 standard; DNA; 20 BP.

XX  
AC AAS29264;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 17615.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GGCCCTGTGTTCGGAAGA 56  
Db 20 GGCCCTGTGTTCGGAAGA 1

RESULT 1309  
AAS29282/c  
ID AAS29282 standard; DNA; 20 BP.

XX  
AC AAS29282;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31717.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 GATCCTGCTGCTTTCGAGC 124  
Db 20 GATCCTGCTGCTTTCGAGC 1

RESULT 1310  
AAS29284/c  
ID AAS29284 standard; DNA; 20 BP.

XX  
AC AAS29284;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31718.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 GCAGCCAGGAGCACCGTCCC 139  
Db 20 GCAGCCAGGAGCACCGTCCC 1

RESULT 1311  
AAS29319/c  
ID AAS29319 standard; DNA; 20 BP.

XX  
AC AAS29319;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31422.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 GACCTGTGTAGACCAAGC 405  
Db 20 GACCTGTGTAGACCAAGC 1

RESULT 1312  
AAS29350/c  
ID AAS29350 standard; DNA; 20 BP.

XX  
AC AAS29350;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31431.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 GGAAGAGAAACCTTCATCTT 759  
Db 20 GGAAGAGAAACCTTCATCTT 1

RESULT 1313





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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1368 GCTGAAGAGGGCTTTGATGT 1387
      |||||
Db 20 GCTGAAGAGGGCTTTGATGT 1

RESULT 1320
AAS29434/c
ID AAS29434 standard; DNA; 20 BP.
XX
AC AAS29434;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31456.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1667 TGGCAAAACAGGACATCTTA 1686
      |||||
Db 20 TGGCAAAACAGGACATCTTA 1

RESULT 1321
AAS29437/c
ID AAS29437 standard; DNA; 20 BP.
XX
AC AAS29437;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31771.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 CCTGCTTTACATGTGCAAG 1709
      |||||
Db 20 CCTGCTTTACATGTGCAAG 1

RESULT 1322
AAS29459/c
ID AAS29459 standard; DNA; 20 BP.
XX
AC AAS29459;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31462.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1898 AGATTTCTTCTCTTAGTAT 1917
      |||||
Db 20 AGATTTCTTCTCTTAGTAT 1
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RESULT 1323
AAS29482/c
ID AAS29482 standard; DNA; 20 BP.
XX
AC AAS29482;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31620.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2123 CCAGGCTGGAGTCAGTGGG 2142
      |||||
Db 20 CCAGGCTGGAGTCAGTGGG 1

RESULT 1324
AAS29499/c
ID AAS29499 standard; DNA; 20 BP.
XX
AC AAS29499;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31471.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2283 CGTGTAGCCAGGATGGTCT 2302
      |||||
Db 20 CGTGTAGCCAGGATGGTCT 1

RESULT 1325
AAS29506/c
ID AAS29506 standard; DNA; 20 BP.
XX
AC AAS29506;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31791.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2341 CAAAGTGCTGGGATTACAGG 2360
      |||||
Db 20 CAAAGTGCTGGGATTACAGG 1

RESULT 1326
AAS29244/c
ID AAS29244 standard; DNA; 20 BP.
XX
AC AAS29244;
XX
DT 21-NOV-2001 (first entry)
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XX Human mdm2 antisense oligonucleotide 16508.
DE
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCTGCTG 114
DB 20 CTCTGACCGAGATCTGCTG 1

RESULT 1327
AAS29260/c
ID AAS29260 standard; DNA; 20 BP.
XX
AC AAS29260;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16524.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2224 AGTCATCTGCCACACACCT 2243
DB 20 AGTCATCTGCCACACACCT 1

RESULT 1328
AAS29272/c
ID AAS29272 standard; DNA; 20 BP.
XX
AC AAS29272;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31712.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCGAGCTTGCTGCTT 23
DB 20 CCGCGCGAGCTTGCTGCTT 1

RESULT 1329
AAS29292/c
ID AAS29292 standard; DNA; 20 BP.
XX
AC AAS29292;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31722.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGGAACTGGGAGTCTTGA 261
DB 20 AGGAACTGGGAGTCTTGA 1

RESULT 1330
AAS29300/c
ID AAS29300 standard; DNA; 20 BP.
XX
AC AAS29300;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31406.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 AGGAGCAGGCAATGTGCAA 319
DB 20 AGGAGCAGGCAATGTGCAA 1

RESULT 1331
AAS29351/c
ID AAS29351 standard; DNA; 20 BP.
XX
AC AAS29351;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31569.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 TTCATCTTCACATTGGTTT 771
DB 20 TTCATCTTCACATTGGTTT 1

RESULT 1332
AAS29370/c
ID AAS29370 standard; DNA; 20 BP.
XX
AC AAS29370;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31744.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 971 GAATCCGATCTTGATGCTG 990
DB 20 GAATCCGATCTTGATGCTG 1

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RESULT 1333
AAS29394/c
ID AAS29394 standard; DNA; 20 BP.
XX
AC AAS29394;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31755.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 TAGCTGACTATTGGAATGC 1226
DB 20 TAGCTGACTATTGGAATGC 1

RESULT 1334
AAS29414/c
ID AAS29414 standard; DNA; 20 BP.
XX
AC AAS29414;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31587.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATAAAATTACACAGCTTC 1468
DB 20 GATAAAATTACACAGCTTC 1

RESULT 1335
AAS29416/c
ID AAS29416 standard; DNA; 20 BP.
XX
AC AAS29416;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31451.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1466 TTCACAAATCACAGAAGTG 1485
DB 20 TTCACAAATCACAGAAGTG 1

RESULT 1336
AAS29442/c
ID AAS29442 standard; DNA; 20 BP.
XX
AC AAS29442;
XX

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DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31459.
XX
AC AAS29394;
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 CCCAGTATGTAGACAACCAA 1755
DB 20 CCCAGTATGTAGACAACCAA 1

RESULT 1337
AAS29243/c
ID AAS29243 standard; DNA; 20 BP.
XX
AC AAS29243;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 16507.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCTGTGTGTCGGAAGA 56
DB 20 GGCCTGTGTGTCGGAAGA 1

RESULT 1338
AAS29301/c
ID AAS29301 standard; DNA; 20 BP.
XX
AC AAS29301;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31407.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GGAGCAGGCAAAATGTGCAAT 320
DB 20 GGAGCAGGCAAAATGTGCAAT 1

RESULT 1339
AAS29329/c
ID AAS29329 standard; DNA; 20 BP.
XX
AC AAS29329;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31425.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

```

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 CAACATATTGTATTTGTTTC 544  
DB 20 CAACATATTGTATTTGTTTC 1

RESULT 1340  
AAS29334/c  
ID AAS29334 standard; DNA; 20 BP.

XX  
AC AAS29334;

DT 21-NOV-2001 (first entry)

DE Human mdm2 antisense oligonucleotide 31731.

KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 GTTGGCGTGCACGCTTCT 585  
DB 20 GTTGGCGTGCACGCTTCT 1

RESULT 1341  
AAS29336/c  
ID AAS29336 standard; DNA; 20 BP.

XX  
AC AAS29336;

DT 21-NOV-2001 (first entry)

DE Human mdm2 antisense oligonucleotide 31732.

KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 587 TGTGAAGACGACAGGAAA 606  
DB 20 TGTGAAGACGACAGGAAA 1

RESULT 1342  
AAS29345/c  
ID AAS29345 standard; DNA; 20 BP.

XX  
AC AAS29345;

DT 21-NOV-2001 (first entry)

DE Human mdm2 antisense oligonucleotide 31567.

KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 AGAACAGGTGTCACCTTGAA 701  
DB 20 AGAACAGGTGTCACCTTGAA 1

RESULT 1343  
AAS29347/c  
ID AAS29347 standard; DNA; 20 BP.

XX  
AC AAS29347;

DT 21-NOV-2001 (first entry)

DE Human mdm2 antisense oligonucleotide 31430.

KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723  
DB 20 TGGGAGTGATCAAAAGGACC 1

RESULT 1344  
AAS29360/c  
ID AAS29360 standard; DNA; 20 BP.

XX  
AC AAS29360;

DT 21-NOV-2001 (first entry)

DE Human mdm2 antisense oligonucleotide 31572.

KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACGCCACAATCTGATAGTA 876  
DB 20 ACGCCACAATCTGATAGTA 1

RESULT 1345  
AAS29381/c  
ID AAS29381 standard; DNA; 20 BP.

XX  
AC AAS29381;

DT 21-NOV-2001 (first entry)

DE Human mdm2 antisense oligonucleotide 31749.

KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1077 TCAGAGATTATAGCCTTAG 1096  
DB 20 TCAGAGATTATAGCCTTAG 1

RESULT 1346  
AAS29385/c  
ID AAS29385 standard; DNA; 20 BP.

XX  
AC AAS29385;

```
XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31751.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 GACAAGAACTCTCAGATGAA 1124
DB 20 GACAAGAACTCTCAGATGAA 1

RESULT 1347
AAS29387/c
ID AAS29387 standard; DNA; 20 BP.
XX
AC AAS29387;
XX
DT 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31752.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 AGATGATGAGGTATATCAAG 1143
DB 20 AGATGATGAGGTATATCAAG 1

RESULT 1348
AAS29397/c
ID AAS29397 standard; DNA; 20 BP.
XX
AC AAS29397;
XX
DT 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31582.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1257 CCATCACAATTGCAACAGATG 1276
DB 20 CCATCACAATTGCAACAGATG 1

RESULT 1349
AAS29420/c
ID AAS29420 standard; DNA; 20 BP.
XX
AC AAS29420;
XX
DT 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31766.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1506 ACTTCTAGTAGCATTATTTA 1525
DB 20 ACTTCTAGTAGCATTATTTA 1

RESULT 1350
AAS29460/c
ID AAS29460 standard; DNA; 20 BP.
XX
AC AAS29460;
XX
DT 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31610.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1905 TTCTCTTTAGTATAATTGAC 1924
DB 20 TTCTCTTTAGTATAATTGAC 1

RESULT 1351
AAS29466/c
ID AAS29466 standard; DNA; 20 BP.
XX
AC AAS29466;
XX
DT 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31613.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1948 ATACTTACTATAATTGACT 1967
DB 20 ATACTTACTATAATTGACT 1

RESULT 1352
AAS29470/c
ID AAS29470 standard; DNA; 20 BP.
XX
AC AAS29470;
XX
DT 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31614.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY - 1982 ATCCTTTACCAACTCCTTA 2001
DB 20 ATCCTTTACCAACTCCTTA 2001
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Db      20 ATCCTTTACACCACTCCTA 1
RESULT 1353
AAS29477/c
ID AAS29477 standard; DNA; 20 BP.
XX
AC
XX AAS29477;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31466.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2059 AATATGTATATGACATTTTAA 2078
Db      20 AATATGTATATGACATTTTAA 1
RESULT 1354
AAS29495/c
ID AAS29495 standard; DNA; 20 BP.
XX
AC
XX AAS29495;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31470.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2232 GCCACACACCTGGCTAATT 2251
Db      20 GCCACACACCTGGCTAATT 1
RESULT 1355
AAS29278/c
ID AAS29278 standard; DNA; 20 BP.
XX
AC
XX AAS29278;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31715.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 50 GGAAGATGGAGCAAGAGC 69
Db      20 GGAAGATGGAGCAAGAGC 1
RESULT 1356
AAS29286/c
ID AAS29286 standard; DNA; 20 BP.
XX
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AC AAS29286;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31719.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 158 CGAGCGCCGAGTGCCTTGGC 177
Db      20 CGAGCGCCGAGTGCCTTGGC 1
RESULT 1357
AAS29296/c
ID AAS29296 standard; DNA; 20 BP.
XX
AC
XX AAS29296;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31402.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 GGTGAGGAGCAGCAATGT 315
Db      20 GGTGAGGAGCAGCAATGT 1
RESULT 1358
AAS29308/c
ID AAS29308 standard; DNA; 20 BP.
XX
AC
XX AAS29308;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31415.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 309 CAAATGTGCAATACCAACAT 328
Db      20 CAAATGTGCAATACCAACAT 1
RESULT 1359
AAS29310/c
ID AAS29310 standard; DNA; 20 BP.
XX
AC
XX AAS29310;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31417.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
```

Db	20	AGGACCTGTACAGAGCTT	1
RESULT 1363			
AAS29364/c			
ID	AAS29364	standard; DNA; 20 BP.	
XX			
XX	AAS29364;		
XX			
DT	21-NOV-2001	(first entry)	
XX			
DE	Human mdm2 antisense oligonucleotide 31742.		
XX			
KW	Human; mdm2; hyperproliferative disorder; cancer; psoriasis;		
KW	atherosclerosis; tumour; cytostatic; anti psoriatic;		
	Query Match	0.8%; Score 20; DB 1; Length 20;	
	Best Local Similarity	100.0%; Pred. No. 1.8e+03;	
	Matches	20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	904	CTCTGTGTGTAATAAGGGAG	923
Db	20	CTCTGTGTGTAATAAGGGAG	1
RESULT 1364			
AAS29379/c			
ID	AAS29379	standard; DNA; 20 BP.	
XX			
AC	AAS29379;		
XX			
DT	21-NOV-2001	(first entry)	
XX			
DE	Human mdm2 antisense oligonucleotide 31748.		
XX			
KW	Human; mdm2; hyperproliferative disorder; cancer; psoriasis;		
KW	atherosclerosis; tumour; cytostatic; anti psoriatic;		
	Query Match	0.8%; Score 20; DB 1; Length 20;	
	Best Local Similarity	100.0%; Pred. No. 1.8e+03;	
	Matches	20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1059	GAAGTTGAATCTCTCGACTC	1078
Db	20	GAAGTTGAATCTCTCGACTC	1
RESULT 1365			
AAS29399/c			
ID	AAS29399	standard; DNA; 20 BP.	
XX			
AC	AAS29399;		
XX			
DT	21-NOV-2001	(first entry)	
XX			
DE	Human mdm2 antisense oligonucleotide 31446.		
XX			
KW	Human; mdm2; hyperproliferative disorder; cancer; psoriasis;		
KW	atherosclerosis; tumour; cytostatic; anti psoriatic;		
	Query Match	0.8%; Score 20; DB 1; Length 20;	
	Best Local Similarity	100.0%; Pred. No. 1.8e+03;	
	Matches	20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1275	TGTTGGGCCCTTCGTGAGAA	1294
Db	20	TGTTGGGCCCTTCGTGAGAA	1
RESULT 1366			
AAS29435/c			
ID	AAS29435	standard; DNA; 20 BP.	

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XX AAS29435;
AC
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31595.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1675 CAGGACATCTTATGCGCTGC 1694
Db 20 CAGGACATCTTATGCGCTGC 1

RESULT 1367
AAS29443/c
ID AAS29443 standard; DNA; 20 BP.
XX
AC AAS29443;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31599.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1745 TAGACAACCAATTCAAATGA 1764
Db 20 TAGACAACCAATTCAAATGA 1

RESULT 1368
AAS29447/c
ID AAS29447 standard; DNA; 20 BP.
XX
AC AAS29447;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31602.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1804 AGAATTATATTTCTTAAT 1823
Db 20 AGAATTATATTTCTTAAT 1

RESULT 1369
AAS29448/c
ID AAS29448 standard; DNA; 20 BP.
XX
AC AAS29448;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31773.
XX

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KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 TTATATATTTCTTAATATAT 1827
Db 20 TTATATATTTCTTAATATAT 1

RESULT 1370
AAS29456/c
ID AAS29456 standard; DNA; 20 BP.
XX
AC AAS29456;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31607.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 AAGTGAGAAAATGCCTCAAT 1891
Db 20 AAGTGAGAAAATGCCTCAAT 1

RESULT 1371
AAS29457/c
ID AAS29457 standard; DNA; 20 BP.
XX
AC AAS29457;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31608.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1883 TGCCTCAATTCACATAGATT 1902
Db 20 TGCCTCAATTCACATAGATT 1

RESULT 1372
AAS29461/c
ID AAS29461 standard; DNA; 20 BP.
XX
AC AAS29461;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31775.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1908 TCCTTAGTATAATTGACCTA 1927
DB 20 TCCTTAGTATAATTGACCTA 1

RESULT 1373
AAS29462/c
ID AAS29462 standard; DNA; 20 BP.
XX
AC AAS29462;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31611.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1913 AGTATAATTGACCTACTTTG 1932
DB 20 AGTATAATTGACCTACTTTG 1

RESULT 1374
AAS29502/c
ID AAS29502 standard; DNA; 20 BP.
XX
AC AAS29502;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31789.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCCGC 2326
DB 20 CTCCTGACCTCGTGATCCGC 1

RESULT 1375
AAS29505/c
ID AAS29505 standard; DNA; 20 BP.
XX
AC AAS29505;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31630.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GGCCTCCCAAGTCTGGGA 2353
DB 20 GGCCTCCCAAGTCTGGGA 1

RESULT 1376
AAS29249/c
ID AAS29249 standard; DNA; 20 BP.
XX
AC AAS29249;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16513.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AGCAGGCAAAATGTGCAATAC 322
DB 20 AGCAGGCAAAATGTGCAATAC 1

RESULT 1377
AAS29250/c
ID AAS29250 standard; DNA; 20 BP.
XX
AC AAS29250;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16514.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACTACTGATGGTGCT 350
DB 20 CTGTACTACTGATGGTGCT 1

RESULT 1378
AAS29253/c
ID AAS29253 standard; DNA; 20 BP.
XX
AC AAS29253;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16517.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTGATTGTAAA 1400
DB 20 TTGATGTTCTGATTGTAAA 1

RESULT 1379
AAS29259/c
ID AAS29259 standard; DNA; 20 BP.
XX
AC AAS29259;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16523.

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XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2132 AGTCAGTGGGTGATCTTGG 2151
DB 20 AGTCAGTGGGTGATCTTGG 1

RESULT 1380
AAS29294/c
ID AAS29294 standard; DNA; 20 BP.
XX
AC AAS29294;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31399.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GATGGTGAGGAGCAGGCANA 312
DB 20 GATGGTGAGGAGCAGGCANA 1

RESULT 1381
AAS29352/c
ID AAS29352 standard; DNA; 20 BP.
XX
AC AAS29352;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31738.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 761 ACATTGGTTTCTAGACCAT 780
DB 20 ACATTGGTTTCTAGACCAT 1

RESULT 1382
AAS29355/c
ID AAS29355 standard; DNA; 20 BP.
XX
AC AAS29355;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31739.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 798 AGAGCAATTAGTGAGACAGA 817
DB 20 AGAGCAATTAGTGAGACAGA 1

RESULT 1383
AAS29398/c
ID AAS29398 standard; DNA; 20 BP.
XX
AC AAS29398;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31757.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 CAACAGATGTTGGCCCTTC 1287
DB 20 CAACAGATGTTGGCCCTTC 1

RESULT 1384
AAS29407/c
ID AAS29407 standard; DNA; 20 BP.
XX
AC AAS29407;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31585.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1358 CTCACACACAGCTGAAGAGG 1377
DB 20 CTCACACACAGCTGAAGAGG 1

RESULT 1385
AAS29410/c
ID AAS29410 standard; DNA; 20 BP.
XX
AC AAS29410;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31586.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GAATGATTCAGAGATCAT 1431
DB 20 GAATGATTCAGAGATCAT 1

RESULT 1386

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 422 ATTAAGTCTGTGTGTGCAC 441
DB 20 ATTAAGTCTGTGTGTGCAC 1

RESULT 1393
AAS29323/c
ID AAS29323 standard; DNA; 20 BP.
XX
AC AAS29323;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31561.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 450 ACTTATCTATGAAAGAGGT 469
DB 20 ACTTATCTATGAAAGAGGT 1

RESULT 1394
AAS29337/c
ID AAS29337 standard; DNA; 20 BP.
XX
AC AAS29337;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31427.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 593 AGAGCACAGGAAATATATA 612
DB 20 AGAGCACAGGAAATATATA 1

RESULT 1395
AAS29368/c
ID AAS29368 standard; DNA; 20 BP.
XX
AC AAS29368;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31437.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 949 GTGAATCTACAGGACGCCA 968
DB 20 GTGAATCTACAGGACGCCA 1
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RESULT 1396
AAS29378/c
ID AAS29378 standard; DNA; 20 BP.
XX
AC AAS29378;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31440.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1051 TAGAATTTGAAGTTGAATCT 1070
DB 20 TAGAATTTGAAGTTGAATCT 1

RESULT 1397
AAS29380/c
ID AAS29380 standard; DNA; 20 BP.
XX
AC AAS29380;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31578.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1068 TCTCTCGACTCAGAAGATTA 1087
DB 20 TCTCTCGACTCAGAAGATTA 1

RESULT 1398
AAS29409/c
ID AAS29409 standard; DNA; 20 BP.
XX
AC AAS29409;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31449.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1401 AAACTATAGTGAATGATTC 1420
DB 20 AAACTATAGTGAATGATTC 1

RESULT 1399
AAS29427/c
ID AAS29427 standard; DNA; 20 BP.
XX
AC AAS29427;
XX
DT 21-NOV-2001 (first entry)
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XX Human mdm2 antisense oligonucleotide 31454.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAAGACAAAGAGAGAG 1585
DB 20 ACCCAAGACAAAGAGAGAG 1

RESULT 1400
AAS29428/c
ID AAS29428 standard; DNA; 20 BP.
XX
XX AAS29428;
AC
XX
XX 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31592.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 AGAGAGTGTGGAATCTAGTT 1599
DB 20 AGAGAGTGTGGAATCTAGTT 1

RESULT 1401
AAS29431/c
ID AAS29431 standard; DNA; 20 BP.
XX
XX AAS29431;
AC
XX
XX 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31593.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1624 GTGTGATTGTCAGGTCGA 1643
DB 20 GTGTGATTGTCAGGTCGA 1

RESULT 1402
AAS29438/c
ID AAS29438 standard; DNA; 20 BP.
XX
XX AAS29438;
AC
XX
XX 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31457.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAGCTAAAGAAA 1721
DB 20 GTGCAAGAGCTAAAGAAA 1

RESULT 1403
AAS29445/c
ID AAS29445 standard; DNA; 20 BP.
XX
XX AAS29445;
AC
XX
XX 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31601.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1787 GTTGACCTGCTATAGAGA 1806
DB 20 GTTGACCTGCTATAGAGA 1

RESULT 1404
AAS29452/c
ID AAS29452 standard; DNA; 20 BP.
XX
XX AAS29452;
AC
XX
XX 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31604.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1840 TTAGACAACCTGAAATTTAT 1859
DB 20 TTAGACAACCTGAAATTTAT 1

RESULT 1405
AAS29454/c
ID AAS29454 standard; DNA; 20 BP.
XX
XX AAS29454;
AC
XX
XX 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31606.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1855 TTTATTTCATATATCAAG 1874
DB 20 TTTATTTCATATATCAAG 1

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RESULT 1406
AAS29472/c
ID AAS29472 standard; DNA; 20 BP.
XX
AC AAS29472;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31615.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1997 TCTAATTTTAAATAATTTC 2016
DB 20 TCTAATTTTAAATAATTTC 1

RESULT 1407
AAS29484/c
ID AAS29484 standard; DNA; 20 BP.
XX
AC AAS29484;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31621.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2140 GGGTGATCTTGGCTCAGTCG 2159
DB 20 GGGTGATCTTGGCTCAGTCG 1

RESULT 1408
AAS29492/c
ID AAS29492 standard; DNA; 20 BP.
XX
AC AAS29492;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31785.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2210 TTAGCTTGGCTACAGTCAT 2229
DB 20 TTAGCTTGGCTACAGTCAT 1

RESULT 1409
AAS29498/c
ID AAS29498 standard; DNA; 20 BP.
XX
AC AAS29498;
XX

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DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31787.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTCACCGTGTTAGCCA 2293
DB 20 GGGTTTCACCGTGTTAGCCA 1

RESULT 1410
AAS29503/c
ID AAS29503 standard; DNA; 20 BP.
XX
AC AAS29503;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31472.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2319 TGATCCGCCACCTCGGCCT 2338
DB 20 TGATCCGCCACCTCGGCCT 1

RESULT 1411
AAS29507/c
ID AAS29507 standard; DNA; 20 BP.
XX
AC AAS29507;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31631.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2351 GGATTACAGCATGAGCCAC 2370
DB 20 GGATTACAGCATGAGCCAC 1

RESULT 1412
AAS29273/c
ID AAS29273 standard; DNA; 20 BP.
XX
AC AAS29273;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31552.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTGGCTGCTTCTGGGGCTG 33
    |||||
Db 20 TTGGCTGCTTCTGGGGCTG 1

RESULT 1413
AAS29290/c
ID AAS29290 standard; DNA; 20 BP.
XX
AC AAS29290;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31721.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 GGCCTCGTGTTCGCGAGTA 227
    |||||
Db 20 GGCCTCGTGTTCGCGAGTA 1

RESULT 1414
AAS29302/c
ID AAS29302 standard; DNA; 20 BP.
XX
AC AAS29302;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31408.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 GAGCAGCAAAATGTGCAATA 321
    |||||
Db 20 GAGCAGCAAAATGTGCAATA 1

RESULT 1415
AAS29312/c
ID AAS29312 standard; DNA; 20 BP.
XX
AC AAS29312;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31419.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 TGTGCAATACCAATGTCT 332
    |||||
Db 20 TGTGCAATACCAATGTCT 1

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RESULT 1416
AAS29317/c
ID AAS29317 standard; DNA; 20 BP.
XX
AC AAS29317;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31559.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 361 CACAGATTCAGCTTCGGAA 380
    |||||
Db 20 CACAGATTCAGCTTCGGAA 1

RESULT 1417
AAS29340/c
ID AAS29340 standard; DNA; 20 BP.
XX
AC AAS29340;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31734.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 TCTACAGGAACCTTGGTAGTA 638
    |||||
Db 20 TCTACAGGAACCTTGGTAGTA 1

RESULT 1418
AAS29357/c
ID AAS29357 standard; DNA; 20 BP.
XX
AC AAS29357;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31571.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 824 TTCAGATGAATTATCTGGTG 843
    |||||
Db 20 TTCAGATGAATTATCTGGTG 1

RESULT 1419
AAS29367/c
ID AAS29367 standard; DNA; 20 BP.
XX
AC AAS29367;

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XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31743.
DE
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 936 AGAAGCAGTACGAGTGAATC 955
DB 20 AGAAGCAGTACGAGTGAATC 1

RESULT 1420
AAS29391/c
ID AAS29391 standard; DNA; 20 BP.
XX
XX AAS29391;
AC
XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31754.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1170 GATACAGATTCATTGGAAGA 1189
DB 20 GATACAGATTCATTGGAAGA 1

RESULT 1421
AAS29403/c
ID AAS29403 standard; DNA; 20 BP.
XX
XX AAS29403;
AC
XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31447.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1311 AAAGGGAAGATAAAGGGGA 1330
DB 20 AAAGGGAAGATAAAGGGGA 1

RESULT 1422
AAS29489/c
ID AAS29489 standard; DNA; 20 BP.
XX
XX AAS29489;
AC
XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31784.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 TCCTGCCTCAGCCTCCCAAT 2210
DB 20 TCCTGCCTCAGCCTCCCAAT 1

RESULT 1423
AAS29496/c
ID AAS29496 standard; DNA; 20 BP.
XX
XX AAS29496;
AC
XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31627.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2253 TTTGTACTTTTAGTAGAGAC 2272
DB 20 TTTGTACTTTTAGTAGAGAC 1

RESULT 1424
AAS29246/c
ID AAS29246 standard; DNA; 20 BP.
XX
XX AAS29246;
AC
XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 16510.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GAGAGTGGATGATCCCGA 200
DB 20 GAGAGTGGATGATCCCGA 1

RESULT 1425
AAS29304/c
ID AAS29304 standard; DNA; 20 BP.
XX
XX AAS29304;
AC
XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31411.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGCAAAATGTGCAATACCA 324
DB 305 CAGGCAAAATGTGCAATACCA 324
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Db      20 CAGCAAAATGTGCAATACCA 1

RESULT 1426
AAS29305/c
ID AAS29305 standard; DNA; 20 BP.
XX
AC AAS29305;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31412.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      306 AGGCAAAATGTGCAATACCA 325
      |||||
Db      20 AGGCAAAATGTGCAATACCA 1

RESULT 1427
AAS29314/c
ID AAS29314 standard; DNA; 20 BP.
XX
AC AAS29314;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31558.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      323 CAACATGCTGTACCTACTG 342
      |||||
Db      20 CAACATGCTGTACCTACTG 1

RESULT 1428
AAS29328/c
ID AAS29328 standard; DNA; 20 BP.
XX
AC AAS29328;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31728.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      515 TGAGAGCAACACACATATTG 534
      |||||
Db      20 TGAGAGCAACACACATATTG 1

RESULT 1429
AAS29332/c
ID AAS29332 standard; DNA; 20 BP.
XX

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AC AAS29332;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31730.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      549 GATCTTCTAGGAGATTGTT 568
      |||||
Db      20 GATCTTCTAGGAGATTGTT 1

RESULT 1430
AAS29342/c
ID AAS29342 standard; DNA; 20 BP.
XX
AC AAS29342;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31566.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      646 AGCAGGAATCATCGGACTCA 665
      |||||
Db      20 AGCAGGAATCATCGGACTCA 1

RESULT 1431
AAS29374/c
ID AAS29374 standard; DNA; 20 BP.
XX
AC AAS29374;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31439.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1017 TTGGATCAGGATTCAGTTTC 1036
      |||||
Db      20 TTGGATCAGGATTCAGTTTC 1

RESULT 1432
AAS29376/c
ID AAS29376 standard; DNA; 20 BP.
XX
AC AAS29376;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31577.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;

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KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1034 TTCAGATCAGTTTAGTGTAG 1053
DB 20 TTCAGATCAGTTTAGTGTAG 1

RESULT 1433
AAS29389/c
ID AAS29389 standard; DNA; 20 BP.
XX
AC AAS29389;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31443.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 GTGTATCAGCGAGGGAGAG 1168
DB 20 GTGTATCAGCGAGGGAGAG 1

RESULT 1434
AAS29396/c
ID AAS29396 standard; DNA; 20 BP.
XX
AC AAS29396;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31756.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1226 CACTTCATGCAATGAATGA 1245
DB 20 CACTTCATGCAATGAATGA 1

RESULT 1435
AAS29429/c
ID AAS29429 standard; DNA; 20 BP.
XX
AC AAS29429;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31769.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 CTTAATGCCATTGAACCTTG 1624
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Db 20 CTTAATGCCATTGAACCTTG 1

RESULT 1436
AAS29444/c
ID AAS29444 standard; DNA; 20 BP.
XX
AC AAS29444;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31600.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1757 TCAAATGATTGTGCTAACTT 1776
DB 20 TCAAATGATTGTGCTAACTT 1

RESULT 1437
AAS29468/c
ID AAS29468 standard; DNA; 20 BP.
XX
AC AAS29468;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31464.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1969 GAATATGTAGCTCATCCTTT 1988
DB 20 GAATATGTAGCTCATCCTTT 1

RESULT 1438
AAS29248/c
ID AAS29248 standard; DNA; 20 BP.
XX
AC AAS29248;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16512.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 TGGTGAGGAGCAGGCAATG 314
DB 20 TGGTGAGGAGCAGGCAATG 1

RESULT 1439
AAS29283/c
ID AAS29283 standard; DNA; 20 BP.
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XX AAS29283;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31396.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 TGTCTTCGACGACGAGCA 132
Db 20 TGTCTTCGACGACGAGCA 1

RESULT 1440
AAS29309/c
ID AAS29309 standard; DNA; 20 BP.
XX
XX AAS29309;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31416.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 310 AAATGTGCAATACCAACATG 329
Db 20 AAATGTGCAATACCAACATG 1

RESULT 1441
AAS29330/c
ID AAS29330 standard; DNA; 20 BP.
XX
XX AAS29330;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31729.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 531 ATTGTATATTGTTCAATGA 550
Db 20 ATTGTATATTGTTCAATGA 1

RESULT 1442
AAS29371/c
ID AAS29371 standard; DNA; 20 BP.
XX
XX AAS29371;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31438.
XX

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KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 983 TGATGCTGGTGAAGTGAAC 1002
Db 20 TGATGCTGGTGAAGTGAAC 1

RESULT 1443
AAS29386/c
ID AAS29386 standard; DNA; 20 BP.
XX
XX AAS29386;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31442.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1115 CTCAGATGAAGATGATGAGG 1134
Db 20 CTCAGATGAAGATGATGAGG 1

RESULT 1444
AAS29402/c
ID AAS29402 standard; DNA; 20 BP.
XX
XX AAS29402;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31759.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1301 TCCTGAAGATAAGGGAAG 1320
Db 20 TCCTGAAGATAAGGGAAG 1

RESULT 1445
AAS29415/c
ID AAS29415 standard; DNA; 20 BP.
XX
XX AAS29415;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31764.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1456 TTACACAAGCTTCACATCA 1475
DB 20 TTACACAAGCTTCACATCA 1

RESULT 1446
AAS29423/c
ID AAS29423 standard; DNA; 20 BP.
XX
XX
AC AAS29423;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31453.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1533 CAAGAAGATGTGAAGAGTT 1552
DB 20 CAAGAAGATGTGAAGAGTT 1

RESULT 1447
AAS29426/c
ID AAS29426 standard; DNA; 20 BP.
XX
XX
AC AAS29426;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31768.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 GAAGAAACCCCAAGACAAGA 1579
DB 20 GAAGAAACCCCAAGACAAGA 1

RESULT 1448
AAS29446/c
ID AAS29446 standard; DNA; 20 BP.
XX
XX
AC AAS29446;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31459.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 TATAAGAGATTATATATTT 1817
DB 20 TATAAGAGATTATATATTT 1

RESULT 1449
AAS29455/c
ID AAS29455 standard; DNA; 20 BP.
XX
XX
AC AAS29455;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31461.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TATATCAAACTGAGAAAATG 1884
DB 20 TATATCAAACTGAGAAAATG 1

RESULT 1450
AAS29474/c
ID AAS29474 standard; DNA; 20 BP.
XX
XX
AC AAS29474;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31616.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2015 TCTACTCTGCTTAAATGAG 2034
DB 20 TCTACTCTGCTTAAATGAG 1

RESULT 1451
AAS29478/c
ID AAS29478 standard; DNA; 20 BP.
XX
XX
AC AAS29478;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31618.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2072 CATTAAATGTAACCTTATTA 2091
DB 20 CATTAAATGTAACCTTATTA 1

RESULT 1452
AAS29485/c
ID AAS29485 standard; DNA; 20 BP.
XX
XX
AC AAS29485;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31468.
```

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2146 TCTTGGCTCACTGCAAGCTC 2165  
 |||||  
 DB 20 TCTTGGCTCACTGCAAGCTC 1

RESULT 1453  
 AAS29490/c  
 ID AAS29490 standard; DNA; 20 BP.  
 XX  
 AC AAS29490;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31469.  
 XX  
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2198 TCAGCCTCCCAATTAGCTTG 2217  
 |||||  
 DB 20 TCAGCCTCCCAATTAGCTTG 1

RESULT 1454  
 AAS29497/c  
 ID AAS29497 standard; DNA; 20 BP.  
 XX  
 AC AAS29497;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31628.  
 XX  
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2265 GTAGAGACAGGGTTTACCG 2284  
 |||||  
 DB 20 GTAGAGACAGGGTTTACCG 1

RESULT 1455  
 AAS29501/c  
 ID AAS29501 standard; DNA; 20 BP.  
 XX  
 AC AAS29501;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31629.  
 XX  
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCTGACCTC 2317  
 |||||  
 DB 20 GGTCTCGATCTCTGACCTC 1

RESULT 1456  
 AAS29297/c  
 ID AAS29297 standard; DNA; 20 BP.  
 XX  
 AC AAS29297;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31403.  
 XX  
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 GTCAGGAGCAGGCAATGTG 316  
 |||||  
 DB 20 GTCAGGAGCAGGCAATGTG 1

RESULT 1457  
 AAS29311/c  
 ID AAS29311 standard; DNA; 20 BP.  
 XX  
 AC AAS29311;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31418.  
 XX  
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTC 331  
 |||||  
 DB 20 ATGTGCAATACCAACATGTC 1

RESULT 1458  
 AAS29341/c  
 ID AAS29341 standard; DNA; 20 BP.  
 XX  
 AC AAS29341;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide 31428.  
 XX  
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 634 TAGTAGTCAATCAGCAGGAA 653  
 |||||  
 DB 20 TAGTAGTCAATCAGCAGGAA 1

RESULT 1459

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AAS29356/c
ID AAS29356 standard; DNA; 20 BP.
XX
AC AAS29356;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31433.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 GAGACAGAGAAATTCAGA 829
Db 20 GAGACAGAGAAATTCAGA 1

RESULT 1460
AAS29373/c
ID AAS29373 standard; DNA; 20 BP.
XX
AC AAS29373;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31745.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1006 CAGGTGATTGGTGGATCAG 1025
Db 20 CAGGTGATTGGTGGATCAG 1

RESULT 1461
AAS29412/c
ID AAS29412 standard; DNA; 20 BP.
XX
AC AAS29412;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31450.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1434 GTTGAGGAAATGATGATAA 1453
Db 20 GTTGAGGAAATGATGATAA 1

RESULT 1462
AAS29417/c
ID AAS29417 standard; DNA; 20 BP.
XX
AC AAS29417;
XX
DT 21-NOV-2001 (first entry)
XX
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DE Human mdm2 antisense oligonucleotide 31588.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AACTGAAGACTATTCTCAGC 1500
Db 20 AAGTGAAGACTATTCTCAGC 1

RESULT 1463
AAS29436/c
ID AAS29436 standard; DNA; 20 BP.
XX
AC AAS29436;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31596.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1684 TTATGGCCTGCTTACATGT 1703
Db 20 TTATGGCCTGCTTACATGT 1

RESULT 1464
AAS29449/c
ID AAS29449 standard; DNA; 20 BP.
XX
AC AAS29449;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31603.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 TTCTAACTATATAACCCCTAG 1835
Db 20 TTCTAACTATATAACCCCTAG 1

RESULT 1465
AAS29451/c
ID AAS29451 standard; DNA; 20 BP.
XX
AC AAS29451;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31460.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1832 CTAGGAATTTAGACAACCTG 1851
Db 20 CTAGGAATTTAGACAACCTG 1

RESULT 1466
AAS29479/c
ID AAS29479 standard; DNA; 20 BP.
XX
AC AAS29479;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31619.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2103 ACCGAGTCTGCTCTGTTC 2122
Db 20 ACCGAGTCTGCTCTGTTC 1

RESULT 1467
AAS29254/c
ID AAS29254 standard; DNA; 20 BP.
XX
AC AAS29254;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16518.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1695 TTATCATGTGCAAGAGCT 1714
Db 20 TTATCATGTGCAAGAGCT 1

RESULT 1468
AAS29255/c
ID AAS29255 standard; DNA; 20 BP.
XX
AC AAS29255;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16519.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1776 TATTTCCCTAGTTGACCTG 1795
Db 20 TATTTCCCTAGTTGACCTG 1

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RESULT 1469
AAS29275/c
ID AAS29275 standard; DNA; 20 BP.
XX
AC AAS29275;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31394.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GCCTGTGTGGCCCTGTGTGT 48
Db 20 GCCTGTGTGGCCCTGTGTGT 1

RESULT 1470
AAS29280/c
ID AAS29280 standard; DNA; 20 BP.
XX
AC AAS29280;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31716.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 CGAGCCCGAGGGCGGCCGC 89
Db 20 CGAGCCCGAGGGCGGCCGC 1

RESULT 1471
AAS29289/c
ID AAS29289 standard; DNA; 20 BP.
XX
AC AAS29289;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31556.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 GCCCAGGCGCTGCTTCC 221
Db 20 GCCCAGGCGCTGCTTCC 1

RESULT 1472
AAS29327/c
ID AAS29327 standard; DNA; 20 BP.
XX
AC AAS29327;
XX
DT 21-NOV-2001 (first entry)

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XX Human mdm2 antisense oligonucleotide 31562.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 503 ACGATTATATGATGAGAGC 522
DB 20 ACGATTATATGATGAGAGC 1

RESULT 1473
AAS29343/c
ID AAS29343 standard; DNA; 20 BP.
XX
AC AAS29343;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31735.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 ATCGGACTCAGGTACATCTG 675
DB 20 ATCGGACTCAGGTACATCTG 1

RESULT 1474
AAS29354/c
ID AAS29354 standard; DNA; 20 BP.
XX
AC AAS29354;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31570.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 CATCTAGAAGGAGGACCAATT 806
DB 20 CATCTAGAAGGAGGACCAATT 1

RESULT 1475
AAS29366/c
ID AAS29366 standard; DNA; 20 BP.
XX
AC AAS29366;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31574.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TGTGTGAAAGAGCAGTAG 946
DB 20 TGTGTGAAAGAGCAGTAG 1

RESULT 1476
AAS29419/c
ID AAS29419 standard; DNA; 20 BP.
XX
AC AAS29419;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31452.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GCCATCAACTTCTAGTAGCA 1518
DB 20 GCCATCAACTTCTAGTAGCA 1

RESULT 1477
AAS29441/c
ID AAS29441 standard; DNA; 20 BP.
XX
AC AAS29441;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31772.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 ATAAAGCCCTGCCCAGTAGT 1745
DB 20 ATAAAGCCCTGCCCAGTAGT 1

RESULT 1478
AAS29464/c
ID AAS29464 standard; DNA; 20 BP.
XX
AC AAS29464;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31463.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 GTAGTGAATAGTGAATACT 1952
DB 20 GTAGTGAATAGTGAATACT 1
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RESULT 1479
AAS29469/C
ID AAS29469 standard; DNA; 20 BP.
XX
XX
AC AAS29469;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31778.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1973 ATGTAGCTCATCCTTTACAC 1992
Db 20 ATGTAGCTCATCCTTTACAC 1

RESULT 1480
AAS29481/C
ID AAS29481 standard; DNA; 20 BP.
XX
XX
AC AAS29481;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31781.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2116 CTGTTACCCAGGCTGGAGTG 2135
Db 20 CTGTTACCCAGGCTGGAGTG 1

RESULT 1481
AAS29494/C
ID AAS29494 standard; DNA; 20 BP.
XX
XX
AC AAS29494;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31786.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2218 GCCTACAGTCATCTGCCACC 2237
Db 20 GCCTACAGTCATCTGCCACC 1

RESULT 1482
AAL40351
ID AAL40351 standard; DNA; 20 BP.
XX
XX
AC AAL40351;
XX

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DT 19-SEP-2002 (first entry)
XX
DE Human caspase 6 antisense inhibition related oligo SEQ ID No 70.
XX
XX
KW Muscular; cytostatic; nootropic; neuroprotective; ophthalmological;
KW antilipaeamic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2340 CCAAAGTGTGGGATTACAG 2359
Db 1 CCAAAGTGTGGGATTACAG 20

RESULT 1483
ABL44004
ID ABL44004 standard; DNA; 20 BP.
XX
XX
AC ABL44004;
XX
DT 11-APR-2002 (first entry)
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1048.
XX
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2337 CTCCCAAGTGTGGGATT 2356
Db 1 CTCCCAAGTGTGGGATT 20

RESULT 1484
ABL44438/C
ID ABL44438 standard; DNA; 20 BP.
XX
XX
AC ABL44438;
XX
DT 11-APR-2002 (first entry)
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1482.
XX
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2142 GTGATCTTGGCTCACTGCAA 2161
Db 20 GTGATCTTGGCTCACTGCAA 1

RESULT 1485
ABA92187
ID ABA92187 standard; DNA; 20 BP.
XX
XX
AC ABA92187;
XX
DT 06-JUN-2002 (first entry)
DE Polymorphism 506B13CA1 reverse PCR primer.
XX
XX
KW NALPN; nyctalopin; human; congenital stationary night blindness; CSNB;
KW glycosylphosphatidylinositol; GPI; proteoglycan; retina; polymorphism;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2338 TCCCAAGTCTGGGATTAC 2357
Db 1 TCCCAAGTCTGGGATTAC 20

RESULT 1486
ABA92208
ID ABA92208 standard; DNA; 20 BP.
XX
AC ABA92208;
XX
DT 06-JUN-2002 (first entry)
DE Reverse PCR primer for polymorphism 506B13CA1.
KW NYX; nyctalopin; human; congenital stationary night blindness; CSNB;
KW glycosylphosphatidylinositol; GPI; retina; SLRP;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2338 TCCCAAGTCTGGGATTAC 2357
Db 1 TCCCAAGTCTGGGATTAC 20

RESULT 1487
ABK86101/c
ID ABK86101 standard; DNA; 20 BP.
XX
AC ABK86101;
XX
DT 23-AUG-2002 (first entry)
DE Human MDM-2 oligonucleotide phosphorothioate 2'-O-MOE gapmer.
KW MDM-2; peptide linked oligomeric compound; ss; human;
KW phosphorothioate 2'-O-MOE gapmer oligonucleotide.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1695 TTTCATGTGCAAGAAGCT 1714
Db 20 TTTCATGTGCAAGAAGCT 1

RESULT 1488
ABL60510/c
ID ABL60510 standard; DNA; 20 BP.
XX
AC ABL60510;
XX
DT 12-AUG-2002 (first entry)
DE Human MDM2 mRNA fragment complementary oligo primer 2.
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 675 GTGAGTGAACAGGTGTCA 694
Db 20 GTGAGTGAACAGGTGTCA 1
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RESULT 1489
ABK91100/c
ID ABK91100 standard; DNA; 20 BP.
XX
AC ABK91100;
XX
DT 05-DEC-2002 (first entry)
DE PCR primer Alu3, for human DNA derived from chromosome 21.
KW Human; fluorescent labelling technique; fluorescent intercalating dye;
KW nucleic acid detection; electrophoresis; diagnostic assay;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2341 CAAAGTCTGGGATTACAGG 2360
Db 20 CAAAGTCTGGGATTACAGG 1

RESULT 1490
ABZ79385
ID ABZ79385 standard; DNA; 20 BP.
XX
AC ABZ79385;
XX
DT 01-MAY-2003 (first entry)
DE Acetyl-Coenzyme A-carboxylase-alpha gene PCR primer, SEQ ID 72.
KW Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer;
KW breast; ovary; PCR; primer; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2338 TCCCAAGTCTGGGATTAC 2357
Db 1 TCCCAAGTCTGGGATTAC 20

RESULT 1491
ACD27753/c
ID ACD27753 standard; DNA; 20 BP.
XX
AC ACD27753;
XX
DT 18-SEP-2003 (first entry)
DE Peptide linked oligomeric compound associated oligonucleotide #2.
KW Peptide linked oligomeric compound; diagnostic; therapeutic;
KW research reagent; protein production inhibitor;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1695 TTTCATGTGCAAGAAGCT 1714
Db 20 TTTCATGTGCAAGAAGCT 1

RESULT 1492
AAL60008/c
ID AAL60008 standard; DNA; 20 BP.
XX
AC AAL60008;
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```
XX 27-AUG-2003 (first entry)
DT Human GH-1 gene amplifying PCR primer, CRV156.lpl.
DE
DE Human; growth hormone 1; GH-1; single nucleotide polymorphism; SNP;
KW gene therapy; PCR; primer; ss.
KW

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2340 CCAAAGTCTGGGATTACAG 2359
DB 20 CCAAAGTCTGGGATTACAG 1
|||||

RESULT 1493
ADD21442/c
ID ADD21442 standard; DNA; 20 BP.
XX
AC ADD21442;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #5.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GAGAGTGGATGATCCCGA 200
DB 20 GAGAGTGGATGATCCCGA 1
|||||

RESULT 1494
ADD21485/c
ID ADD21485 standard; DNA; 20 BP.
XX
AC ADD21485;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #48.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 GCCCAGGCGTGGCTTCC 221
DB 20 GCCCAGGCGTGGCTTCC 1
|||||

RESULT 1495
ADD21486/c
ID ADD21486 standard; DNA; 20 BP.
XX
AC ADD21486;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #49.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GCGTCGTCTTCCGAGTA 227
DB 20 GCGTCGTCTTCCGAGTA 1
|||||

RESULT 1496
ADD21522/c
ID ADD21522 standard; DNA; 20 BP.
XX
AC ADD21522;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #85.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGACTAAACGATTATATGAT 515
DB 20 TGACTAAACGATTATATGAT 1
|||||

RESULT 1497
ADD21553/c
ID ADD21553 standard; DNA; 20 BP.
XX
AC ADD21553;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #116.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 824 TTCAGATGAATTATCTGGTG 843
DB 20 TTCAGATGAATTATCTGGTG 1
|||||

RESULT 1498
ADD21554/c
ID ADD21554 standard; DNA; 20 BP.
XX
AC ADD21554;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #117.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 ATTATCTGCTGAACGACAAA 852
DB 20 ATTATCTGCTGAACGACAAA 1
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Db      20 ATTATCTGGTGAAGACAAA 1

RESULT 1499
ADD21555/c
ID      ADD21555 standard; DNA; 20 BP.
XX
XX
AC      ADD21555;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #118.
DE
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      844 AACGACAAAGAAAGCCAC 863
Db      20 AACGACAAAGAAAGCCAC 1

RESULT 1500
ADD21567/c
ID      ADD21567 standard; DNA; 20 BP.
XX
XX
AC      ADD21567;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #130.
DE
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      983 TGATGCTGGTGAAGTGAAC 1002
Db      20 TGATGCTGGTGAAGTGAAC 1

RESULT 1501
ADD21568/c
ID      ADD21568 standard; DNA; 20 BP.
XX
XX
AC      ADD21568;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #131.
DE
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      996 AGTGACATTTCAGGTGATTG 1015
Db      20 AGTGACATTTCAGGTGATTG 1

RESULT 1502
ADD21579/c
ID      ADD21579 standard; DNA; 20 BP.
XX

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AC      ADD21579;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #142.
DE
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1092 CTTAGTGAAGACGACAAGA 1111
Db      20 CTTAGTGAAGACGACAAGA 1

RESULT 1503
ADD21596/c
ID      ADD21596 standard; DNA; 20 BP.
XX
XX
AC      ADD21596;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #159.
DE
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1283 CCTTCGTGAGATTGGCTTC 1302
Db      20 CCTTCGTGAGATTGGCTTC 1

RESULT 1504
ADD21616/c
ID      ADD21616 standard; DNA; 20 BP.
XX
XX
AC      ADD21616;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #179.
DE
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1506 ACTTCTAGTAGCATTATTTA 1525
Db      20 ACTTCTAGTAGCATTATTTA 1

RESULT 1505
ADD21634/c
ID      ADD21634 standard; DNA; 20 BP.
XX
XX
AC      ADD21634;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #197.
DE
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAGCTAAAGAA 1721
DB 20 GTGCAAGAGCTAAAGAA 1

RESULT 1506
ADD21641/c
ID ADD21641 standard; DNA; 20 BP.
XX
AC ADD21641;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #204.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1787 GTTGACCTGTATAGAGA 1806
DB 20 GTTGACCTGTATAGAGA 1

RESULT 1507
ADD21646/c
ID ADD21646 standard; DNA; 20 BP.
XX
AC ADD21646;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #209.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1823 TATATAACCTTAGGAATTTA 1842
DB 20 TATATAACCTTAGGAATTTA 1

RESULT 1508
ADD21650/c
ID ADD21650 standard; DNA; 20 BP.
XX
AC ADD21650;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #213.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1855 TTTATTACATATATCAAG 1874

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAGCTAAAGAA 1721
DB 20 GTGCAAGAGCTAAAGAA 1

RESULT 1509
ADD21702/c
ID ADD21702 standard; DNA; 20 BP.
XX
AC ADD21702;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #265.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
DB 20 CAAAGTCTGGGATTACAGG 1

RESULT 1510
ADD21712/c
ID ADD21712 standard; DNA; 20 BP.
XX
AC ADD21712;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #268.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 CACCTCACAGATTCAGCTT 375
DB 20 CACCTCACAGATTCAGCTT 1

RESULT 1511
ADD21719/c
ID ADD21719 standard; DNA; 20 BP.
XX
AC ADD21719;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #275.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 AGATTCAGCTTCGAACAA 383
DB 20 AGATTCAGCTTCGAACAA 1

RESULT 1512
ADD21734/c
ID ADD21734 standard; DNA; 20 BP.
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XX ADD21734;
AC
DT 15-JAN-2004 (first entry)
DE
XX Human mdm2 antisense oligonucleotide #290.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249
Db 20 TCATGCAATGAATGAATCC 1

RESULT 1513
ADD21748/c
ID ADD21748 standard; DNA; 20 BP.
XX
AC ADD21748;
XX
DT 15-JAN-2004 (first entry)
DE
XX Human mdm2 antisense oligonucleotide #304.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1742 ATGTAGACAACCAATTCAAA 1761
Db 20 ATGTAGACAACCAATTCAAA 1

RESULT 1514
ADD21750/c
ID ADD21750 standard; DNA; 20 BP.
XX
AC ADD21750;
XX
DT 15-JAN-2004 (first entry)
DE
XX Human mdm2 antisense oligonucleotide #306.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1762 TGATTGTGCTAACTATTTC 1781
Db 20 TGATTGTGCTAACTATTTC 1

RESULT 1515
ADD21438/c
ID ADD21438 standard; DNA; 20 BP.
XX
AC ADD21438;
XX
DT 15-JAN-2004 (first entry)
DE
XX Human mdm2 antisense oligonucleotide #1.

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KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGCGCTG 20
Db 20 GCACCGCGGAGCTTGCGCTG 1

RESULT 1516
ADD21451/c
ID ADD21451 standard; DNA; 20 BP.
XX
AC ADD21451;
XX
DT 15-JAN-2004 (first entry)
DE
XX Human mdm2 antisense oligonucleotide #14.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1776 TATTTCCCTAGTTGACCTG 1795
Db 20 TATTTCCCTAGTTGACCTG 1

RESULT 1517
ADD21495/c
ID ADD21495 standard; DNA; 20 BP.
XX
AC ADD21495;
XX
DT 15-JAN-2004 (first entry)
DE
XX Human mdm2 antisense oligonucleotide #58.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 GAGGAGCAGCGCAAAATGTGCA 318
Db 20 GAGGAGCAGCGCAAAATGTGCA 1

RESULT 1518
ADD21566/c
ID ADD21566 standard; DNA; 20 BP.
XX
AC ADD21566;
XX
DT 15-JAN-2004 (first entry)
DE
XX Human mdm2 antisense oligonucleotide #129.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 971 GAATCCGATCTTGATCTG 990
Db 20 GAATCCGATCTTGATCTG 1

RESULT 1519
ADD21569/c
ID ADD21569 standard; DNA; 20 BP.
XX
AC
XX
AC ADD21569;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #132.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1006 CAGGTGATTGTTGGATCAG 1025
Db 20 CAGGTGATTGTTGGATCAG 1

RESULT 1520
ADD21595/c
ID ADD21595 standard; DNA; 20 BP.
XX
AC
XX
AC ADD21595;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #158.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1275 TGTGGGCCCTTCGTGAGAA 1294
Db 20 TGTGGGCCCTTCGTGAGAA 1

RESULT 1521
ADD21627/c
ID ADD21627 standard; DNA; 20 BP.
XX
AC
XX
AC ADD21627;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #190.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1624 GTGTGATTGTCAAGGTGCA 1643
Db 20 GTGTGATTGTCAAGGTGCA 1

RESULT 1522
ADD21651/c
ID ADD21651 standard; DNA; 20 BP.
XX
AC
XX
AC ADD21651;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #214.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1865 TATATCAAAAGTGAGAAAATG 1884
Db 20 TATATCAAAAGTGAGAAAATG 1

RESULT 1523
ADD21653/c
ID ADD21653 standard; DNA; 20 BP.
XX
AC
XX
AC ADD21653;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #216.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1883 TGCCTCAATTACATAGATT 1902
Db 20 TGCCTCAATTACATAGATT 1

RESULT 1524
ADD21701/c
ID ADD21701 standard; DNA; 20 BP.
XX
AC
XX
AC ADD21701;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #264.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2334 GGCCTCCCAAAGTGTGGGA 2353
Db 20 GGCCTCCCAAAGTGTGGGA 1

RESULT 1525
ADD21726/c
ID ADD21726 standard; DNA; 20 BP.
XX
AC
XX
AC ADD21726;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #282.
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XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 482 TGGCCAGTATATGACTA 501  
DB 20 TGGCCAGTATATGACTA 1  
RESULT 1526  
ADD21728/c  
ID ADD21728 standard; DNA; 20 BP.  
XX  
AC ADD21728;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #284.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 780 TCTACCTCATCTAGAAGGAG 799  
DB 20 TCTACCTCATCTAGAAGGAG 1  
RESULT 1527  
ADD21733/c  
ID ADD21733 standard; DNA; 20 BP.  
XX  
AC ADD21733;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #289.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1203 TCCTTAGCTGACTATTGGAA 1222  
DB 20 TCCTTAGCTGACTATTGGAA 1  
RESULT 1528  
ADD21752/c  
ID ADD21752 standard; DNA; 20 BP.  
XX  
AC ADD21752;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #308.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1782 CCTAGTTGACCTGTCTATA 1801  
DB 20 CCTAGTTGACCTGTCTATA 1  
RESULT 1529  
ADD21445/c  
ID ADD21445 standard; DNA; 20 BP.  
XX  
AC ADD21445;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #8.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 303 AGCAGGCAAAATGTGCAATAC 322  
DB 20 AGCAGGCAAAATGTGCAATAC 1  
RESULT 1530  
ADD21478/c  
ID ADD21478 standard; DNA; 20 BP.  
XX  
AC ADD21478;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #41.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 105 GATCCTGCTGCTTTGCGAGC 124  
DB 20 GATCCTGCTGCTTTGCGAGC 1  
RESULT 1531  
ADD21493/c  
ID ADD21493 standard; DNA; 20 BP.  
XX  
AC ADD21493;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #56.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 297 GTGAGGAGCAGGCAATGTG 316  
DB 20 GTGAGGAGCAGGCAATGTG 1  
RESULT 1532
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ADD21505/c
ID  ADD21505 standard; DNA; 20 BP.
XX
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
AC  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX  ADD21505;
DT  15-JAN-2004 (first entry)
DE  Human mdm2 antisense oligonucleotide #68.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  310 AAATGTGCAATACCAACATG 329
Db  20 AAATGTGCAATACCAACATG 1

RESULT 1533
ADD21524/c
ID  ADD21524 standard; DNA; 20 BP.
XX
XX  ADD21524;
DT  15-JAN-2004 (first entry)
DE  Human mdm2 antisense oligonucleotide #87.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  515 TGAGAGCAACAAACATATTG 534
Db  20 TGAGAGCAACAAACATATTG 1

RESULT 1534
ADD21533/c
ID  ADD21533 standard; DNA; 20 BP.
XX
XX  ADD21533;
DT  15-JAN-2004 (first entry)
DE  Human mdm2 antisense oligonucleotide #96.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  593 AGAGCAGAGAAATATATA 612
Db  20 AGAGCAGAGAAATATATA 1

RESULT 1535
ADD21540/c
ID  ADD21540 standard; DNA; 20 BP.
XX
XX  ADD21540;
DT  15-JAN-2004 (first entry)
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE  Human mdm2 antisense oligonucleotide #103.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  669 ACATCTGTGAGTGAGAACAG 688
Db  20 ACATCTGTGAGTGAGAACAG 1

RESULT 1536
ADD21550/c
ID  ADD21550 standard; DNA; 20 BP.
XX
XX  ADD21550;
DT  15-JAN-2004 (first entry)
DE  Human mdm2 antisense oligonucleotide #113.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  787 CATCTAGAGGAGGAGCAATT 806
Db  20 CATCTAGAGGAGGAGCAATT 1

RESULT 1537
ADD21573/c
ID  ADD21573 standard; DNA; 20 BP.
XX
XX  ADD21573;
DT  15-JAN-2004 (first entry)
DE  Human mdm2 antisense oligonucleotide #136.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1046 TAGTGTAGAATTGGAAGTTG 1065
Db  20 TAGTGTAGAATTGGAAGTTG 1

RESULT 1538
ADD21574/c
ID  ADD21574 standard; DNA; 20 BP.
XX
XX  ADD21574;
DT  15-JAN-2004 (first entry)
DE  Human mdm2 antisense oligonucleotide #137.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1051 TAGAATTTGACGTTGAATCT 1070
Db 20 TAGAATTTGAAGTTGAATCT 1
RESULT 1539
ADD21581/c
ID ADD21581 standard; DNA; 20 BP.
XX
AC ADD21581;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #144.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1105 GACAAGAACTCTCAGATGAA 1124
Db 20 GACAAGAACTCTCAGATGAA 1
RESULT 1540
ADD21594/c
ID ADD21594 standard; DNA; 20 BP.
XX
AC ADD21594;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #157.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1268 CAACAGATGTTGGCCCTTC 1287
Db 20 CAACAGATGTTGGCCCTTC 1
RESULT 1541
ADD21615/c
ID ADD21615 standard; DNA; 20 BP.
XX
AC ADD21615;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #178.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1499 GCCATCAACTTCTAGTAGCA 1518
Db 20 GCCATCAACTTCTAGTAGCA 1
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RESULT 1542
ADD21625/c
ID ADD21625 standard; DNA; 20 BP.
XX
AC ADD21625;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #188.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1605 CTTAATGCCATTGAACCTTG 1624
Db 20 CTTAATGCCATTGAACCTTG 1
RESULT 1543
ADD21628/c
ID ADD21628 standard; DNA; 20 BP.
XX
AC ADD21628;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #191.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1648 AAAATGTTGCATTGTCCAT 1667
Db 20 AAAATGTTGCATTGTCCAT 1
RESULT 1544
ADD21637/c
ID ADD21637 standard; DNA; 20 BP.
XX
AC ADD21637;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #200.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1726 ATAAGCCCTGCCCATGTATGT 1745
Db 20 ATAAGCCCTGCCCATGTATGT 1
RESULT 1545
ADD21668/c
ID ADD21668 standard; DNA; 20 BP.
XX
AC ADD21668;
XX
DT 15-JAN-2004 (first entry)
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```
XX Human mdm2 antisense oligonucleotide #231.
DE
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1997 TCCTAAATTTTAAATAATTTTC 2016
DB 20 TCCTAAATTTTAAATAATTTTC 1
RESULT 1546
ADD21685/c
ID ADD21685 standard; DNA; 20 BP.
XX
AC ADD21685;
XX
XX 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #248.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2191 TCCTGCCTCAGCCTCCCAAT 2210
DB 20 TCCTGCCTCAGCCTCCCAAT 1
RESULT 1547
ADD21697/c
ID ADD21697 standard; DNA; 20 BP.
XX
AC ADD21697;
XX
XX 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #260.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2298 GGTCTCGATCTCTGACCTC 2317
DB 20 GGTCTCGATCTCTGACCTC 1
RESULT 1548
ADD21721/c
ID ADD21721 standard; DNA; 20 BP.
XX
AC ADD21721;
XX
XX 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #277.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1695 TTTTACATGTGCAAGAAGCT 1714
DB 20 TTTTACATGTGCAAGAAGCT 1
XX Human mdm2 antisense oligonucleotide #231.
DE
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 366 ATTCAGCTTCGGAACAAGA 385
DB 20 ATTCAGCTTCGGAACAAGA 1
RESULT 1549
ADD21741/c
ID ADD21741 standard; DNA; 20 BP.
XX
AC ADD21741;
XX
XX 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #297.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1662 GTCCATGGCAAAACAGGACA 1681
DB 20 GTCCATGGCAAAACAGGACA 1
RESULT 1550
ADD21743/c
ID ADD21743 standard; DNA; 20 BP.
XX
AC ADD21743;
XX
XX 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #299.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1682 TCTTATGGCTGCTTTACAT 1701
DB 20 TCTTATGGCTGCTTTACAT 1
RESULT 1551
ADD21450/c
ID ADD21450 standard; DNA; 20 BP.
XX
AC ADD21450;
XX
XX 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #13.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1695 TTTTACATGTGCAAGAAGCT 1714
DB 20 TTTTACATGTGCAAGAAGCT 1
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RESULT 1552
ADD21460/c
ID ADD21460 standard; DNA; 20 BP.
XX
AC ADD21460;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #23.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 GGCCCTGTGTCTCGGAAGA 56
DB 20 GGCCCTGTGTCTCGGAAGA 1

RESULT 1553
ADD21476/c
ID ADD21476 standard; DNA; 20 BP.
XX
AC ADD21476;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #39.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 CGAGCCCGAGGGCGGCGGC 89
DB 20 CGAGCCCGAGGGCGGCGGC 1

RESULT 1554
ADD21477/c
ID ADD21477 standard; DNA; 20 BP.
XX
AC ADD21477;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #40.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 TGACCGAGATCTGTGTT 117
DB 20 TGACCGAGATCTGTGTT 1

RESULT 1555
ADD21521/c
ID ADD21521 standard; DNA; 20 BP.
XX
AC ADD21521;
XX
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DT 15-JAN-2004 (first entry)
XX
XX Human mdm2 antisense oligonucleotide #84.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 490 ATATTATGACTAAACGATTA 509
DB 20 ATATTATGACTAAACGATTA 1

RESULT 1556
ADD21570/c
ID ADD21570 standard; DNA; 20 BP.
XX
AC ADD21570;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #133.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1017 TTGGATCAGGATTCAGTTTC 1036
DB 20 TTGGATCAGGATTCAGTTTC 1

RESULT 1557
ADD21585/c
ID ADD21585 standard; DNA; 20 BP.
XX
AC ADD21585;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #148.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1149 GTGTATCAGCGGCGAGAG 1168
DB 20 GTGTATCAGCGGCGAGAG 1

RESULT 1558
ADD21593/c
ID ADD21593 standard; DNA; 20 BP.
XX
AC ADD21593;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #156.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1257 CCATCATTGCAACAGTG 1276
DB 20 CCATCATTGCAACAGTG 1

RESULT 1559
ADD21614/c
ID ADD21614 standard; DNA; 20 BP.
XX
AC ADD21614;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #177.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1489 ACTATTCTCAGCCATCACT 1508
DB 20 ACTATTCTCAGCCATCACT 1

RESULT 1560
ADD21618/c
ID ADD21618 standard; DNA; 20 BP.
XX
AC ADD21618;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #181.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 TTTATAGCAGCCAGAAGAT 1541
DB 20 TTTATAGCAGCCAGAAGAT 1

RESULT 1561
ADD21620/c
ID ADD21620 standard; DNA; 20 BP.
XX
AC ADD21620;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #183.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1541 TGTGAAGAGTTTGAAGGG 1560
DB 20 TGTGAAGAGTTTGAAGGG 1

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1562
ADD21630/c
ID ADD21630 standard; DNA; 20 BP.
XX
AC ADD21630;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #193.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 TGGCAAAACAGGACATCTTA 1686
DB 20 TGGCAAAACAGGACATCTTA 1

RESULT 1563
ADD21635/c
ID ADD21635 standard; DNA; 20 BP.
XX
AC ADD21635;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #198.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1710 AAGCTAAAGAAAGGAATAA 1729
DB 20 AAGCTAAAGAAAGGAATAA 1

RESULT 1564
ADD21647/c
ID ADD21647 standard; DNA; 20 BP.
XX
AC ADD21647;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #210.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1832 CTAGGAATTTAGACAACCTG 1851
DB 20 CTAGGAATTTAGACAACCTG 1

RESULT 1565
ADD21652/c
ID ADD21652 standard; DNA; 20 BP.
XX
AC ADD21652;
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```
XX 15-JAN-2004 (first entry)
DT Human mdm2 antisense oligonucleotide #215.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 AAGTGAGAAATGCCTCAAT 1891
DB 20 AAGTGAGAAATGCCTCAAT 1

RESULT 1566
ADD21699/c
ID ADD21699 standard; DNA; 20 BP.
XX
AC ADD21699;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #262.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 TGATCGCCCACTCGGCT 2338
DB 20 TGATCGCCCACTCGGCT 1

RESULT 1567
ADD21735/c
ID ADD21735 standard; DNA; 20 BP.
XX
AC ADD21735;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #291.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1341 AAAGCCAACTGGAACAATC 1360
DB 20 AAAGCCAACTGGAACAATC 1

RESULT 1568
ADD21446/c
ID ADD21446 standard; DNA; 20 BP.
XX
AC ADD21446;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #9.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
```

```
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACTACTGATGGTCT 350
DB 20 CTGTACTACTGATGGTCT 1

RESULT 1569
ADD21481/c
ID ADD21481 standard; DNA; 20 BP.
XX
AC ADD21481;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #44.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
```

```
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 AGTGGTACGAGCGCCAGT 169
DB 20 AGTGGTACGAGCGCCAGT 1
```

```
RESULT 1570
ADD21512/c
ID ADD21512 standard; DNA; 20 BP.
```

```
XX AC ADD21512;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #75.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
```

```
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 351 GTAAACCACCTCACAGATTCC 370
DB 20 GTAAACCACCTCACAGATTCC 1
```

```
RESULT 1571
ADD21516/c
ID ADD21516 standard; DNA; 20 BP.
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```
XX AC ADD21516;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #79.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
```

```
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 GGTAGACCAAGCCATTGC 411
```

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Db      20  GGTTAGACCAAGCCATTGC 1

RESULT 1572
ADD21527/c
ID  ADD21527 standard; DNA; 20 BP.
XX
XX  ADD21527;
AC
XX
XX  15-JAN-2004 (first entry)
DT
XX  Human mdm2 antisense oligonucleotide #90.
DE
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX  Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      538  ATTGTTCAAAATGATCTTCTA 557
Db      20  ATTGTTCAAAATGATCTTCTA 1

RESULT 1573
ADD21528/c
ID  ADD21528 standard; DNA; 20 BP.
XX
XX  ADD21528;
AC
XX
XX  15-JAN-2004 (first entry)
DT
XX  Human mdm2 antisense oligonucleotide #91.
DE
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX  Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      549  GATCTTCTAGGAGATTGTT 568
Db      20  GATCTTCTAGGAGATTGTT 1

RESULT 1574
ADD21529/c
ID  ADD21529 standard; DNA; 20 BP.
XX
XX  ADD21529;
AC
XX
XX  15-JAN-2004 (first entry)
DT
XX  Human mdm2 antisense oligonucleotide #92.
DE
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX  Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      559  GAGATTGTTGGCGTGCCA 578
Db      20  GAGATTGTTGGCGTGCCA 1

RESULT 1575
ADD21534/c
ID  ADD21534 standard; DNA; 20 BP.
XX
XX  ADD21534;
AC
XX
XX  15-JAN-2004 (first entry)
DT
XX  Human mdm2 antisense oligonucleotide #97.
DE
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX  Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      600  AGGAAAATATATACCATGAT 619
Db      20  AGGAAAATATATACCATGAT 1

RESULT 1576
ADD21546/c
ID  ADD21546 standard; DNA; 20 BP.
XX
XX  ADD21546;
AC
XX
XX  15-JAN-2004 (first entry)
DT
XX  Human mdm2 antisense oligonucleotide #109.
DE
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX  Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      740  GGAAGAGAAACCTTCATCTT 759
Db      20  GGAAGAGAAACCTTCATCTT 1

RESULT 1577
ADD21556/c
ID  ADD21556 standard; DNA; 20 BP.
XX
XX  ADD21556;
AC
XX
XX  15-JAN-2004 (first entry)
DT
XX  Human mdm2 antisense oligonucleotide #119.
DE
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX  Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      857  ACCGCCAAATCTGTAGTA 876
Db      20  ACCGCCAAATCTGTAGTA 1

RESULT 1578
ADD21606/c
ID  ADD21606 standard; DNA; 20 BP.
XX
XX  ADD21606;
AC
XX
XX  15-JAN-2004 (first entry)
DT
XX  Human mdm2 antisense oligonucleotide #169.
DE
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GAATGATTCACAGAGTGCAT 1431
Db 20 GAATGATTCACAGAGTGCAT 1

RESULT 1579
ADD21617/c
ID ADD21617 standard; DNA; 20 BP.
XX
AC ADD21617;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #180.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 CATTATTATAGCAGCCCAAG 1536
Db 20 CATTATTATAGCAGCCCAAG 1

RESULT 1580
ADD21669/c
ID ADD21669 standard; DNA; 20 BP.
XX
AC ADD21669;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #232.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2004 TTATAATAATTCTACTCTG 2023
Db 20 TTATAATAATTCTACTCTG 1

RESULT 1581
ADD21676/c
ID ADD21676 standard; DNA; 20 BP.
XX
AC ADD21676;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #239.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTACCCAGGCTG 2130
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Db 20 TTGCTCTGTACCCAGGCTG 1

RESULT 1582
ADD21739/c
ID ADD21739 standard; DNA; 20 BP.
XX
AC ADD21739;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #295.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 GACCTAAAAATGTTGCATT 1661
Db 20 GACCTAAAAATGTTGCATT 1

RESULT 1583
ADD21441/c
ID ADD21441 standard; DNA; 20 BP.
XX
AC ADD21441;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #4.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATTAGTCCGTACGAGGCCCC 166
Db 20 ATTAGTCCGTACGAGGCCCC 1

RESULT 1584
ADD21473/c
ID ADD21473 standard; DNA; 20 BP.
XX
AC ADD21473;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #36.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GTGTGTCGGAAGATGAGC 62
Db 20 GTGTGTCGGAAGATGAGC 1

RESULT 1585
ADD21474/c
ID ADD21474 standard; DNA; 20 BP.
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XX ADD21474;
AC
XX
DT
XX
XX
DE
XX
XX
KW antisenase oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GGAAGATGGAGCAAGAAGC 69
Db 20 GGAAGATGGAGCAAGAAGC 1

RESULT 1586
ADD21491/c
ID ADD21491 standard; DNA; 20 BP.
XX
AC ADD21491;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisenase oligonucleotide #54.
XX
KW antisenase oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 ATGGTGAGGAGCAGGCAAAAT 313
Db 20 ATGGTGAGGAGCAGGCAAAAT 1

RESULT 1587
ADD21500/c
ID ADD21500 standard; DNA; 20 BP.
XX
AC ADD21500;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisenase oligonucleotide #63.
XX
KW antisenase oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGCAAAATGCAATACCA 324
Db 20 CAGGCAAAATGCAATACCA 1

RESULT 1588
ADD21513/c
ID ADD21513 standard; DNA; 20 BP.
XX
AC ADD21513;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisenase oligonucleotide #76.
XX

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KW antisenase oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 CACAGATTCAGCTTCGGAA 380
Db 20 CACAGATTCAGCTTCGGAA 1

RESULT 1589
ADD21519/c
ID ADD21519 standard; DNA; 20 BP.
XX
AC ADD21519;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisenase oligonucleotide #82.
XX
KW antisenase oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 ACTTATCTATGAAAGAGGT 469
Db 20 ACTTATCTATGAAAGAGGT 1

RESULT 1590
ADD21536/c
ID ADD21536 standard; DNA; 20 BP.
XX
AC ADD21536;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisenase oligonucleotide #99.
XX
KW antisenase oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 TCTACAGGAACCTGGTAGTA 638
Db 20 TCTACAGGAACCTGGTAGTA 1

RESULT 1591
ADD21541/c
ID ADD21541 standard; DNA; 20 BP.
XX
AC ADD21541;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisenase oligonucleotide #104.
XX
KW antisenase oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 682 AGAACAGGTGTCACCTTGAA 701
Db |||||
20 AGAACAGGTGTCACCTTGAA 1

RESULT 1592
ADD21547/c
ID ADD21547 standard; DNA; 20 BP.
XX
AC ADD21547;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #110.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 TTCATCTTCACATTTGGTTT 771
Db |||||
20 TTCATCTTCACATTTGGTTT 1

RESULT 1593
ADD21558/c
ID ADD21558 standard; DNA; 20 BP.
XX
AC ADD21558;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #121.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 CCCTTTCCTTTGATGAAGC 899
Db |||||
20 CCCTTTCCTTTGATGAAGC 1

RESULT 1594
ADD21563/c
ID ADD21563 standard; DNA; 20 BP.
XX
AC ADD21563;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #126.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 936 AGAAGCAGTAGCAGTGAATC 955
Db |||||
20 AGAAGCAGTAGCAGTGAATC 1

RESULT 1595
ADD21589/c

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ID ADD21589 standard; DNA; 20 BP.
XX
AC ADD21589;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #152.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 TGAATTTTCCTTAGCTGACT 1215
Db |||||
20 TGAATTTTCCTTAGCTGACT 1

RESULT 1596
ADD21597/c
ID ADD21597 standard; DNA; 20 BP.
XX
AC ADD21597;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #160.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 GAATTCGCTTCCTGAAGATA 1311
Db |||||
20 GAATTCGCTTCCTGAAGATA 1

RESULT 1597
ADD21598/c
ID ADD21598 standard; DNA; 20 BP.
XX
AC ADD21598;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #161.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1301 TCCTGAAGATAAAGGGAAG 1320
Db |||||
20 TCCTGAAGATAAAGGGAAG 1

RESULT 1598
ADD21603/c
ID ADD21603 standard; DNA; 20 BP.
XX
AC ADD21603;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #166.

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XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1358 CTCACACAAGCTGAAGAGG 1377  
 Db 20 CTCACACAAGCTGAAGAGG 1

## RESULT 1599

ADD21611/c  
 ID ADD21611 standard; DNA; 20 BP.

XX  
 AC ADD21611;

XX  
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #174.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1456 TTACACAAGCTTCACAATCA 1475  
 Db 20 TTACACAAGCTTCACAATCA 1

## RESULT 1600

ADD21631/c  
 ID ADD21631 standard; DNA; 20 BP.

XX  
 AC ADD21631;

XX  
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #194.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1675 CAGGACATCTTATGCGCTGC 1694  
 Db 20 CAGGACATCTTATGCGCTGC 1

## RESULT 1601

ADD21655/c  
 ID ADD21655 standard; DNA; 20 BP.

XX  
 AC ADD21655;

XX  
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #218.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1898 AGATTTCTTCTTTAGTAT 1917  
 Db 20 AGATTTCTTCTTTAGTAT 1

## RESULT 1602

ADD21656/c  
 ID ADD21656 standard; DNA; 20 BP.

XX  
 AC ADD21656;

XX  
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #219.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1905 TTCTTTTACTATAATTGAC 1924  
 Db 20 TTCTTTTACTATAATTGAC 1

## RESULT 1603

ADD21660/c  
 ID ADD21660 standard; DNA; 20 BP.

XX  
 AC ADD21660;

XX  
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #223.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1933 GTAGTGAATAGTGAATACT 1952  
 Db 20 GTAGTGAATAGTGAATACT 1

## RESULT 1604

ADD21664/c  
 ID ADD21664 standard; DNA; 20 BP.

XX  
 AC ADD21664;

XX  
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #227.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1969 GAATATGATGATCATCCTTT 1988  
 Db 20 GAATATGATGATCATCCTTT 1

## RESULT 1605

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ADD21667/c
ID ADD21667 standard; DNA; 20 BP.
XX
AC ADD21667;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #230.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1990 CACCAACTCCTAATTTTAA 209
DB 20 CACCAACTCCTAATTTTAA 1
RESULT 1606
ADD21672/c
ID ADD21672 standard; DNA; 20 BP.
XX
AC ADD21672;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #235.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2051 TTTTCTTAATATGTATATG 2070
DB 20 TTTTCTTAATATGTATATG 1
RESULT 1607
ADD21674/c
ID ADD21674 standard; DNA; 20 BP.
XX
AC ADD21674;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #237.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2072 CATTAAATGTAACCTATTAT 2091
DB 20 CATTAAATGTAACCTATTAT 1
RESULT 1608
ADD21677/c
ID ADD21677 standard; DNA; 20 BP.
XX
AC ADD21677;
XX
DT 15-JAN-2004 (first entry)
XX
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DE Human mdm2 antisense oligonucleotide #240.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2116 CTGTTACCCAGGCTGGAGTG 2135
DB 20 CTGTTACCCAGGCTGGAGTG 1
RESULT 1609
ADD21684/c
ID ADD21684 standard; DNA; 20 BP.
XX
AC ADD21684;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #247.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2185 CCATTCTCTGCTCAGCCT 2204
DB 20 CCATTCTCTGCTCAGCCT 1
RESULT 1610
ADD21715/c
ID ADD21715 standard; DNA; 20 BP.
XX
AC ADD21715;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #271.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 359 CTCACAGATTCCAGCTTCGG 378
DB 20 CTCACAGATTCCAGCTTCGG 1
RESULT 1611
ADD21720/c
ID ADD21720 standard; DNA; 20 BP.
XX
AC ADD21720;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #276.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 365 GATTCAGCTTCGGAACAAG 384
Db 20 GATTCAGCTTCGGAACAAG 1

RESULT 1612
ADD21723/c
ID ADD21723 standard; DNA; 20 BP.
XX
AC ADD21723;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #279.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 TCCAGCTTCGGAACAAGAGA 387
Db 20 TCCAGCTTCGGAACAAGAGA 1

RESULT 1613
ADD21747/c
ID ADD21747 standard; DNA; 20 BP.
XX
AC ADD21747;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #303.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1732 CCTGCCAGTATGTAGACAA 1751
Db 20 CCTGCCAGTATGTAGACAA 1

RESULT 1614
ADD21447/c
ID ADD21447 standard; DNA; 20 BP.
XX
AC ADD21447;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #10.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 617 GATCTACAGGAACCTGGTAG 636
Db 20 GATCTACAGGAACCTGGTAG 1

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1615
ADD21453/c
ID ADD21453 standard; DNA; 20 BP.
XX
AC ADD21453;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #16.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1818 CTAACCTATATACCCCTAGGA 1837
Db 20 CTAACCTATATACCCCTAGGA 1

RESULT 1616
ADD21472/c
ID ADD21472 standard; DNA; 20 BP.
XX
AC ADD21472;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #35.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 TGTGGCCCTGTGTGCGAA 53
Db 20 TGTGGCCCTGTGTGCGAA 1

RESULT 1617
ADD21483/c
ID ADD21483 standard; DNA; 20 BP.
XX
AC ADD21483;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #46.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 CCAGTGCCTGCGCCGAGA 184
Db 20 CCAGTGCCTGCGCCGAGA 1

RESULT 1618
ADD21484/c
ID ADD21484 standard; DNA; 20 BP.
XX
AC ADD21484;
XX
DT 15-JAN-2004 (first entry)

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XX Human mdm2 antisense oligonucleotide #47.
DE
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 174 TGGCCCGGAGAGTGAATGA 193
Db 20 TGGCCCGGAGAGTGAATGA 1
RESULT 1619
ADD21490/c
ID ADD21490 standard; DNA; 20 BP.
XX
AC ADD21490;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #53.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 293 GATGGTGAGGAGCAGGCATA 312
Db 20 GATGGTGAGGAGCAGGCATA 1
RESULT 1620
ADD21492/c
ID ADD21492 standard; DNA; 20 BP.
XX
AC ADD21492;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #55.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 296 GGTGAGGAGCAGGCATAATGT 315
Db 20 GGTGAGGAGCAGGCATAATGT 1
RESULT 1621
ADD21496/c
ID ADD21496 standard; DNA; 20 BP.
XX
AC ADD21496;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #59.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 300 AGGAGCAGGCAAAATGTGCAA 319
Db 20 AGGAGCAGGCAAAATGTGCAA 1
RESULT 1622
ADD21510/c
ID ADD21510 standard; DNA; 20 BP.
XX
AC ADD21510;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #73.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 323 CAACATGCTGTACTACTG 342
Db 20 CAACATGCTGTACTACTG 1
RESULT 1623
ADD21518/c
ID ADD21518 standard; DNA; 20 BP.
XX
AC ADD21518;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #81.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 422 ATTAAGTCTGTGTGTGCAC 441
Db 20 ATTAAGTCTGTGTGTGCAC 1
RESULT 1624
ADD21542/c
ID ADD21542 standard; DNA; 20 BP.
XX
AC ADD21542;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #105.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 691 GTCACCTTGAAGGTGGAGT 710
Db 20 GTCACCTTGAAGGTGGAGT 1
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RESULT 1625
ADD21551/c
ID ADD21551 standard; DNA; 20 BP.
XX
AC ADD21551;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #114.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 798 AGAGCAATTAGTGACAGAGA 817
Db 20 AGAGCAATTAGTGACAGAGA 1

RESULT 1626
ADD21575/c
ID ADD21575 standard; DNA; 20 BP.
XX
AC ADD21575;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #138.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1059 GAAGTTGAATCTCTCGACTC 1078
Db 20 GAAGTTGAATCTCTCGACTC 1

RESULT 1627
ADD21586/c
ID ADD21586 standard; DNA; 20 BP.
XX
AC ADD21586;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #149.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1161 GGGGAGAGTGATACAGATTC 1180
Db 20 GGGGAGAGTGATACAGATTC 1

RESULT 1628
ADD21604/c
ID ADD21604 standard; DNA; 20 BP.
XX
AC ADD21604;
XX

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DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #167.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1368 GCTGAAGAGGGCTTTGATGT 1387
Db 20 GCTGAAGAGGGCTTTGATGT 1

RESULT 1629
ADD21605/c
ID ADD21605 standard; DNA; 20 BP.
XX
AC ADD21605;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #168.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1401 AAAACTATAGTGAATGATTC 1420
Db 20 AAAACTATAGTGAATGATTC 1

RESULT 1630
ADD21638/c
ID ADD21638 standard; DNA; 20 BP.
XX
AC ADD21638;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #201.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 CCCAGTATGTAGACAACCAA 1755
Db 20 CCCAGTATGTAGACAACCAA 1

RESULT 1631
ADD21642/c
ID ADD21642 standard; DNA; 20 BP.
XX
AC ADD21642;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #205.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 TATAAGAGAATTATATATTT 1817
DB 20 TATAAGAGAATTATATATTT 1

RESULT 1632
ADD21681/c
ID ADD21681 standard; DNA; 20 BP.
XX
AC ADD21681;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #244.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2146 TCTTGGCTCACTGCAAGCTC 2165
DB 20 TCTTGGCTCACTGCAAGCTC 1

RESULT 1633
ADD21696/c
ID ADD21696 standard; DNA; 20 BP.
XX
AC ADD21696;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #259.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGGTCTCGATCTC 2309
DB 20 GCCAGGATGGTCTCGATCTC 1

RESULT 1634
ADD21703/c
ID ADD21703 standard; DNA; 20 BP.
XX
AC ADD21703;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #266.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCAC 2370
DB 20 GGATTACAGGCATGAGCCAC 1
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RESULT 1635
ADD21732/c
ID ADD21732 standard; DNA; 20 BP.
XX
AC ADD21732;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #288.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 TTCCTTAGCTGACTATTGGA 1221
DB 20 TTCCTTAGCTGACTATTGGA 1

RESULT 1636
ADD21742/c
ID ADD21742 standard; DNA; 20 BP.
XX
AC ADD21742;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #298.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 AAACAGGACATCTTATGGCC 1691
DB 20 AAACAGGACATCTTATGGCC 1

RESULT 1637
ADD21753/c
ID ADD21753 standard; DNA; 20 BP.
XX
AC ADD21753;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #309.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 CCTGTCTATAGAGAAATTAT 1811
DB 20 CCTGTCTATAGAGAAATTAT 1

RESULT 1638
ADD21767/c
ID ADD21767 standard; DNA; 20 BP.
XX
AC ADD21767;
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XX 15-JAN-2004 (first entry)
XX Mouse mdm2 antisense oligonucleotide #8.
XX antisense oligonucleotide; mouse; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 GAAGAGAAACCTTCATCTTC 760
DB 20 GAAGAGAAACCTTCATCTTC 1

RESULT 1639
ADD21443/C
ID ADD21443 standard; DNA; 20 BP.
XX
XX AC ADD21443;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #6.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCCAAGCGCGAAACCCCG 292
DB 20 CTCCAAGCGCGAAACCCCG 1

RESULT 1640
ADD21531/C
ID ADD21531 standard; DNA; 20 BP.
XX
XX AC ADD21531;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #94.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 GCCAAGCTTCTCTGTGAAG 594
DB 20 GCCAAGCTTCTCTGTGAAG 1

RESULT 1641
ADD21532/C
ID ADD21532 standard; DNA; 20 BP.
XX
XX AC ADD21532;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #95.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;

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XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 587 TGTGAAAGAGACACAGGAAA 606
DB 20 TGTGAAAGAGACACAGGAAA 1

RESULT 1642
ADD21571/C
ID ADD21571 standard; DNA; 20 BP.
XX
XX AC ADD21571;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #134.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1023 CAGGATTCAGTTTCAGATCA 1042
DB 20 CAGGATTCAGTTTCAGATCA 1

RESULT 1643
ADD21582/C
ID ADD21582 standard; DNA; 20 BP.
XX
XX AC ADD21582;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #145.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 CTCAGATGAAGATGATGAGG 1134
DB 20 CTCAGATGAAGATGATGAGG 1

RESULT 1644
ADD21583/C
ID ADD21583 standard; DNA; 20 BP.
XX
XX AC ADD21583;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #146.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 AGATGATGAGGTATATCAAG 1143
DB 20 AGATGATGAGGTATATCAAG 1

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Db      20 AGATGATGAGGTATATCAAG 1

RESULT 1645
ADD21592/c
ID      ADD21592 standard; DNA; 20 BP.
XX
XX
AC      ADD21592;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #155.
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1226 CACTTCATGCAATGAATGA 1245
      |||||
Db      20 CACTTCATGCAATGAATGA 1

RESULT 1646
ADD21601/c
ID      ADD21601 standard; DNA; 20 BP.
XX
XX
AC      ADD21601;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #164.
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1333 TCTCTGAGAAAGCCAAACTG 1352
      |||||
Db      20 TCTCTGAGAAAGCCAAACTG 1

RESULT 1647
ADD21624/c
ID      ADD21624 standard; DNA; 20 BP.
XX
XX
AC      ADD21624;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #187.
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1580 AGAGAGTGTGGAATCTAGTT 1599
      |||||
Db      20 AGAGAGTGTGGAATCTAGTT 1

RESULT 1648
ADD21643/c
ID      ADD21643 standard; DNA; 20 BP.
XX
XX
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AC      ADD21643;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #206.
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1804 AGAATTATATATTTCTTAAC 1823
      |||||
Db      20 AGAATTATATATTTCTTAAC 1

RESULT 1649
ADD21654/c
ID      ADD21654 standard; DNA; 20 BP.
XX
XX
AC      ADD21654;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #217.
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1889 AATTCACATAGATTCTTCT 1908
      |||||
Db      20 AATTCACATAGATTCTTCT 1

RESULT 1650
ADD21690/c
ID      ADD21690 standard; DNA; 20 BP.
XX
XX
AC      ADD21690;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #253.
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2218 GCCTACAGTCATCTGCCACC 2237
      |||||
Db      20 GCCTACAGTCATCTGCCACC 1

RESULT 1651
ADD21469/c
ID      ADD21469 standard; DNA; 20 BP.
XX
XX
AC      ADD21469;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #32.
DE      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      antisense oligonucleotide; human; mdm2; hyperproliferation;
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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TTGGCTGCTTCTGGGGCTG 33
Db 20 TTGGCTGCTTCTGGGGCTG 1

RESULT 1652
ADD21475/c
ID ADD21475 standard; DNA; 20 BP.
XX
AC ADD21475;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #38.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CAAGAAGCCGAGCCGAGGG 81
Db 20 CAAGAAGCCGAGCCGAGGG 1

RESULT 1653
ADD21487/c
ID ADD21487 standard; DNA; 20 BP.
XX
AC ADD21487;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #50.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CTTCCGCAGTAGTCAGTCCC 236
Db 20 CTTCCGCAGTAGTCAGTCCC 1

RESULT 1654
ADD21499/c
ID ADD21499 standard; DNA; 20 BP.
XX
AC ADD21499;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #62.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAATGTGCAATACC 323
Db 20 GCAGGCAATGTGCAATACC 1

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAAATGTGCAATACCAACAT 328
Db 20 CAAATGTGCAATACCAACAT 1

RESULT 1655
ADD21515/c
ID ADD21515 standard; DNA; 20 BP.
XX
AC ADD21515;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #78.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 GACCCCTGGTTAGACCAAGC 405
Db 20 GACCCCTGGTTAGACCAAGC 1

RESULT 1657
ADD21535/c
ID ADD21535 standard; DNA; 20 BP.
XX
AC ADD21535;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #98.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 609 TATACCATGATCTACAGGAA 628
Db 20 TATACCATGATCTACAGGAA 1

RESULT 1658
ADD21544/c
ID ADD21544 standard; DNA; 20 BP.

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XX ADD21544;
AC
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #107.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 718 AGGACCTTGTAAGAGCTT 737
Db 20 AGGACCTTGTAAGAGCTT 1

RESULT 1659
ADD21587/c
ID ADD21587 standard; DNA; 20 BP.
XX
XX AC ADD21587;
XX AC
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #150.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1170 GATACAGATTTCATTGGAAGA 1189
Db 20 GATACAGATTTCATTGGAAGA 1

RESULT 1660
ADD21602/c
ID ADD21602 standard; DNA; 20 BP.
XX
XX AC ADD21602;
XX AC
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #165.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1346 CAAACTGGAAACTCAACAC 1365
Db 20 CAAACTGGAAACTCAACAC 1

RESULT 1661
ADD21623/c
ID ADD21623 standard; DNA; 20 BP.
XX
XX AC ADD21623;
XX AC
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #186.
XX

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KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAGACAAAGAAGAGAG 1585
Db 20 ACCCAGACAAAGAAGAGAG 1

RESULT 1662
ADD21666/c
ID ADD21666 standard; DNA; 20 BP.
XX
XX AC ADD21666;
XX AC
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #229.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1982 ATCCTTTACACCAACTCCTA 2001
Db 20 ATCCTTTACACCAACTCCTA 1

RESULT 1663
ADD21678/c
ID ADD21678 standard; DNA; 20 BP.
XX
XX AC ADD21678;
XX AC
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #241.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2123 CCAGGCTGGAGTGCAGTGGG 2142
Db 20 CCAGGCTGGAGTGCAGTGGG 1

RESULT 1664
ADD21682/c
ID ADD21682 standard; DNA; 20 BP.
XX
XX AC ADD21682;
XX AC
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #245.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2153 TCACTGCAAGCTCTGCCCTC 2172  
 Db 20 TCACTGCAAGCTCTGCCCTC 1

## RESULT 1665

ADD21700/c

ID ADD21700 standard; DNA; 20 BP.

XX

AC ADD21700;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #263.

XX

KW antisense oligonucleotide; human; mdm2; hyperproliferation;

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2325 GCCCACCCTCGCCTCCCAA 2344

Db 20 GCCCACCCTCGCCTCCCAA 1

## RESULT 1666

ADD21717/c

ID ADD21717 standard; DNA; 20 BP.

XX

AC ADD21717;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #273.

XX

KW antisense oligonucleotide; human; mdm2; hyperproliferation;

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 ACAGATCCAGCTTCGGAAC 381

Db 20 ACAGATCCAGCTTCGGAAC 1

## RESULT 1667

ADD21745/c

ID ADD21745 standard; DNA; 20 BP.

XX

AC ADD21745;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #301.

XX

KW antisense oligonucleotide; human; mdm2; hyperproliferation;

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1712 GCTAAAGAAAGGAATAGC 1731

Db 20 GCTAAAGAAAGGAATAGC 1

## RESULT 1668

ADD21746/c

ID ADD21746 standard; DNA; 20 BP.

XX

AC ADD21746;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #302.

XX

KW antisense oligonucleotide; human; mdm2; hyperproliferation;

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1722 AGGAATAAGCCCTGCCCAGT 1741

Db 20 AGGAATAAGCCCTGCCCAGT 1

## RESULT 1669

ADD21790/c

ID ADD21790 standard; DNA; 20 BP.

XX

AC ADD21790;

XX

DT 15-JAN-2004 (first entry)

XX

DE Mouse mdm2 antisense oligonucleotide #31.

XX

KW antisense oligonucleotide; mouse; mdm2; hyperproliferation;

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1758 CAAATGATTGTGCTAACTTA 1777

Db 20 CAAATGATTGTGCTAACTTA 1

## RESULT 1670

ADD21448/c

ID ADD21448 standard; DNA; 20 BP.

XX

AC ADD21448;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #11.

XX

KW antisense oligonucleotide; human; mdm2; hyperproliferation;

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1047 AGTGTAGAAATTTGAAGTTGA 1066

Db 20 AGTGTAGAAATTTGAAGTTGA 1

## RESULT 1671

ADD21501/c

ID ADD21501 standard; DNA; 20 BP.

XX

AC ADD21501;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #64.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 AGGCAATGTGCAATACCA 325  
DB 20 AGGCAATGTGCAATACCA 1

RESULT 1672

ADD21507/c  
ID ADD21507 standard; DNA; 20 BP.

XX  
AC ADD21507;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #70.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAATGTC 331  
DB 20 ATGTGCAATACCAATGTC 1

RESULT 1673

ADD21523/c  
ID ADD21523 standard; DNA; 20 BP.

XX  
AC ADD21523;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #86.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 503 ACGATTATATGATGAGAAGC 522  
DB 20 ACGATTATATGATGAGAAGC 1

RESULT 1674

ADD21548/c  
ID ADD21548 standard; DNA; 20 BP.

XX  
AC ADD21548;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #111.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 761 ACATTGGTTTCTAGACCAT 780  
DB 20 ACATTGGTTTCTAGACCAT 1

RESULT 1675

ADD21552/c  
ID ADD21552 standard; DNA; 20 BP.

XX  
AC ADD21552;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #115.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 GAGACAGAGAAAATTCAGA 829  
DB 20 GAGACAGAGAAAATTCAGA 1

RESULT 1676

ADD21608/c  
ID ADD21608 standard; DNA; 20 BP.

XX  
AC ADD21608;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #171.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1434 GTTGAGGAAAATGATGATAA 1453  
DB 20 GTTGAGGAAAATGATGATAA 1

RESULT 1677

ADD21662/c  
ID ADD21662 standard; DNA; 20 BP.

XX  
AC ADD21662;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #225.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1948 ATACTTACTATATTTGACT 1967  
DB 20 ATACTTACTATATTTGACT 1

RESULT 1678

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ADD21665/c
ID  ADD21665 standard; DNA; 20 BP.
XX
AC  ADD21665;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #228.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1773 ATGTAGCTCATCCTTTACAC 1992
Db  20 ATGTAGCTCATCCTTTACAC 1

RESULT 1679
ADD21671/c
ID  ADD21671 standard; DNA; 20 BP.
XX
AC  ADD21671;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #234.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2020 TCTGCTCTTAATGAGAGTA 2039
Db  20 TCTGCTCTTAATGAGAGTA 1

RESULT 1680
ADD21716/c
ID  ADD21716 standard; DNA; 20 BP.
XX
AC  ADD21716;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #272.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  360 TCACAGATTCACGCTTCGA 379
Db  20 TCACAGATTCACGCTTCGA 1

RESULT 1681
ADD21730/c
ID  ADD21730 standard; DNA; 20 BP.
XX
AC  ADD21730;
XX
DT  15-JAN-2004 (first entry)
XX
XX

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DE  Human mdm2 antisense oligonucleotide #286.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1200 ATTTCTTACGCTGACTATTG 1219
Db  20 ATTTCTTACGCTGACTATTG 1

RESULT 1682
ADD21749/c
ID  ADD21749 standard; DNA; 20 BP.
XX
AC  ADD21749;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #305.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1752 CCAATTCAATGATTGTGCT 1771
Db  20 CCAATTCAATGATTGTGCT 1

RESULT 1683
ADD21751/c
ID  ADD21751 standard; DNA; 20 BP.
XX
AC  ADD21751;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #307.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1772 AACCTATTTCCCTAGTTGA 1791
Db  20 AACCTATTTCCCTAGTTGA 1

RESULT 1684
ADD21482/c
ID  ADD21482 standard; DNA; 20 BP.
XX
AC  ADD21482;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #45.
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 CGAGCGCCAGTGCCTGGC 177
Db 20 CGAGCGCCAGTGCCTGGC 1

RESULT 1685
ADD21539/c
ID ADD21539 standard; DNA; 20 BP.
XX
AC ADD21539;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #102.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 ATCGGACTCAGGTACATCTG 675
Db 20 ATCGGACTCAGGTACATCTG 1

RESULT 1686
ADD21561/c
ID ADD21561 standard; DNA; 20 BP.
XX
AC ADD21561;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #124.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 ATAAGGAGATATGTTGTGA 934
Db 20 ATAAGGAGATATGTTGTGA 1

RESULT 1687
ADD21562/c
ID ADD21562 standard; DNA; 20 BP.
XX
AC ADD21562;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #125.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TGTGTGAAGACAGTAG 946
Db 20 TGTGTGAAGACAGTAG 1
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RESULT 1688
ADD21565/c
ID ADD21565 standard; DNA; 20 BP.
XX
AC ADD21565;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #128.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 964 CGCATCGAATCCGATCTT 983
Db 20 CGCATCGAATCCGATCTT 1

RESULT 1689
ADD21572/c
ID ADD21572 standard; DNA; 20 BP.
XX
AC ADD21572;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #135.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1034 TTCAGATCAGTTAGTGTAG 1053
Db 20 TTCAGATCAGTTAGTGTAG 1

RESULT 1690
ADD21580/c
ID ADD21580 standard; DNA; 20 BP.
XX
AC ADD21580;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #143.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 AGAAGGACAAAGACTCTCAG 1119
Db 20 AGAAGGACAAAGACTCTCAG 1

RESULT 1691
ADD21584/c
ID ADD21584 standard; DNA; 20 BP.
XX
AC ADD21584;
XX
DT 15-JAN-2004 (first entry)
```



XX Human mdm2 antisense oligonucleotide #147.  
 DE antisense oligonucleotide; human; mdm2; hyperproliferation;  
 XX hyperproliferative disorder; cancer; psoriasis; fibrosis;  
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1135 TATATCAAGTTACTGTGTAT 1154  
 Db 20 TATATCAAGTTACTGTGTAT 1

RESULT 1692  
 ADD21590/c  
 ID ADD21590 standard; DNA; 20 BP.

XX

AC ADD21590;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #153.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1207 TAGCTGACTATTGGAATGC 1226

Db 20 TAGCTGACTATTGGAATGC 1

RESULT 1693

ADD21591/c

ID ADD21591 standard; DNA; 20 BP.

XX

AC ADD21591;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #154.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1220 GAAATGCATTCATGCAATG 1239

Db 20 GAAATGCATTCATGCAATG 1

RESULT 1694

ADD21607/c

ID ADD21607 standard; DNA; 20 BP.

XX

AC ADD21607;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #170.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1421 CAGAGAGTCATGCTTTCAGG 1440

Db 20 CAGAGAGTCATGCTTTCAGG 1

RESULT 1695

ADD21621/c

ID ADD21621 standard; DNA; 20 BP.

XX

AC ADD21621;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #184.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1550 GTTTGAAAGGGAAGAAACCC 1569

Db 20 GTTTGAAAGGGAAGAAACCC 1

RESULT 1696

ADD21633/c

ID ADD21633 standard; DNA; 20 BP.

XX

AC ADD21633;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #196.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 CCTGCTTTACATGTGCAAG 1709

Db 20 CCTGCTTTACATGTGCAAG 1

RESULT 1697

ADD21645/c

ID ADD21645 standard; DNA; 20 BP.

XX

AC ADD21645;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human mdm2 antisense oligonucleotide #208.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1816 TTCTAACTATATACCCCTAG 1835

Db 20 TTCTAACTATATACCCCTAG 1

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RESULT 1698
ADD21658/c
ID ADD21658 standard; DNA; 20 BP.
XX
XX
AC ADD21658;
XX
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #221.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1913 AGTATAATTGACCTACTTTG 1932
DB 20 AGTATAATTGACCTACTTTG 1
XX
RESULT 1699
ADD21661/c
ID ADD21661 standard; DNA; 20 BP.
XX
XX
AC ADD21661;
XX
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #224.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1940 AATAGTGAATCTTACTATA 1959
DB 20 AATAGTGAATCTTACTATA 1
XX
RESULT 1700
ADD21670/c
ID ADD21670 standard; DNA; 20 BP.
XX
XX
AC ADD21670;
XX
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #233.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2015 TCTACTCTGCTTAATGAG 2034
DB 20 TCTACTCTGCTTAATGAG 1
XX
RESULT 1701
ADD21673/c
ID ADD21673 standard; DNA; 20 BP.
XX
XX
AC ADD21673;
XX

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DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #236.
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2059 AATATGTATATGACATTAA 2078
DB 20 AATATGTATATGACATTAA 1
XX
RESULT 1702
ADD21675/c
ID ADD21675 standard; DNA; 20 BP.
XX
XX
AC ADD21675;
XX
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #238.
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2103 ACCGAGTCTTGCTCTGTAC 2122
DB 20 ACCGAGTCTTGCTCTGTAC 1
XX
RESULT 1703
ADD21683/c
ID ADD21683 standard; DNA; 20 BP.
XX
XX
AC ADD21683;
XX
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #246.
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2176 GGGTTGCGACCATTCCTG 2195
DB 20 GGGTTGCGACCATTCCTG 1
XX
RESULT 1704
ADD21687/c
ID ADD21687 standard; DNA; 20 BP.
XX
XX
AC ADD21687;
XX
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #250.
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

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Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2202 CCTCCCAATTAGCTTGGCCT 2221
Db 20 CCTCCCAATTAGCTTGGCCT 1

RESULT 1705:
ADD21693/c
ID ADD21693 standard; DNA; 20 BP.
XX
AC ADD21693;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #256.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2265 GTAGAGACAGGGTTTCACCG 2284
Db 20 GTAGAGACAGGGTTTCACCG 1

RESULT 1706
ADD21698/c
ID ADD21698 standard; DNA; 20 BP.
XX
AC ADD21698;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #261.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2307 CTCCTGACCTCGTGATCCGC 2326
Db 20 CTCCTGACCTCGTGATCCGC 1

RESULT 1707
ADD21713/c
ID ADD21713 standard; DNA; 20 BP.
XX
AC ADD21713;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #269.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 ACCTCAGATTCAGCTTC 376
Db 20 ACCTCAGATTCAGCTTC 1

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 367 TTCAGCTTCGGAACAAGAG 386
Db 20 TTCAGCTTCGGAACAAGAG 1

RESULT 1708
ADD21722/c
ID ADD21722 standard; DNA; 20 BP.
XX
AC ADD21722;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #278.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1381 TTCATGTTCTGATTGTAA 1400
Db 20 TTCATGTTCTGATTGTAA 1

RESULT 1710
ADD21470/c
ID ADD21470 standard; DNA; 20 BP.
XX
AC ADD21470;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #33.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1381 TTCATGTTCTGATTGTAA 1400
Db 20 TTCATGTTCTGATTGTAA 1

RESULT 1711
ADD21489/c
ID ADD21489 standard; DNA; 20 BP.
XX
AC ADD21489;

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XX 15-JAN-2004 (first entry)  
DT Human mdm2 antisense oligonucleotide #52.  
XX  
DE  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 CCCGATGCTGAGGACGAG 308  
DB 20 CCCGATGCTGAGGACGAG 1

RESULT 1712  
ADD21494/c  
ID ADD21494 standard; DNA; 20 BP.

XX  
AC ADD21494;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #57.

DE  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TGAGGAGCAGGCAATGTGC 317  
DB 20 TGAGGAGCAGGCAATGTGC 1

RESULT 1713  
ADD21517/c  
ID ADD21517 standard; DNA; 20 BP.

XX  
AC ADD21517;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #80.

DE  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGCCATTGCTTTGAAGTTA 422  
DB 20 AGCCATTGCTTTGAAGTTA 1

RESULT 1714  
ADD21530/c  
ID ADD21530 standard; DNA; 20 BP.

XX  
AC ADD21530;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #93.

DE  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 GTTTGGCGTGCCCAAGCTTCT 585  
DB 20 GTTTGGCGTGCCCAAGCTTCT 1

RESULT 1715

ADD21545/c

ID ADD21545 standard; DNA; 20 BP.

XX  
AC ADD21545;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #108.

DE  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 TACAAGAGCTTCAGGAAGAG 746  
DB 20 TACAAGAGCTTCAGGAAGAG 1

RESULT 1716

ADD21559/c

ID ADD21559 standard; DNA; 20 BP.

XX  
AC ADD21559;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #122.

DE  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 AAAGCCTGGCTCTGTGTGTA 914  
DB 20 AAAGCCTGGCTCTGTGTGTA 1

RESULT 1717

ADD21564/c

ID ADD21564 standard; DNA; 20 BP.

XX  
AC ADD21564;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #127.

DE  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 949 GTGAATCTACAGGACGCCCA 968

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Db      20 GTGAATCTACAGGAGCGCCA 1

RESULT 1718
ADD21609/c
XX ADD21609 standard; DNA; 20 BP.
XX AC ADD21609;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #172.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1439 GGAATAATGATGATAAATTA 1458
Db      20 GGAATAATGATGATAAATTA 1

RESULT 1719
ADD21619/c
XX ADD21619 standard; DNA; 20 BP.
XX AC ADD21619;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #182.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1533 CAAGAAGATGTGAAGAGTT 1552
Db      20 CAAGAAGATGTGAAGAGTT 1

RESULT 1720
ADD21622/c
XX ADD21622 standard; DNA; 20 BP.
XX AC ADD21622;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #185.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1560 GAAGAAACCCAGCAAGA 1579
Db      20 GAAGAAACCCAGCAAGA 1

RESULT 1721
ADD21626/c
XX ADD21626 standard; DNA; 20 BP.
XX

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AC ADD21626;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #189.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1617 GAACCTTGTGTGATTGTCA 1636
Db      20 GAACCTTGTGTGATTGTCA 1

RESULT 1722
ADD21629/c
XX ADD21629 standard; DNA; 20 BP.
XX AC ADD21629;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #192.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1657 GCATTGTCCATGCCAAACA 1676
Db      20 GCATTGTCCATGCCAAACA 1

RESULT 1723
ADD21636/c
XX ADD21636 standard; DNA; 20 BP.
XX AC ADD21636;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #199.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1720 AAAGGAATAAGCCCTGCCCA 1739
Db      20 AAAGGAATAAGCCCTGCCCA 1

RESULT 1724
ADD21640/c
XX ADD21640 standard; DNA; 20 BP.
XX AC ADD21640;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #203.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;

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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1757 TCAATGATTGGCTAACTT 1776
DB 20 TCAATGATTGGCTAACTT 1
  RESULT 1725
  ADD21649/c
  ID ADD21649 standard; DNA; 20 BP.
  XX AC ADD21649;
  XX DT 15-JAN-2004 (first entry)
  XX DE Human mdm2 antisense oligonucleotide #212.
  XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
  KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1850 TGAATTTTATTCACATATAT 1869
DB 20 TGAATTTTATTCACATATAT 1
  RESULT 1726
  ADD21688/c
  ID ADD21688 standard; DNA; 20 BP.
  XX AC ADD21688;
  XX DT 15-JAN-2004 (first entry)
  XX DE Human mdm2 antisense oligonucleotide #251.
  XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
  KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2210 TTAGCTTGGCTACAGTCAT 2229
DB 20 TTAGCTTGGCTACAGTCAT 1
  RESULT 1727
  ADD21740/c
  ID ADD21740 standard; DNA; 20 BP.
  XX AC ADD21740;
  XX DT 15-JAN-2004 (first entry)
  XX DE Human mdm2 antisense oligonucleotide #296.
  XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
  KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1652 TGGTTGCATTGTCCATGCA 1671
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DB 20 TGGTTGCATTGTCCATGCA 1
  RESULT 1728
  ADD21439/c
  ID ADD21439 standard; DNA; 20 BP.
  XX AC ADD21439;
  XX DT 15-JAN-2004 (first entry)
  XX DE Human mdm2 antisense oligonucleotide #2.
  XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
  KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 GGCCTGTGTGTCGGAAGA 56
DB 20 GGCCTGTGTGTCGGAAGA 1
  RESULT 1729
  ADD21440/c
  ID ADD21440 standard; DNA; 20 BP.
  XX AC ADD21440;
  XX DT 15-JAN-2004 (first entry)
  XX DE Human mdm2 antisense oligonucleotide #3.
  XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
  KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 95 CTCTGACCGAGATCCTGCTG 114
DB 20 CTCTGACCGAGATCCTGCTG 1
  RESULT 1730
  ADD21454/c
  ID ADD21454 standard; DNA; 20 BP.
  XX AC ADD21454;
  XX DT 15-JAN-2004 (first entry)
  XX DE Human mdm2 antisense oligonucleotide #17.
  XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
  KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1934 TAGTGAATAGTGAATACCTT 1953
DB 20 TAGTGAATAGTGAATACCTT 1
  RESULT 1731
  ADD21457/c
  ID ADD21457 standard; DNA; 20 BP.
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XX AC ADD21457;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #20.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2256 GTACTTTTAGTAGACAGG 2275
Db 20 GTACTTTTAGTAGACAGG 1

RESULT 1732
ADD21497/c
ID ADD21497 standard; DNA; 20 BP.
XX AC ADD21497;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #60.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 301 GGAGCAGGCAATGTGCAAT 320
Db 20 GGAGCAGGCAATGTGCAAT 1

RESULT 1733
ADD21511/c
ID ADD21511 standard; DNA; 20 BP.
XX AC ADD21511;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #74.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 TACCTACTGATGGTGCTGTA 353
Db 20 TACCTACTGATGGTGCTGTA 1

RESULT 1734
ADD21549/c
ID ADD21549 standard; DNA; 20 BP.
XX AC ADD21549;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #112.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 774 AGACCATCTACCTCATCTAG 793
Db 20 AGACCATCTACCTCATCTAG 1

RESULT 1735
ADD21557/c
ID ADD21557 standard; DNA; 20 BP.
XX AC ADD21557;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #120.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 867 TCTGATAGTATTTCCTTTC 886
Db 20 TCTGATAGTATTTCCTTTC 1

RESULT 1736
ADD21576/c
ID ADD21576 standard; DNA; 20 BP.
XX AC ADD21576;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #139.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1068 TCTCTCGACTCAGAGATTA 1087
Db 20 TCTCTCGACTCAGAGATTA 1

RESULT 1737
ADD21577/c
ID ADD21577 standard; DNA; 20 BP.
XX AC ADD21577;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #140.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1077 TCAGAAGATTATAGCCTTAG 1096
DB 20 TCAGAAGATTATAGCCTTAG 1

RESULT 1738
ADD21613/c
ID ADD21613 standard; DNA; 20 BP.
XX
AC ADD21613;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #176.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAGTGAAGACTATTCTCAGC 1500
DB 20 AAGTGAAGACTATTCTCAGC 1

RESULT 1739
ADD21632/c
ID ADD21632 standard; DNA; 20 BP.
XX
AC ADD21632;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #195.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1684 TTATGGCTGCTTTACATGT 1703
DB 20 TTATGGCTGCTTTACATGT 1

RESULT 1740
ADD21639/c
ID ADD21639 standard; DNA; 20 BP.
XX
AC ADD21639;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #202.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1745 TAGACAACCAATTCAAATGA 1764
DB 20 TAGACAACCAATTCAAATGA 1

RESULT 1741
ADD21648/c
ID ADD21648 standard; DNA; 20 BP.
XX
AC ADD21648;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #211.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1840 TTAGACAACCTGAAATTTAT 1859
DB 20 TTAGACAACCTGAAATTTAT 1

RESULT 1742
ADD21663/c
ID ADD21663 standard; DNA; 20 BP.
XX
AC ADD21663;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #226.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1956 TATAATTTGACTTGAATATG 1975
DB 20 TATAATTTGACTTGAATATG 1

RESULT 1743
ADD21680/c
ID ADD21680 standard; DNA; 20 BP.
XX
AC ADD21680;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #243.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2140 GGGTGATCTTGGCTCACTGC 2159
DB 20 GGGTGATCTTGGCTCACTGC 1

RESULT 1744
ADD21691/c
ID ADD21691 standard; DNA; 20 BP.
XX
AC ADD21691;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #254.

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XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2232 GCCACCAACCTGGCTAATT 2251
Db 20 GCCACCAACCTGGCTAATT 1

RESULT 1745
ADD21694/c
ID ADD21694 standard; DNA; 20 BP.
XX
AC ADD21694;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #257.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTTCCCGTGTAGCCA 2293
Db 20 GGGTTTCCCGTGTAGCCA 1

RESULT 1746
ADD21695/c
ID ADD21695 standard; DNA; 20 BP.
XX
AC ADD21695;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #258.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2283 CGTGTAGCCAGGATGGTCT 2302
Db 20 CGTGTAGCCAGGATGGTCT 1

RESULT 1747
ADD21711/c
ID ADD21711 standard; DNA; 20 BP.
XX
AC ADD21711;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #267.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 315 TGCAATACCAACATGCTGT 334
Db 20 TGCAATACCAACATGCTGT 1

RESULT 1748
ADD21724/c
ID ADD21724 standard; DNA; 20 BP.
XX
AC ADD21724;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #280.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 369 CCAGCTTCGGAACAAGAGAC 388
Db 20 CCAGCTTCGGAACAAGAGAC 1

RESULT 1749
ADD21731/c
ID ADD21731 standard; DNA; 20 BP.
XX
AC ADD21731;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #287.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1201 TTTCTTAGCTGACTATTGG 1220
Db 20 TTTCTTAGCTGACTATTGG 1

RESULT 1750
ADD21736/c
ID ADD21736 standard; DNA; 20 BP.
XX
AC ADD21736;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #292.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1342 AAGCCAACTGGAAACTCA 1361
Db 20 AAGCCAACTGGAAACTCA 1

RESULT 1751

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ADD21737/c
ID ADD21737 standard; DNA; 20 BP.
XX
AC ADD21737;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #293.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1622 TTGTGTGATTGTTCAGGTC 1641
DB 20 TTGTGTGATTGTTCAGGTC 1

RESULT 1752
ADD21444/c
ID ADD21444 standard; DNA; 20 BP.
XX
XX AC ADD21444;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #7.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 TGGTGAGGAGCAGGCAATG 314
DB 20 TGGTGAGGAGCAGGCAATG 1

RESULT 1753
ADD21455/c
ID ADD21455 standard; DNA; 20 BP.
XX
XX AC ADD21455;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #18.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2132 AGTGCAGTGGGTGATCTTGG 2151
DB 20 AGTGCAGTGGGTGATCTTGG 1

RESULT 1754
ADD21468/c
ID ADD21468 standard; DNA; 20 BP.
XX
XX AC ADD21468;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #77.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Human mdm2 antisense oligonucleotide #31.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCGAGCTTGCTGCTT 23
DB 20 CCGCGCGAGCTTGCTGCTT 1

RESULT 1755
ADD21503/c
ID ADD21503 standard; DNA; 20 BP.
XX
XX AC ADD21503;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #66.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 GCAAAATGTGCAATACCAACA 327
DB 20 GCAAAATGTGCAATACCAACA 1

RESULT 1756
ADD21506/c
ID ADD21506 standard; DNA; 20 BP.
XX
XX AC ADD21506;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #69.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 AATGTGCAATACCAACATGT 330
DB 20 AATGTGCAATACCAACATGT 1

RESULT 1757
ADD21514/c
ID ADD21514 standard; DNA; 20 BP.
XX
XX AC ADD21514;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #77.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 372 GCTTCGGAACAAGAGACCTT 391
| | | | | | | | | | | | | | | | | |
Db 20 GCTTCGGAACAAGAGACCTT 1

RESULT 1758
ADD21520/c
ID ADD21520 standard; DNA; 20 BP.
XX
AC ADD21520;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #83.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 477 TATCTTGGCCAGTATATAT 496
| | | | | | | | | | | | | | | | | |
Db 20 TATCTTGGCCAGTATATAT 1

RESULT 1759
ADD21526/c
ID ADD21526 standard; DNA; 20 BP.
XX
AC ADD21526;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #89.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 531 ATTGTATATTGTTCAATGA 550
| | | | | | | | | | | | | | | | | |
Db 20 ATTGTATATTGTTCAATGA 1

RESULT 1760
ADD21588/c
ID ADD21588 standard; DNA; 20 BP.
XX
AC ADD21588;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #151.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1184 TGAAGAAGATCCTGAAATTT 1203
| | | | | | | | | | | | | | | | | |
Db 20 TGAAGAAGATCCTGAAATTT 1
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RESULT 1761
ADD21610/c
ID ADD21610 standard; DNA; 20 BP.
XX
AC ADD21610;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #173.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1449 GATAAAATTTACACAGCTTC 1468
| | | | | | | | | | | | | | | | | |
Db 20 GATAAAATTTACACAGCTTC 1

RESULT 1762
ADD21659/c
ID ADD21659 standard; DNA; 20 BP.
XX
AC ADD21659;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #222.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1920 TTGACCTACTTTGGTAGTGG 1939
| | | | | | | | | | | | | | | | | |
Db 20 TTGACCTACTTTGGTAGTGG 1

RESULT 1763
ADD21679/c
ID ADD21679 standard; DNA; 20 BP.
XX
AC ADD21679;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #242.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2133 GTGCAGTGGGTGATCTTGGC 2152
| | | | | | | | | | | | | | | | | |
Db 20 GTGCAGTGGGTGATCTTGGC 1

RESULT 1764
ADD21452/c
ID ADD21452 standard; DNA; 20 BP.
XX
AC ADD21452;
XX
DT 15-JAN-2004 (first entry)
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XX Human mdm2 antisense oligonucleotide #15.
DE
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1785 TAGTTGACCTGTCTATAGA 1804
Db 20 TAGTTGACCTGTCTATAGA 1
RESULT 1765
ADD21471/c
ID ADD21471 standard; DNA; 20 BP.
XX
AC ADD21471;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #34.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 GCCTGTGTGGCCCTGTGTGT 48
Db 20 GCCTGTGTGGCCCTGTGTGT 1
RESULT 1766
ADD21480/c
ID ADD21480 standard; DNA; 20 BP.
XX
AC ADD21480;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #43.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 GCAGCCAGGACCGTCCC 139
Db 20 GCAGCCAGGACCGTCCC 1
RESULT 1767
ADD21488/c
ID ADD21488 standard; DNA; 20 BP.
XX
AC ADD21488;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #51.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 242 AGGAAACTGGGAGTCTTGA 261
Db 20 AGGAAACTGGGAGTCTTGA 1
RESULT 1768
ADD21509/c
ID ADD21509 standard; DNA; 20 BP.
XX
AC ADD21509;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #72.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 314 GTGCAATACCAACATGTCTG 333
Db 20 GTGCAATACCAACATGTCTG 1
RESULT 1769
ADD21538/c
ID ADD21538 standard; DNA; 20 BP.
XX
AC ADD21538;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #101.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 646 AGCAGGAATCATCGGACTCA 665
Db 20 AGCAGGAATCATCGGACTCA 1
RESULT 1770
ADD21578/c
ID ADD21578 standard; DNA; 20 BP.
XX
AC ADD21578;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #141.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 ATTATAGCCTTAGTGAAGAA 1103
Db 20 ATTATAGCCTTAGTGAAGAA 1
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RESULT 1771
ADD21600/c
ID ADD21600 standard; DNA; 20 BP.
XX
AC ADD21600;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #163.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1325 AGGGGAATCTCTGAGAAAG 1344
Db 20 AGGGGAATCTCTGAGAAAG 1

RESULT 1772
ADD21644/c
ID ADD21644 standard; DNA; 20 BP.
XX
AC ADD21644;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #207.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1808 TTATATATTTCTAACTATAT 1827
Db 20 TTATATATTTCTAACTATAT 1

RESULT 1773
ADD21657/c
ID ADD21657 standard; DNA; 20 BP.
XX
AC ADD21657;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #220.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1908 TCCTTAGTATAATTGACCTA 1927
Db 20 TCCTTAGTATAATTGACCTA 1

RESULT 1774
ADD21689/c
ID ADD21689 standard; DNA; 20 BP.
XX
AC ADD21689;
XX

RESULT 1775
ADD21692/c
ID ADD21692 standard; DNA; 20 BP.
XX
AC ADD21692;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #255.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2213 GCTTGGCCTACATCATCTG 2232
Db 20 GCTTGGCCTACATCATCTG 1

RESULT 1776
ADD21718/c
ID ADD21718 standard; DNA; 20 BP.
XX
AC ADD21718;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #274.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2253 TTTGTACTTTTACTAGAGAC 2272
Db 20 TTTGTACTTTTACTAGAGAC 1

RESULT 1777
ADD21725/c
ID ADD21725 standard; DNA; 20 BP.
XX
AC ADD21725;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #281.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 363 CAGATTCCAGCTTCGGAACA 382
Db 20 CAGATTCCAGCTTCGGAACA 1

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TTGCCAGTATATTATGACT 500
DB 20 TTGCCAGTATATTATGACT 1

RESULT 1778
ADD21738/c
ID ADD21738 standard; DNA; 20 BP.
XX
AC ADD21738;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #294.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1632 TGTCAAGTCGACCTAATAAA 1651
DB 20 TGTCAAGTCGACCTAATAAA 1

RESULT 1779
ADD21744/c
ID ADD21744 standard; DNA; 20 BP.
XX
AC ADD21744;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #300.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 TGTCTTACATGTGCAAGAA 1711
DB 20 TGTCTTACATGTGCAAGAA 1

RESULT 1780
ADD21456/c
ID ADD21456 standard; DNA; 20 BP.
XX
AC ADD21456;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #19.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2224 AGTCATCTGCCACACACCT 2243
DB 20 AGTCATCTGCCACACACCT 1
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RESULT 1781
ADD21479/c
ID ADD21479 standard; DNA; 20 BP.
XX
AC ADD21479;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #42.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TGCTTTCCGAGCCGAGGACA 132
DB 20 TGCTTTCCGAGCCGAGGACA 1

RESULT 1782
ADD21498/c
ID ADD21498 standard; DNA; 20 BP.
XX
AC ADD21498;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #61.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GAGCAGGCAAAATGTGCAATA 321
DB 20 GAGCAGGCAAAATGTGCAATA 1

RESULT 1783
ADD21502/c
ID ADD21502 standard; DNA; 20 BP.
XX
AC ADD21502;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #65.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAAAATGTGCAATACCAAC 326
DB 20 GGCAAAATGTGCAATACCAAC 1

RESULT 1784
ADD21508/c
ID ADD21508 standard; DNA; 20 BP.
XX
AC ADD21508;
```

```
XX 15-JAN-2004 (first entry)
DT Human mdm2 antisense oligonucleotide #71.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 313 TGTGCAATACCAATGTCT 332
DB 20 TGTGCAATACCAATGTCT 1
RESULT 1785
ADD21525/c
ID ADD21525 standard; DNA; 20 BP.
XX
AC ADD21525;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #88.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 525 CAACATATTGTATTTGTC 544
DB 20 CAACATATTGTATTTGTC 1
RESULT 1786
ADD21537/c
ID ADD21537 standard; DNA; 20 BP.
XX
AC ADD21537;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #106.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 634 TAGTAGTCAATCAGCAGAA 653
DB 20 TAGTAGTCAATCAGCAGAA 1
RESULT 1787
ADD21543/c
ID ADD21543 standard; DNA; 20 BP.
XX
AC ADD21543;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #106.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 704 TGGGAGTGATCAAAAGGACC 723
DB 20 TGGGAGTGATCAAAAGGACC 1
RESULT 1788
ADD21560/c
ID ADD21560 standard; DNA; 20 BP.
XX
AC ADD21560;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #123.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 904 CTCTGTGTGTATAAGGGAG 923
DB 20 CTCTGTGTGTATAAGGGAG 1
RESULT 1789
ADD21599/c
ID ADD21599 standard; DNA; 20 BP.
XX
AC ADD21599;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #162.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1311 AAAGGGAAGATAAAGGGGA 1330
DB 20 AAAGGGAAGATAAAGGGGA 1
RESULT 1790
ADD21612/c
ID ADD21612 standard; DNA; 20 BP.
XX
AC ADD21612;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #175.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1466 TTCAATCAATCAAGAAAGTG 1485
DB 20 TTCAATCAATCAAGAAAGTG 1
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Db      20 TTCAATCAACAGAAAGTG 1

RESULT 1791
ADD21686/c
ID      ADD21686 standard; DNA; 20 BP.
XX
XX
AC      ADD21686;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Human mdm2 antisense oligonucleotide #249.
XX
KW      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2198 TCAGCTCCCAATTAGCTTG 2217
      |||||
Db      20 TCAGCTCCCAATTAGCTTG 1

RESULT 1792
ADD21714/c
ID      ADD21714 standard; DNA; 20 BP.
XX
XX
AC      ADD21714;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Human mdm2 antisense oligonucleotide #270.
XX
KW      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      358 CCTCACAGATCCAGCTTCG 377
      |||||
Db      20 CCTCACAGATCCAGCTTCG 1

RESULT 1793
ADD21727/c
ID      ADD21727 standard; DNA; 20 BP.
XX
XX
AC      ADD21727;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Human mdm2 antisense oligonucleotide #283.
XX
KW      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      483 GGCCAGTATATTACTAA 502
      |||||
Db      20 GGCCAGTATATTACTAA 1

RESULT 1794
ADD21729/c
ID      ADD21729 standard; DNA; 20 BP.
XX
XX
AC      ADD21729;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Human mdm2 antisense oligonucleotide #285.
XX
KW      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      781 CTACCTCATCTAGAGGAGA 800
      |||||
Db      20 CTACCTCATCTAGAGGAGA 1

RESULT 1795
ADE86781/c
ID      ADE86781 standard; DNA; 20 BP.
XX
XX
AC      ADE86781;
XX
DT      29-JAN-2004 (first entry)
XX
DE      GATA primer #1.
XX
KW      ss; primer; molecular phenotyping; brain; lung; CD31+ cell;
KW      lineage committed cell; survival; proliferation; differentiation;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2344 AGTGCTGGGATTACAGGCAT 2363
      |||||
Db      20 AGTGCTGGGATTACAGGCAT 1

RESULT 1796
AAD64979
ID      AAD64979 standard; DNA; 20 BP.
XX
XX
AC      AAD64979;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Human mouse double minute (MDM2) sense oligonucleotide S7.
XX
KW      MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW      therapeutic; antisense therapy; human; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1018 TGGATCAGGATTCAGTTTCA 1037
      |||||
Db      1 TGGATCAGGATTCAGTTTCA 20

RESULT 1797
AAD65012/c
ID      AAD65012 standard; DNA; 20 BP.
XX
XX
AC      AAD65012;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Human mouse double minute (MDM2) antisense oligonucleotide ASS-4.
XX
KW      MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;

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KW therapeutic; antisense therapy; human; antisense; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 685 ACAGGTGTCACCTTGAGGT 704  
 DB 20 ACAGGTGTCACCTTGAGGT 1  
 RESULT 1798  
 AAD64999  
 ID AAD64999 standard; DNA; 20 BP.  
 XX  
 AC  
 AAD64999;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX Human mouse double minute (MDM2) sense oligonucleotide S7-5.  
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;  
 KW therapeutic; antisense therapy; human; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1038 GATCAGTTTGTAGTGAATT 1057  
 DB 1 GATCAGTTTGTAGTGAATT 20  
 RESULT 1799  
 AAD65006/C  
 ID AAD65006 standard; DNA; 20 BP.  
 XX  
 AC  
 AAD65006;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX Human mouse double minute (MDM2) antisense oligonucleotide AS3.  
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;  
 KW therapeutic; antisense therapy; human; antisense; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 780 TCTACCTCATCTAGAGGAG 799  
 DB 20 TCTACCTCATCTAGAGGAG 1  
 RESULT 1800  
 AAD64978  
 ID AAD64978 standard; DNA; 20 BP.  
 XX  
 AC  
 AAD64978;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX Human mouse double minute (MDM2) sense oligonucleotide S5.  
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;  
 KW therapeutic; antisense therapy; human; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 695 CCTTGAAGGTGGGAGTGATC 714

DB 1 CCTTGAAGGTGGGAGTGATC 20  
 RESULT 1801  
 AAD64996  
 ID AAD64996 standard; DNA; 20 BP.  
 XX  
 AC  
 AAD64996;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX Human mouse double minute (MDM2) sense oligonucleotide S7-2.  
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;  
 KW therapeutic; antisense therapy; human; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1003 ATTACAGTGTGTTGGAT 1022  
 DB 1 ATTACAGTGTGTTGGAT 20  
 RESULT 1802  
 AAD65005/C  
 ID AAD65005 standard; DNA; 20 BP.  
 XX  
 AC  
 AAD65005;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX Human mouse double minute (MDM2) antisense oligonucleotide AS1.  
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;  
 KW therapeutic; antisense therapy; human; antisense; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 ACCTACAGATTCAGCTTC 376  
 DB 20 ACCTACAGATTCAGCTTC 1  
 RESULT 1803  
 AAD65009/C  
 ID AAD65009 standard; DNA; 20 BP.  
 XX  
 AC  
 AAD65009;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX Human mouse double minute (MDM2) antisense oligonucleotide AS5-1.  
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;  
 KW therapeutic; antisense therapy; human; antisense; ss.  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 669 ACATCTGTGAGTGAGAACAG 688  
 DB 20 ACATCTGTGAGTGAGAACAG 1  
 RESULT 1804  
 AAD64984  
 ID AAD64984 standard; DNA; 20 BP.

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XX AAD64984;
XX AC
XX DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) sense oligonucleotide S3.
XX DM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
XX KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 TCTACCTCATCTAGAGGAG 799
Db 1 TCTACCTCATCTAGAGGAG 20

RESULT 1805
AAD64988
ID AAD64988 standard; DNA; 20 BP.
XX AC
XX AAD64988;
XX DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) sense oligonucleotide S5-1.
XX DM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
XX KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGACAG 688
Db 1 ACATCTGTGAGTGAGACAG 20

RESULT 1806
AAD65007/c
ID AAD65007 standard; DNA; 20 BP.
XX AC
XX AAD65007;
XX DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) antisense oligonucleotide AS6.
XX DM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
XX KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 TCCTTAGCTGACTATTGGAA 1222
Db 20 TCCTTAGCTGACTATTGGAA 1

RESULT 1807
AAD65008/c
ID AAD65008 standard; DNA; 20 BP.
XX AC
XX AAD65008;
XX DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) antisense oligonucleotide AS8.
XX
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KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249
Db 20 TCATGCAATGAATGAATCC 1

RESULT 1808
AAD65015/c
ID AAD65015 standard; DNA; 20 BP.
XX AC
XX AAD65015;
XX DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) antisense oligonucleotide AS5-7.
XX DM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
XX KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 AAGGACCTTGTACAAGAGCT 736
Db 20 AAGGACCTTGTACAAGAGCT 1

RESULT 1809
AAD65013/c
ID AAD65013 standard; DNA; 20 BP.
XX AC
XX AAD65013;
XX DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) antisense oligonucleotide AS5-5.
XX DM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
XX KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723
Db 20 TGGGAGTGATCAAAAGGACC 1

RESULT 1810
AAD65014/c
ID AAD65014 standard; DNA; 20 BP.
XX AC
XX AAD65014;
XX DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) antisense oligonucleotide AS5-6.
XX DM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
XX KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 709 GTGATCAAAAGGACCTTGTA 728
Db 20 GTGATCAAAAGGACCTTGTA 1

RESULT 1811
AAD65020/c
ID AAD65020 standard; DNA; 20 BP.
XX
AC
XX AAD65020;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7-5.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 GATCAGTTTACTGTGAGATT 1057
Db 20 GATCAGTTTACTGTGAGATT 1

RESULT 1812
AAD64990
ID AAD64990 standard; DNA; 20 BP.
XX
AC
XX AAD64990;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-3.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 680 TGAGAACAGGTGTCACTTG 699
Db 1 TGAGAACAGGTGTCACTTG 20

RESULT 1813
AAD64977
ID AAD64977 standard; DNA; 20 BP.
XX
AC
XX AAD64977;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S4.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 481 TTGCCAGTATATTATGACT 500
Db 1 TTGCCAGTATATTATGACT 20

RESULT 1814
AAD65021/c

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ID AAD65021 standard; RNA; 20 BP.
XX
AC
XX AAD65021;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense RNA oligonucleotide AS2-2H.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 675 GTGAGTGAGAACAGGTGTCA 694
Db 20 GTGAGTGAGAACAGGTGTCA 1

RESULT 1815
AAD64983
ID AAD64983 standard; DNA; 20 BP.
XX
AC
XX AAD64983;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S2.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 369 CCAGCTTCGGAAACAAGAGAC 388
Db 1 CCAGCTTCGGAAACAAGAGAC 20

RESULT 1816
AAD64986
ID AAD64986 standard; DNA; 20 BP.
XX
AC
XX AAD64986;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S8.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1230 TCATGCAATGAATGAATCC 1249
Db 1 TCATGCAATGAATGAATCC 20

RESULT 1817
AAD64992
ID AAD64992 standard; DNA; 20 BP.
XX
AC
XX AAD64992;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-5.

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XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGATGATCAAAAGGACC 723
Db 1 TGGGATGATCAAAAGGACC 20

RESULT 1818
AAD64993
ID AAD64993 standard; DNA; 20 BP.
XX
AC AAD64993;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-6.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 GTGATCAAAAGGACCTTGTA 728
Db 1 GTGATCAAAAGGACCTTGTA 20

RESULT 1819
AAD65004/c
ID AAD65004 standard; DNA; 20 BP.
XX
AC AAD65004;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 TGGATCAGGATTCAGTTTCA 1037
Db 20 TGGATCAGGATTCAGTTTCA 1

RESULT 1820
AAD65017/c
ID AAD65017 standard; DNA; 20 BP.
XX
AC AAD65017;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7-2.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1003 ATTCAAGTGATTGGTTGGAT 1022
Db 20 ATTCAAGTGATTGGTTGGAT 1

RESULT 1821
AAD64991
ID AAD64991 standard; DNA; 20 BP.
XX
AC AAD64991;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-4.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 ACAGGTGTCACTTGAAGGT 704
Db 1 ACAGGTGTCACTTGAAGGT 20

RESULT 1822
AAD65003/c
ID AAD65003 standard; DNA; 20 BP.
XX
AC AAD65003;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS5.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 695 CCTTGAAGGTGGAGTGATC 714
Db 20 CCTTGAAGGTGGAGTGATC 1

RESULT 1823
AAD65019/c
ID AAD65019 standard; DNA; 20 BP.
XX
AC AAD65019;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7-4.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATTCAAGTTTCAGATCAGTTT 1046
Db 20 ATTCAAGTTTCAGATCAGTTT 1

RESULT 1824
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AAD64985
ID AAD64985 standard; DNA; 20 BP.
XX
AC AAD64985;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S6.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 TCCTTAGCTGACTATTGGAA 1222
Db 1 TCCTTAGCTGACTATTGGAA 20

RESULT 1825
AAD65002/c
ID AAD65002 standard; DNA; 20 BP.
XX
AC AAD65002;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS4.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TTGCCAGTATATTGACT 500
Db 20 TTGCCAGTATATTGACT 1

RESULT 1826
AAD65010/c
ID AAD65010 standard; DNA; 20 BP.
XX
AC AAD65010;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS5-2.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTCAGAACACAGGTGTCA 694
Db 20 GTGAGTCAGAACACAGGTGTCA 1

RESULT 1827
AAD65026/c
ID AAD65026 standard; RNA; 20 BP.
XX
AC AAD65026;
XX
DT 11-MAR-2004 (first entry)
XX

DE Mouse double minute (MDM2) antisense RNA oligonucleotide AS.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTCAGAACACAGGTGTCA 694
Db 20 GTGAGTCAGAACACAGGTGTCA 1

RESULT 1828
AAD64994
ID AAD64994 standard; DNA; 20 BP.
XX
AC AAD64994;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-7.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 AAGGACCTTGTACAGAGCT 736
Db 1 AAGGACCTTGTACAGAGCT 20

RESULT 1829
AAD65011/c
ID AAD65011 standard; DNA; 20 BP.
XX
AC AAD65011;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS5-3.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGAACAGGTGTACCTTG 699
Db 20 TGAGAACAGGTGTACCTTG 1

RESULT 1830
AAD64982
ID AAD64982 standard; DNA; 20 BP.
XX
AC AAD64982;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S1.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTCAGAACACAGGTGTCA 694
Db 20 GTGAGTCAGAACACAGGTGTCA 1

RESULT 1827
AAD65026/c
ID AAD65026 standard; RNA; 20 BP.
XX
AC AAD65026;
XX
DT 11-MAR-2004 (first entry)
XX

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 357 ACCTCACAGATTCAGCTTC 376
Db 1 ACCTCACAGATTCAGCTTC 20

RESULT 1831
AAD64995
ID AAD64995 standard; DNA; 20 BP.
XX
AC AAD64995;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) sense oligonucleotide S7-1.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 998 TGAACATTCAGGTGATTGGT 1017
Db 1 TGAACATTCAGGTGATTGGT 20

RESULT 1832
AAD64998
ID AAD64998 standard; DNA; 20 BP.
XX
AC AAD64998;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) sense oligonucleotide S7-4.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1027 ATTCAGTTTCAGATCAGTTT 1046
Db 1 ATTCAGTTTCAGATCAGTTT 20

RESULT 1833
AAD65016/c
ID AAD65016 standard; DNA; 20 BP.
XX
AC AAD65016;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7-1.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 998 TGAACATTCAGGTGATTGGT 1017
Db 20 TGAACATTCAGGTGATTGGT 1

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RESULT 1834
AAD64989
ID AAD64989 standard; DNA; 20 BP.
XX
AC AAD64989;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) sense oligonucleotide S5-2.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 675 GTGAGTGAGAACAGGTGTCA 694
Db 1 GTGAGTGAGAACAGGTGTCA 20

RESULT 1835
AAD50276/c
ID AAD50276 standard; DNA; 20 BP.
XX
AC AAD50276;
XX
DT 24-MAR-2003 (first entry)
DE Oligonucleotide #3, used in the invention.
XX
KW Therapy; research reagent; diagnostic; phosphorothioate backbone; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1695 TTTACATGTGCAAGAAGCT 1714
Db 20 TTTACATGTGCAAGAAGCT 1

RESULT 1836
ABZ99055
ID ABZ99055 standard; DNA; 20 BP.
XX
AC ABZ99055;
XX
DT 17-OCT-2003 (first entry)
DE Human PDE4C oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
Db 1 CCCAGGCTGGAGTGCAGTGG 20

RESULT 1837
ABZ97964
ID ABZ97964 standard; DNA; 20 BP.
XX
AC ABZ97964;
XX
DT 17-OCT-2003 (first entry)

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XX DE Human RANTES oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTGGCTCAGCCTCC 2206
Db 1 ATTCTCTGCTGGCTCAGCCTCC 20

RESULT 1838
ADM65742
ID ADM65742 standard; DNA; 20 BP.
XX
AC ADM65742;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human Y chromosome non-recombining region polymorphic fragment #301.
XX
KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
Db 1 CAAAGTCTGGGATTACAGG 20

RESULT 1839
ADM65739
ID ADM65739 standard; DNA; 20 BP.
XX
AC ADM65739;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human Y chromosome non-recombining region polymorphic fragment #300.
XX
KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
Db 1 CAAAGTCTGGGATTACAGG 20

RESULT 1840
ADM65575/c
ID ADM65575 standard; DNA; 20 BP.
XX
AC ADM65575;
XX
DT 03-JUN-2004 (first entry)
XX
DE NRY polymorphism detection primer #489.
XX
KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;

Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGC 2361
Db 20 AAAGTCTGGGATTACAGGC 1

RESULT 1841
ADM65745
ID ADM65745 standard; DNA; 20 BP.
XX
AC ADM65745;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human Y chromosome non-recombining region polymorphic fragment #302.
XX
KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
Db 1 CAAAGTCTGGGATTACAGG 20

RESULT 1842
ADM65578/c
ID ADM65578 standard; DNA; 20 BP.
XX
AC ADM65578;
XX
DT 03-JUN-2004 (first entry)
XX
DE NRY polymorphism detection primer #491.
XX
KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGC 2361
Db 20 AAAGTCTGGGATTACAGGC 1

RESULT 1843
ABD30995
ID ABD30995 standard; DNA; 20 BP.
XX
AC ABD30995;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human RANTES-derived oligonucleotide SEQ ID 13206.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTCAGCCTCC 2206
Db 1 ATTCTCTGCTCAGCCTCC 20

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RESULT 1844
ABD32086
ID ABD32086 standard; DNA; 20 BP.
XX
XX ABD32086;
AC
XX
XX
DT 29-JUL-2004 (first entry)
XX
XX Human PDE4C-derived oligonucleotide SEQ ID 14297.
DE
DE Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW Human respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
Db 1 CCCAGGCTGGAGTGCAGTGG 20

RESULT 1845
ADI80086/c
ID ADI80086 standard; DNA; 20 BP.
XX
XX ADI80086;
AC
XX
XX
DT 22-APR-2004 (first entry)
XX
XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 87.
DE
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; nontropic; neuroprotective; immunosuppressive;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2333 CGGCTCCCAAGTGTGG 2352
Db 20 CGGCTCCCAAGTGTGG 1

RESULT 1846
ADI80221
ID ADI80221 standard; DNA; 20 BP.
XX
XX ADI80221;
AC
XX
XX
DT 22-APR-2004 (first entry)
XX
XX Human transforming growth factor-beta 2 target DNA region, SEQ ID No 222.
DE
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; nontropic; neuroprotective; immunosuppressive;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2333 CGGCTCCCAAGTGTGG 2352
Db 1 CGGCTCCCAAGTGTGG 20

RESULT 1847
ADI30045/c
ID ADI30045 standard; DNA; 20 BP.
XX
XX ADI30045;
AC
XX
XX

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DT 22-APR-2004 (first entry)
XX
XX Human dual specific phosphatase 4 DNA, antisense oligonucleotide #65.
DE
XX Antisense therapy; human; dual specific phosphatase 4;
KW hyperproliferative disorder; developmental disorder; apoptosis;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2280 CACCCTGTTAGCCAGGATGG 2299
Db 20 CACCCTGTTAGCCAGGATGG 1

RESULT 1848
ADJ59829
ID ADJ59829 standard; DNA; 20 BP.
XX
XX ADJ59829;
AC
XX
XX
DT 06-MAY-2004 (first entry)
XX
XX Oligonucleotide associated to RANTES #78.
DE
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTCAGCCTCC 2206
Db 1 ATTCTCTGCTCAGCCTCC 20

RESULT 1849
ADJ60940
ID ADJ60940 standard; DNA; 20 BP.
XX
XX ADJ60940;
AC
XX
XX
DT 06-MAY-2004 (first entry)
XX
XX Oligonucleotide associated to PDE4C #6.
DE
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
Db 1 CCCAGGCTGGAGTGCAGTGG 20

RESULT 1850
ADL23339
ID ADL23339 standard; DNA; 20 BP.
XX
XX ADL23339;
AC
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX Primer #1 for amplification of D6S105.
DE
XX ss; primer; diagnosis; cervical intraepithelial neoplasia; CIN;
KW allelic deletion; PHIT; fragile histidine triad gene; PR;

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XX 01-JUL-2004 (first entry)
DT Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1145.
DE
XX
XX Chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2331 CTCGGCCTCCCAAGTGCTG 2350
DB 20 CTCGGCCTCCCAAGTGCTG 1

RESULT 1858
ADO46429
ID ADO46429 standard; DNA; 20 BP.
XX
XX ADO46429;
AC
XX
DT 15-JUL-2004 (first entry)
DE Human oligonucleotide #1795.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
DB 1 CCCAGGCTGGAGTGCAGTGG 20

RESULT 1859
ADO45319
ID ADO45319 standard; DNA; 20 BP.
XX
XX ADO45319;
AC
XX
DT 15-JUL-2004 (first entry)
DE Human oligonucleotide #685.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 ATTCCTCGCTCAGCTCC 2206
DB 1 ATTCCTCGCTCAGCTCC 20

RESULT 1860
ADP12093/c
ID ADP12093 standard; DNA; 20 BP.
XX
XX ADP12093;
AC
XX
DT 12-AUG-2004 (first entry)
DE Set 2 right PCR primer for marker probe #199.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1598 TTGCCCCCTTAATGCCATTG 1617
DB 20 TTGCCCCCTTAATGCCATTG 1

RESULT 1861
ADP10937
ID ADP10937 standard; DNA; 20 BP.
XX
XX ADP10937;
AC
XX
DT 12-AUG-2004 (first entry)
DE Set 1 left PCR primer for marker probe #282.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1660 TTGTCCATGCGCAAAACAGGA 1679
DB 1 TTGTCCATGCGCAAAACAGGA 20

RESULT 1862
ADP11268/c
ID ADP11268 standard; DNA; 20 BP.
XX
XX ADP11268;
AC
XX
DT 12-AUG-2004 (first entry)
DE Set 1 right PCR primer for marker probe #282.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 AAGGAATAAGCCCTGCCCAG 1740
DB 20 AAGGAATAAGCCCTGCCCAG 1

RESULT 1863
ADN30395/c
ID ADN30395 standard; DNA; 20 BP.
XX
XX ADN30395;
AC
XX
DT 12-AUG-2004 (first entry)
DE Human Notch2 DNA antisense oligonucleotide #67.
XX
KW Human; Notch2; ss; antisense oligonucleotide; phosphorothioate linkage;
KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; autoimmune disorder;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2294 GGATGCTCGATCTCTGA 2313
DB 1 GGATGCTCGATCTCTGA 2313

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Db      20 GGATGCTCGATCTCTCTGA 1

RESULT 1864
ADQ75057/c
ID      ADQ75057 standard; DNA; 20 BP.
XX
AC      ADQ75057;
XX
XX      23-SEP-2004 (first entry)
XX
DE      Ligand conjugated oligomeric compound associated oligo seqid 7.
DE
KW      virucide; oligonucleotide binder; protein binder; serum binder;
KW      vascular protein binder; cellular protein binder; oligomeric compound;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1695 TTTACATGTGCAGGAAGCT 1714
      |||||
Db      20 TTTACATGTGCAGGAAGCT 1

RESULT 1865
AAF84350/c
ID      AAF84350 standard; DNA; 22 BP.
XX
AC      AAF84350;
XX
XX      20-JUN-2001 (first entry)
XX
DE      Human CYP2C18i PCR primer #6.
DE
KW      Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C18i; ss.

Query Match      0.8%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2346 TGCTGGGATTACAGGCATGA 2365
      |||||
Db      20 TGCTGGGATTACAGGCATGA 1

RESULT 1866
AAS11629
ID      AAS11629 standard; DNA; 22 BP.
XX
AC      AAS11629;
XX
XX      24-OCT-2001 (first entry)
XX
DE      Human CYP2B6 allele sequencing primer seqCYP2B6-7p for exon 7.
DE
KW      CYP2B6; cytostatic; gene therapy; genotyping; cancer; metabolism; ss;
KW      human; cancer susceptibility; environmental carcinogen;

Query Match      0.8%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2352 GATTACAGGCATGACCCACC 2371
      |||||
Db      1 GATTACAGGCATGACCCACC 20

RESULT 1867
ADB04761
ID      ADB04761 standard; DNA; 25 BP.
XX

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AC      ADB04761;
XX
XX      20-NOV-2003 (first entry)
XX
DE      Human MDZ7 scanning oligonucleotide SEQ ID 5747.
DE
KW      Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW      zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      0.8%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2274 GGGTTTCACCGTGTAGCCCA 2293
      |||||
Db      6 GGGTTTCACCGTGTAGCCCA 25

RESULT 1868
ABL60500/c
ID      ABL60500 standard; DNA; 26 BP.
XX
AC      ABL60500;
XX
XX      12-AUG-2002 (first entry)
XX
DE      Human MDM2 mRNA fragment complementary oligo 12.
DE
KW      Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW      nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 20; DB 1; Length 26;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      674 TGTGAGTGAGAACAGGTGTCA 694
      |||||
Db      21 TGTGAGTGAGAACAGGTGTCA 1

RESULT 1869
AAH37414
ID      AAH37414 standard; DNA; 23 BP.
XX
AC      AAH37414;
XX
XX      14-AUG-2001 (first entry)
XX
DE      SNP specific lower PCR primer SEQ ID 210.
DE
KW      Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW      SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2345 GTCTGGGATTACAGGCATGAGC 2367
      |||||
Db      1 GTGATGGGATTATAGGCATGAGC 23

RESULT 1870
ABZ83516
ID      ABZ83516 standard; DNA; 23 BP.
XX
AC      ABZ83516;
XX
XX      14-MAY-2003 (first entry)
XX
DE      Toxicologically relevant human PCR primer #675.
DE
KW      Toxicologically relevant gene; toxicological response; PCR primer; ss.

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XX  
Query Match 0.8%; Score 19.8; DB 1; Length 23;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2292 CAGGATGGTCTCGATCTCTCGAC 2314  
DB 1 CAGGATGGTCTCGATCTCTCGAC 23  
RESULT 1871  
AAI71673/c  
ID AAI71673 standard; DNA; 24 BP.  
XX AAI71673;  
XX  
XX  
DT 15-JAN-2002 (first entry)  
DE Human myosin heavy chain 12-14 coding sequence PCR primer #1.  
XX Human; myosin heavy chain 12-14; Prader Willi syndrome; PCR primer;  
KW Klinefelter syndrome; inflammation; kinetic illness; gene therapy; ss.  
Query Match 0.8%; Score 19.8; DB 1; Length 24;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2147 CTGGCTCACTGCAAGCTCTGCC 2169  
DB 24 CTGGCTCACTGCAAGCTCTGCC 2  
RESULT 1872  
AAS00333  
ID AAS00333 standard; DNA; 24 BP.  
XX AAS00333;  
XX  
XX  
DT 17-MAY-2001 (first entry)  
DE PCR primer #2, used to amplify human RAD51 gene at position -2339.  
XX Human; RAD51; breast cancer; BRCA1; BRCA2; PCR primer; ss.  
Query Match 0.8%; Score 19.8; DB 1; Length 24;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2193 CTGCTCAGCTCTCCCAATTAGCT 2215  
DB 1 CTGCTCAGCTCTCCCAAGTACT 23  
RESULT 1873  
AAD42696  
ID AAD42696 standard; DNA; 24 BP.  
XX AAD42696;  
XX  
XX  
DT 15-NOV-2002 (first entry)  
DE Primer #2 used to construct Hdm2 mutant plasmid.  
XX Human; detection; cancer; ARF-p19 protein; cell cycle regulator; tumour;  
KW cell cycle arrest; cell growth; hyperproliferative signal; therapeutic;  
Query Match 0.8%; Score 19.8; DB 1; Length 24;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 307 GGCAATGTGCAATACCAACATG 329

DB 2 GCCATATGTGCAATACCAACATG 24  
RESULT 1874  
ABL50916  
ID ABL50916 standard; DNA; 24 BP.  
XX ABL50916;  
XX  
XX  
DT 24-JUN-2002 (first entry)  
DE Human dihydropyrrrole-5-carboxylate reductase 15 PCR primer 1.  
XX Human; dihydropyrrrole-5-carboxylate reductase 15; cancer; enzyme;  
KW human immunodeficiency virus infection; HIV infection; PCR primer; ss.  
Query Match 0.8%; Score 19.8; DB 1; Length 24;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2263 TAGTAGACAGAGGGTTTCACCGT 2285  
DB 2 TAGTAGACAGAGGATTTTCCACAT 24  
RESULT 1875  
ABV74727  
ID ABV74727 standard; DNA; 24 BP.  
XX AC ABV74727;  
XX  
XX  
DT 03-FEB-2003 (first entry)  
DE Human clathrin light chain 13.64 PCR primer #2.  
XX Human; clathrin light chain 13.64; tumour; haemopathy; HIV infection;  
KW immunological disease; inflammation; cytostatic; anti-HIV; PCR; primer;  
Query Match 0.8%; Score 19.8; DB 1; Length 24;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2092 TTTTCTTGGACCGAGTCTTGC 2114  
DB 1 TTTTCTTGGACCGAGTCTTGC 23  
RESULT 1876  
ADB04581  
ID ADB04581 standard; DNA; 25 BP.  
XX AC ADB04581;  
XX  
XX  
DT 20-NOV-2003 (first entry)  
DE Human MDZ7 scanning oligonucleotide SEQ ID 5567.  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
Query Match 0.8%; Score 19.8; DB 1; Length 25;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2089 TTATTTTGGACCGAGTCT 2111  
DB 1 TTTTCTTGGACCGAGTCT 23  
RESULT 1877  
ADB04735  
ID ADB04735 standard; DNA; 25 BP.

XX ADB04735;  
AC  
XX  
DT 20-NOV-2003 (first entry)  
DE Human MD27 scanning oligonucleotide SEQ ID 5721.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
Query Match 0.8%; Score 19.8; DB 1; Length 25;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2246 CTAATTTTGTACTTTAGTAG 2268  
DB 3 CTAATATTTGTATTTAGTAG 25  
RESULT 1878  
ADB04662  
ID ADB04662 standard; DNA; 25 BP.  
XX  
AC ADB04662;  
XX  
DT 20-NOV-2003 (first entry)  
DE Human MD27 scanning oligonucleotide SEQ ID 5648.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
Query Match 0.8%; Score 19.8; DB 1; Length 25;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2173 CCCGGGTTCCACATTCCTCTG 2195  
DB 3 CCTGGGTTCCACATTCCTCTG 25  
RESULT 1879  
ADB04580  
ID ADB04580 standard; DNA; 25 BP.  
XX  
AC ADB04580;  
XX  
DT 20-NOV-2003 (first entry)  
DE Human MD27 scanning oligonucleotide SEQ ID 5566.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
Query Match 0.8%; Score 19.8; DB 1; Length 25;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2089 TTATTTTGTGACCGAGTCT 2111  
DB 2 TTTTGTGACCGAGTCT 24  
RESULT 1880  
AB222656/C  
ID AB222656 standard; DNA; 26 BP.  
XX  
AC AB222656;  
XX  
DT 31-MAR-2003 (first entry)  
DE Human PEPT1 PCR primer PEPT1#1 R.  
XX

KW Human; PEPT1; PEPT2; intestinal peptide transporter; transport;  
KW transporter; PCR primer; ss.  
Query Match 0.8%; Score 19.8; DB 1; Length 26;  
Best Local Similarity 91.3%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2350 GGGATTACAGGCATGAGCCACCG 2372  
DB 26 GGGATTACAGGCCTTGAGCTACCG 4  
RESULT 1881  
AAA39394/C  
ID AAA39394 standard; DNA; 26 BP.  
XX  
AC AAA39394;  
XX  
DT 04-OCT-2000 (first entry)  
DE Alu repeat 3' end consensus oligonucleotide SEQ ID NO:7.  
XX  
KW Alu 3' end primer; human genome; allele; phenotype; screening;  
KW polymorphic; characterisation; ss.  
Query Match 0.8%; Score 19.6; DB 1; Length 26;  
Best Local Similarity 84.6%; Pred. No. 1.9e+03;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2099 TGAGACCGAGTCTGCTGTATACC 2124  
DB 26 TGAGACCGAGTCTGCTGTATGCC 1  
RESULT 1882  
AAA62473/C  
ID AAA62473 standard; DNA; 26 BP.  
XX  
AC AAA62473;  
XX  
DT 21-NOV-2000 (first entry)  
DE Human SECX 2826468 probe.  
XX  
KW Human; secreted protein; SECX; cancer; cytostatic; vaccine; probe;  
KW expression analysis; ss.  
Query Match 0.8%; Score 19.6; DB 1; Length 26;  
Best Local Similarity 84.6%; Pred. No. 1.9e+03;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2269 AGACAGCGTTTACCGTGTAGCCAG 2294  
DB 26 ACATGGGGTCTCACCGTGTAGCCAG 1  
RESULT 1883  
AAF64089/C  
ID AAF64089 standard; DNA; 26 BP.  
XX  
AC AAF64089;  
XX  
DT 06-APR-2001 (first entry)  
DE Primer #33.  
XX  
KW Human; lipoprotein lipase; LPL; stenosis; ss.  
Query Match 0.8%; Score 19.6; DB 1; Length 26;  
Best Local Similarity 84.6%; Pred. No. 1.9e+03;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;



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XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGGC 2361
DB 1 CAAAGTCTGGGATTACAGGC 21

RESULT 1891
AAH40070
ID AAH40070 standard; DNA; 21 BP.
XX
AC AAH40070;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific lower PCR primer SEQ ID 2866.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2283 CGTGTAGCCAGGATGCTCTC 2303
DB 1 CATGTTAGCCAGGATGCTCTC 21

RESULT 1892
AAH24567/c
ID AAH24567 standard; DNA; 21 BP.
XX
AC AAH24567;
XX
DT 07-AUG-2001 (first entry)
DE Human Alu sequence-specific primer Alu-Sense.
KW Human; Alu; metastatic potential determination; cancer;
KW chorioallantoic membrane; CAM; avian embryo; intravasation;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2343 AAGTGCTGGGATTACAGCAT 2363
DB 21 AAGTGCTGGGATTACAGCGT 1

RESULT 1893
ABQ74069
ID ABQ74069 standard; DNA; 21 BP.
XX
AC ABQ74069;
XX
DT 11-OCT-2002 (first entry)
DE Microsatellite typing and sequencing D6S105 5' primer.
KW Homozygous stem cell; major histocompatibility complex; MHC; HLA;
KW human leukocyte antigen; immunotype; genotype; microsatellite; probe;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2350 GGGATTACAGGCATGAGCCAC 2370
DB 1 GGGATTACAGGCAGGAGCCAC 21

RESULT 1894
ABS98158
ID ABS98158 standard; DNA; 21 BP.
XX
AC ABS98158;
XX
DT 23-DEC-2002 (first entry)
DE Human multidrug resistance gene polymorphic sequence #60.
XX
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTACCCAGGATG 2298
DB 1 TTCACCGTGTACCCAGGATG 21

RESULT 1895
ABS97183
ID ABS97183 standard; DNA; 21 BP.
XX
AC ABS97183;
XX
DT 23-DEC-2002 (first entry)
DE Human CYP450A2 promoter polymorphism #1.
XX
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTC 2339
DB 1 TGATCCGCCACCTCGGCTC 21

RESULT 1896
ABS98107/c
ID ABS98107 standard; DNA; 21 BP.
XX
AC ABS98107;
XX
DT 23-DEC-2002 (first entry)
DE Human multidrug resistance gene polymorphic sequence #9.
XX
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2174 CCGGGTTCCGACCATCTCTCT 2194
DB 21 CCGGGTTCCGACCATCTCTCT 1

RESULT 1897

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ABS98163
ID ABS98163 standard; DNA; 21 BP.
XX
AC ABS98163;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human multidrug resistance gene polymorphic sequence #65.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCGTGGCCACC 2371
DB 1 GGATTACAGGCGTGGCCACC 21

RESULT 1898
ABS98105/c
ID ABS98105 standard; DNA; 21 BP.
XX
AC ABS98105;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human multidrug resistance gene polymorphic sequence #7.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2314 CCTCGTGATCCGCCACCTCG 2334
DB 21 CCTCGTGATCCGCCCGCTCG 1

RESULT 1899
ADE14130/c
ID ADE14130 standard; DNA; 21 BP.
XX
AC ADE14130;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #239.
XX
KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
SNP; glaucoma; progressive ocular hypertensive disorder;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAGTGTGGG 2352
DB 21 TCGGCTCCCAAGTGTGGG 1

RESULT 1900
ADH59601/c
ID ADH59601 standard; DNA; 21 BP.
XX
AC ADH59601;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Y chromosome non-recombining region polymorphic fragment #247.
XX
KW ethnic origin determination; polymorphic site determination;
Y chromosome; paternity testing; forensic; diagnosis;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DE Non-nucleotide probe of the invention #5.
XX
KW non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
KW probe.

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGGTTTC 2280
DB 21 TTTTAGTAGACAGGGTTTC 1

RESULT 1901
ADH59613
ID ADH59613 standard; DNA; 21 BP.
XX
AC ADH59613;
XX
DT 25-MAR-2004 (first entry)
XX
DE Non-nucleotide probe of the invention #17.
XX
KW non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
KW probe.

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGGTTTC 2280
DB 1 TTTTAGTAGACAGGGTTTC 21

RESULT 1902
ADH59613
ID ADH59613 standard; DNA; 21 BP.
XX
AC ADH59613;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human LPDLR PCR primer #19.
XX
KW lipase; LPDL; lipase deficiency; atherosclerosis;
fatty liver disease; dyslipidaemia; hypercholesterolaemia;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2352 GATTACAGGCGTGGCCACC 2372
DB 1 GATTACAGGCGTGGCCACC 21

RESULT 1903
ADH59613
ID ADH59613 standard; DNA; 21 BP.
XX
AC ADH59613;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human Y chromosome non-recombining region polymorphic fragment #247.
XX
KW ethnic origin determination; polymorphic site determination;
Y chromosome; paternity testing; forensic; diagnosis;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2277 TTTCCCGTGTAGCCAGGAT 2297
    ||||| ||||| ||||| |||||
Db 1 TTTCCCTTGTAGCCAGGAT 21

RESULT 1904
AD055495
ID AD055495 standard; DNA; 21 BP.
XX
AC AD055495;
XX
DT 26-AUG-2004 (first entry)
XX
DE HIV gene expression analysis primer SB704 following siRNA inhibition.
XX
KW ss; primer; anti-HIV; virucide; gene therapy; small interfering RNA;
KW siRNA; HIV; genome; diagnosis.

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2346 TGCTGGGATTACAGGATGAG 2366
    ||||| ||||| ||||| |||||
Db 1 TGCTGGGATTACAGGCGTGAG 21

RESULT 1905
AAX09910/c
ID AAX09910 standard; DNA; 22 BP.
XX
AC AAX09910;
XX
DT 24-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic marker downstream primer #216.
XX
KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;

Query Match 0.8%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2234 CACCACACCTGGCTAAATTTT 2254
    ||||| ||||| ||||| |||||
Db 21 CACCACACCTGGTTAAATTTT 1

RESULT 1906
AAF29797/c
ID AAF29797 standard; DNA; 22 BP.
XX
AC AAF29797;
XX
DT 09-APR-2001 (first entry)
XX
DE Preseniline-1 gene promoter PCR primer Prom22R.
XX
KW Human; PSEN1; Alzheimer's disease; polymorphism; diagnosis;
KW preseniline-1; chromosome 14; PCR primer; ss.

Query Match 0.8%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2260 TTTTAGTAGACAGCGGTTTC 2280
    ||||| ||||| ||||| |||||
Db 21 TTTTAGTAGACAGCGGGTTTC 1

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RESULT 1907
ADC24360
ID ADC24360 standard; DNA; 22 BP.
XX
AC ADC24360;
XX
DT 18-DEC-2003 (first entry)
XX
DE PCR primer for amplifying the BRCA1 gene #SEQ ID 50.
XX
KW DNA amplification; copy number; polymerase chain reaction; PCR; primer;
KW ss.

Query Match 0.8%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2340 CCAAAGTGTGGGATTACAGG 2360
    ||||| ||||| ||||| |||||
Db 1 CCAAAGTGTAGGATTACAGG 21

RESULT 1908
ADH13395/c
ID ADH13395 standard; DNA; 23 BP.
XX
AC ADH13395;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human malignant neoplasia-related PCR primer SeqID244.
XX
KW malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
KW gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;

Query Match 0.8%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2145 ATCTTGGCTCACTGCAAGCTC 2165
    ||||| ||||| ||||| |||||
Db 23 ATCTTGGCTCACTGCAACCTC 3

RESULT 1909
ABS56410
ID ABS56410 standard; DNA; 24 BP.
XX
AC ABS56410;
XX
DT 23-JAN-2003 (first entry)
XX
DE Human DNA mismatch repair gene 10.45 specific RT-PCR primer, #2.
XX
KW Human; RT-PCR; ss; DNA mismatch repair gene 10.45; tumour; haemopathy;
KW human immunodeficiency virus; HIV; immunological disease; inflammation;

Query Match 0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2103 ACCGAGTCTTGTCTGTACC 2123
    ||||| ||||| ||||| |||||
Db 1 ACCGAGTCTTGTCTGTACC 21

RESULT 1910
ABK14172
ID ABK14172 standard; DNA; 24 BP.
XX
AC ABK14172;
XX
DT 21-MAY-2002 (first entry)

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XX Insulin like growth factor binding protein 11.88 cDNA RT-PCR primer #2.
DE
XX
KW Insulin like growth factor binding protein 11.88; primer; ss; cytotstatic;
KW embryo development dysmorphia; malignant tumour; gene therapy; cancer;

Query Match      0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATACCCAG 2126
DB 4 GAGTCTTGCTCTGTATACCCAG 24
|||||
|||||

RESULT 1911
ABV76761/c
ID ABV76761 standard; DNA; 24 BP.
XX
AC ABV76761;
XX
DT 07-MAR-2003 (first entry)
XX
DE Ras GTP enzyme-activating protein 20.68 RT-PCR primer, SEQ ID NO:3.
XX
DE Ras GTP enzyme-activating protein 20.68; cancer suppressor protein-20.68;
KW recombinant production; gene therapy; cancer; tumour; HIV infection;
KW

Query Match      0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTCTCCTGCTCAGCTCC 2207
DB 21 ATTCTCCTGCTCAGCTCC 1
|||||
|||||

RESULT 1912
ABL42193
ID ABL42193 standard; DNA; 24 BP.
XX
AC ABL42193;
XX
DT 12-JUN-2002 (first entry)
XX
DE PCR primer #2 for human cartilage connective protein 10.67 cDNA.
XX
KW Human; cartilage connective protein 10.67; disease; PCR primer; ss.
XX

Query Match      0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATACCCAG 2126
DB 4 GAGTCTTGCTCTGTATACCCAG 24
|||||
|||||

RESULT 1913
ABS55854
ID ABS55854 standard; DNA; 24 BP.
XX
AC ABS55854;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human SOX3 protein 13.31 cDNA RT-PCR primer #1.
XX
DE Human; SOX3 protein 13.31; primer; ss; malignant tumour; haemopathy;
KW HIV infection; human immunodeficiency virus; immunological disease;
KW

Query Match      0.8%; Score 19.4; DB 1; Length 24;

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Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGCATGAGCCACC 2371
DB 1 GGATTACAGCATGAGCCACC 21
|||||
|||||

RESULT 1914
ABZ24886
ID ABZ24886 standard; DNA; 24 BP.
XX
AC ABZ24886;
XX
DT 25-MAR-2003 (first entry)
XX
DE High-mobility component protein 12.87 PCR primer #2.
XX
DE High-mobility component protein 12.87; cancer; HIV infection; cytostatic;
KW anti-HIV; PCR; primer; ss.
KW

Query Match      0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATACCCAG 2126
DB 4 GAGTCTTGCTCTGTATACCCAG 24
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RESULT 1915
AAT63214
ID AAT63214 standard; DNA; 20 BP.
XX
AC AAT63214;
XX
DT 17-JUN-1997 (first entry)
XX
DE Primer Alu 5' used in Inter-Alu PCR for PAC isolation.
XX
KW S182 gene; familial Alzheimer's disease; diagnosis; transgenic animal;
KW polymerase chain reaction; PCR; primer; artificial chromosome; PAC; ss.
KW

Query Match      0.8%; Score 19.2; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2351 GGATTACAGCATGAGCCAC 2370
DB 1 GGATTACAGCATGAGCCAC 20
|||||
|||||

RESULT 1916
ADL72189/c
ID ADL72189 standard; DNA; 23 BP.
XX
AC ADL72189;
XX
DT 20-MAY-2004 (first entry)
XX
DE Alu-specific primer AD-1.
XX
KW Nucleic acid amplification; Alu; fluorescence in-situ hybridization;
KW FISH; primer; PCR; ss.
KW

Query Match      0.8%; Score 19.2; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 2e+03;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2098 TTGAGACCGAGTCTTGTCTGT 2119
DB 22 TTGAGACCGAGTCTTGTCTGT 1
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RESULT 1917
AAV52725/c
ID AAV52725 standard; DNA; 24 BP.
XX
XX
AC AAV52725;
XX
DT 21-DEC-1998 (first entry)
XX
XX Hepatocyte nuclear factor 1 alpha gene STS UC-39 forward primer.
DE
XX
KW Hepatocyte nuclear factor 1 alpha; HNF-1 alpha; MODY3; human;
KW transcription factor; maturity onset diabetes of the young; diabetes;
KW

Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2099 TGAGACGAGTCTTGCTCTGTTC 2122
DB 24 TGAGATGGAGTCTTGCTCTGTTC 1

RESULT 1918
AAX27978
ID AAX27978 standard; cDNA; 24 BP.
XX
XX
AC AAX27978;
XX
DT 08-JUN-1999. (first entry)
XX
XX PCR primer for B18hum coding sequence.
DE
XX B18hum; bronchoalveolar protein; peroxisome-associated polypeptide;
KW lung injury; oxidative stress-related disorder; inflammatory disease;
KW

Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2267 AGAGACAGGGTTTCACCGTCTTAG 2290
DB 1 AGAGACAGGGTTTCACCATCTGG 24

RESULT 1919
AAA27181
ID AAA27181 standard; DNA; 24 BP.
XX
XX
AC AAA27181;
XX
DT 11-SEP-2000 (first entry)
XX
DE Reverse primer P2 for target sequence human P2 gene.
KW
KW P2; CX5C chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;
KW allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;
KW

Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2115 TCTGTTACCCAGGCTGGAGTGCAG 2138
DB 1 TATGTCACCCAGGCTGGGGTGCAG 24

RESULT 1920
AAF92846
ID AAF92846 standard; DNA; 24 BP.
XX
XX
AC AAF92846;
XX
XX

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DT 17-MAY-2001 (first entry)
XX
XX Human ABC1 transcription factor binding site #9.
XX
XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX

Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2293 AGGATGGTCTCGATCTCTGACCT 2316
DB 1 AGGTTCGTTTCGAACCTCTGACCT 24

RESULT 1921
AAH40034/c
ID AAH40034 standard; DNA; 24 BP.
XX
XX
AC AAH40034;
XX
DT 14-AUG-2001 (first entry)
XX
XX SNP specific lower PCR primer SEQ ID 2830.
DE
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW

Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2334 GGCTCCCAAGCTCTGGGATTAC 2357
DB 24 GGACTCTCTAAAGTCTGGGAATTAC 1

RESULT 1922
AAI66532
ID AAI66532 standard; DNA; 24 BP.
XX
XX
AC AAI66532;
XX
DT 11-DEC-2001 (first entry)
XX
DE Human pterin-molybdenum oxidoreductase 10 cDNA PCR primer #2.
KW
KW Human; pterin-molybdenum oxidoreductase 10; cancer; haemopathy;
KW immunological disease; HIV infection; inflammation; gene therapy;
KW

Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2117 TGTATCCAGGCTGGAGTGCAGTG 2140
DB 1 TGTATCCAGGCTGGAGTGCAGTG 24

RESULT 1923
ABA82841/c
ID ABA82841 standard; DNA; 24 BP.
XX
XX
AC ABA82841;
XX
XX
DT 07-FEB-2002 (first entry)
XX
XX Human protective DNA sequence CNI-00746 fragment #6.
DE
XX Human; protective sequence; cell death; cancer; autoimmune disease;
KW neurological disorder; stroke; cytostatic; neuroprotective; gene therapy;
KW

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Query Match 0.8%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2262 TTAGTAGACACGAGGTTTCACCGT 2285  
DB 24 TTAGTAGACACGAGGTTTCACCAT 1

RESULT 1924  
ABL41332  
ID ABL41332 standard; DNA; 24 BP.  
XX  
AC ABL41332;  
XX  
DT 22-MAY-2002 (first entry)  
XX  
DE Human mitochondrial ATPase coupling factor F69.35 PCR primer 2.  
XX  
KW Human; mitochondrial ATPase coupling factor F69.35; sugar; fat; protein;  
KW metabolic disturbance; PCR; primer; ss.

Query Match 0.8%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2102 GACCGAGTCTTGCTCTGTACCA 2125  
DB 1 GACAGAGTCTTGTCTGTGTGCCA 24

RESULT 1925  
ABS56119  
ID ABS56119 standard; DNA; 24 BP.  
XX  
AC ABS56119;  
XX  
DT 22-JAN-2003 (first entry)  
XX  
DE RT-PCR primer #2 for cDNA encoding human zinc finger protein 11.55.  
XX  
KW Human; zinc finger protein 11.55; malignant tumour; haemopathy;  
KW human immunodeficiency virus infection; HIV infection;

Query Match 0.8%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2100 GACCGAGTCTTGCTCTGTACCA 2123  
DB 1 GACCGAGTCTTGCTCTGTGTGCCA 24

RESULT 1926  
ABS56756  
ID ABS56756 standard; DNA; 24 BP.  
XX  
AC ABS56756;  
XX  
DT 30-JAN-2003 (first entry)  
XX  
DE DNA topoisomerase II-beta (TOP2B), 9.02 RT-PCR primer #2.  
XX  
KW DNA topoisomerase II-beta 9.02; TOP2B 9.02; cancer; HIV infection; PCR;  
KW primer; amplification; ss.

Query Match 0.8%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTTGCTCTGTACCA 2126  
DB 1 ACAGAGTCTTGCTCTGTGTGCCA 24

RESULT 1927  
ABK52730  
ID ABK52730 standard; DNA; 24 BP.  
XX  
AC ABK52730;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Human Mch2 protein 11.55. RT-PCR primer #2.  
XX  
KW Human; Mch2 protein 11.55; cancer; human immunodeficiency virus; HIV;  
KW reverse transcriptase PCR; RT-PCR; primer; ss.

Query Match 0.8%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2100 GACCGAGTCTTGCTCTGTACCA 2123  
DB 1 GACCGAGTCTTGCTCTGTGTGCC 24

RESULT 1928  
ABQ77952  
ID ABQ77952 standard; DNA; 24 BP.  
XX  
AC ABQ77952;  
XX  
DT 30-JAN-2003 (first entry)  
XX  
DE Mitochondrial translation initiation factor 10.01 RT-PCR primer 2.  
XX  
KW Human; mitochondrial translation initiation factor 10.01;  
KW recombinant production; gene therapy; sugar metabolism disorder;

Query Match 0.8%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2104 CCGAGTCTTGCTCTGTACCA 2127  
DB 1 CCGAGTCTTGCTCTGTGTGCCA 24

RESULT 1929  
ABL41338  
ID ABL41338 standard; DNA; 24 BP.  
XX  
AC ABL41338;  
XX  
DT 22-MAY-2002 (first entry)  
XX  
DE Human TFIIID subunit p30beta protein 12.54 PCR primer SEQ ID NO 3.  
XX  
KW Human; TFIIID subunit p30beta protein 12.54; tumour; inflammation;  
KW protein metabolism dysfunction; immunological disease; haemopathy; HIV;

Query Match 0.8%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2108 GTCTCTCTGTGTACCA 2131  
DB 1 GTCTCTCTGTGTGTGCCA 24

RESULT 1930  
ABK89466  
ID ABK89466 standard; DNA; 24 BP.  
XX  
AC ABK89466;

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XX 05-NOV-2002 (first entry)
XX Human large protein 17.6 specific RT-PCR primer, #1.
DE Human; RT-PCR; ss; large protein 17.6; embryonic development deformity;
XX protein metabolism disturbance; tumour; antagonist;
KW
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2104 CCGAGTCTTGCTCTGTACCCAG 2127
DB 1 CAGGGTCTTGCTCTGTACCCAG 24
RESULT 1931
ABA94088
ID ABA94088 standard; DNA; 24 BP.
XX
AC ABA94088;
XX
DT 08-MAY-2002 (first entry)
XX Human tumour suppressor factor 11.77 PCR primer 2 SEQ ID NO:4.
DE Human; tumour suppressor factor 11.77; cytostatic; haemostatic; virucide;
KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2103 ACCGAGTCTTGCTCTGTACCCAG 2126
DB 1 ACGGAGTCTTGCTCTGTGCCCCAG 24
RESULT 1932
ABS56496
ID ABS56496 standard; DNA; 24 BP.
XX
AC ABS56496;
XX
DT 22-JAN-2003 (first entry)
XX Human cell signal/architecture protein 10.56 RT-PCR primer #2.
DE Human; ss; cell signal/architecture protein 10.56; PCR; primer;
KW nervous disorder; RT-PCR; reverse transcriptase PCR.
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2102 GACCGAGTCTTGCTCTGTACCCA 2125
DB 1 GATGGAGTCTTGCTCTGTGCCCCA 24
RESULT 1933
ABA01638
ID ABA01638 standard; DNA; 24 BP.
XX
AC ABA01638;
XX
DT 05-FEB-2002 (first entry)
XX Human tyrosinase 12 PCR primer 2 SEQ ID NO:4.
DE Human; tyrosinase 12; cytostatic; virucidal; immunomodulatory;
KW antiinflammatory; haemostatic; diagnosis; malignancy; haemopathy;

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Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2103 ACCGAGTCTTGCTCTGTACCCAG 2126
DB 1 ACAGGGTCTTGCTCTGTACCCAG 24
RESULT 1934
ABK90209
ID ABK90209 standard; DNA; 24 BP.
XX
AC ABK90209;
XX
DT 21-OCT-2002 (first entry)
XX Human transcription binding factor (CBF-C) RT-PCR primer #1.
DE Human; ss; primer; CBF-C; 13.42; transcription binding factor;
KW gamma subunit; protein metabolism disorder; reverse transcriptase PCR.
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2108 GTCTTGTCTTGCTCTGTACCCAGCTGG 2131
DB 1 GTCTCGTCTTGCTCGCCAGGCTGG 24
RESULT 1935
ABV74685
ID ABV74685 standard; DNA; 24 BP.
XX
AC ABV74685;
XX
DT 03-FEB-2003 (first entry)
XX Human SOX3 protein 10.67 PCR primer #2.
DE Human; SOX3 protein 10.67; haemophilia A; PCR; primer;
KW pseudohypertrophic muscular dystrophy; bo-Fu-Lai syndrome; ss.
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2103 ACCGAGTCTTGCTCTGTACCCAG 2126
DB 1 ACAGTGTCTTGCTCTGTACCCAG 24
RESULT 1936
AAS19678/c
ID AAS19678 standard; DNA; 24 BP.
XX
AC AAS19678;
XX
DT 09-APR-2002 (first entry)
XX RT-PCR primer #2 for cDNA encoding human tyrosinase 12.
DE Human; tyrosinase 12; malignant tumour; haemopathy; HIV infection;
KW human immunodeficiency virus; cytostatic; immunological disease;
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2125 AGGCTGAGTGCAGTGGTGATCT 2148
DB 1 AGGCTGAGTGCAGTGGTGATCT 2148

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Db      24 AGGCTGGAGTGCATGCTGTGATCT 1

RESULT 1937
ABK12883
ID ABK12883 standard; DNA; 24 BP.
XX
XX
AC ABK12883;
XX
XX
DT 18-JUN-2002 (first entry)
XX
DE Ras GTP activator protein 12, RT-PCR primer 2.
XX
KW Ras GTP activator protein 12; malignant tumour; haemopathy; HIV;
human immunodeficiency virus infection; immunological disease;
Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2102 GACCGAGTCTTGCTCTGTACCCA 2125
      ||| ||| ||| ||| ||| ||| ||| |||
Db      1 GACGGGTCTTACTCTGTACCCA 24

RESULT 1938
ABA05003
ID ABA05003 standard; DNA; 24 BP.
XX
XX
AC ABA05003;
XX
XX
DT 20-FEB-2002 (first entry)
XX
DE Human tyrosine kinase 14 coding sequence PCR primer #2.
XX
KW Human; tyrosine kinase 14; cancer; haemopathy; HIV infection;
immunological disease; inflammation; developmental disorder; cytostatic;
Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2102 GACCGAGTCTTGCTCTGTACCCA 2125
      ||| ||| ||| ||| ||| ||| ||| |||
Db      1 GATGGAGTCTTGCTCTGTACCCA 24

RESULT 1939
ABA95476
ID ABA95476 standard; DNA; 24 BP.
XX
XX
AC ABA95476;
XX
XX
DT 04-APR-2002 (first entry)
XX
DE Human dihydroorotase 11 PCR primer #1.
XX
KW Human; dihydroorotase 11; cytostatic; haemostatic; virucide; PCR primer;
immunomodulatory; antiinflammatory; gene therapy; enzyme; tumour;
Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2100 GAGACCGAGTCTTGCTCTGTACCC 2123
      ||| ||| ||| ||| ||| ||| ||| |||
Db      1 GAGACAGAGTCTCGCTCTGTACCC 24

RESULT 1940
ADC48698
ID ADC48698 standard; DNA; 24 BP.
XX

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AC ADC48698;
XX
XX
DT 18-DEC-2003 (first entry)
XX
XX
DE Human epilepsy associated protein-11.77, RT-PCR primer #2.
XX
KW Human; epilepsy associated protein-11.77; cancer; haematopathy;
HIV infection; immune disease; reverse transcriptase-PCR; RT-PCR; primer;
Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2102 GACCGAGTCTTGCTCTGTACCCA 2125
      ||| ||| ||| ||| ||| ||| ||| |||
Db      1 GACGGAGCCTTGCTCTGTACCCA 24

RESULT 1941
ABZ57061
ID ABZ57061 standard; DNA; 24 BP.
XX
XX
AC ABZ57061;
XX
XX
DT 24-MAR-2003 (first entry)
XX
DE Excitatory amino acid transport protein 13.53 RT-PCR primer, SEQ ID NO:4.
XX
KW Human; excitatory amino acid transport protein 13.53;
recombinant production; gene therapy; glutamic acid transport disorder;
Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2322 TCCGCCACCTCGGCTCCCAAG 2345
      ||| ||| ||| ||| ||| ||| ||| |||
Db      1 TCCTCCACCTTGCTTCCCAAG 24

RESULT 1942
ADG83872
ID ADG83872 standard; DNA; 24 BP.
XX
XX
AC ADG83872;
XX
XX
DT 11-MAR-2004 (first entry)
XX
DE Human SLC6A14 forward PCR primer SEQ ID NO:13.
XX
KW differentiation; ulcerative colitis; Crohn's disease;
target genetic marker gene; human; PCR primer; ss.
Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2345 GTCTGGATTACAGGCATGAGCC 2368
      ||| ||| ||| ||| ||| ||| ||| |||
Db      1 GTCTGAGATTACAGGTGTGAGCC 24

RESULT 1943
ADB04577
ID ADB04577 standard; DNA; 25 BP.
XX
XX
AC ADB04577;
XX
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5563.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;

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KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
Query Match 0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2086 TTATTATTTTGTGACCGAGT 2109
DB 2 TTTTGTGACGAGT 25

RESULT 1944
ADB04583
ID ADB04583 standard; DNA; 25 BP.
XX AC ADB04583;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD27 scanning oligonucleotide SEQ ID 5569.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2092 TTTTGTGACCGAGTCTGTCT 2115
DB 2 TTTTGTGACGAGTCTGTCT 25

RESULT 1945
ADB04677
ID ADB04677 standard; DNA; 25 BP.
XX AC ADB04677;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD27 scanning oligonucleotide SEQ ID 5663.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2186 CATTCCTGCTCAGCTCCCA 2209
DB 1 CATTCCTGCTCAGTCTCCGA 24

RESULT 1946
ADB04586
ID ADB04586 standard; DNA; 25 BP.
XX AC ADB04586;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD27 scanning oligonucleotide SEQ ID 5572.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2094 TTTTGTGACCGAGTCTGTCT 2117
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Db 1 TTTTGTGACGAGTCTGTCT 24

RESULT 1947
ADB04747
ID ADB04747 standard; DNA; 25 BP.
XX AC ADB04747;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD27 scanning oligonucleotide SEQ ID 5733.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2256 GTATTTTGTAGAGACGGGTT 2279
DB 1 GTATTTTGTAGACGGGGTT 24

RESULT 1948
AAT94763
ID AAT94763 standard; DNA; 19 BP.
XX AC AAT94763;
XX DT 25-MAR-2003 (revised)
XX DT 18-FEB-1998 (first entry)
XX DE Human progesterone receptor gene primer.
XX KW Human; progesterone receptor; breast cancer; ovarian cancer; mutant;

Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGG 2360
DB 1 AAAGTCTGGGATTACAGG 19

RESULT 1949
AAT84754
ID AAT84754 standard; DNA; 19 BP.
XX AC AAT84754;
XX DT 04-NOV-1997 (first entry)
XX DE FISH primer for human progesterone receptor intron G.
XX KW Breast; ovarian; cancer; diagnosis; risk; predisposition; human;
KW detection; point mutation; progesterone; receptor; FISH; primer;

Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGG 2360
DB 1 AAAGTCTGGGATTACAGG 19

RESULT 1950
AAH38677
ID AAH38677 standard; DNA; 19 BP.
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XX AAH38677;
AC
XX 14-AUG-2001 (first entry)
DT
XX SNP specific upper PCR primer SEQ ID 1473.
DE
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agamaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGGATTACAGCATG 2364
DB 1 TGCTGGGATTACAGCATG 19

RESULT 1951
AAH38221
ID AAH38221 standard; DNA; 19 BP.
XX
XX AAH38221;
AC
XX 14-AUG-2001 (first entry)
DT
XX SNP specific upper PCR primer SEQ ID 1017.
DE
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agamaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGGATTACAGCATG 2364
DB 1 TGCTGGGATTACAGCATG 19

RESULT 1952
ABL44474/c
ID ABL44474 standard; DNA; 19 BP.
XX
XX ABL44474;
AC
XX 11-APR-2002 (first entry)
DT
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1518.
DE
XX Human chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTGTGGGATT 2355
DB 19 CTCCCAAAGTGTGGGATT 1

RESULT 1953
ADK41249/c
ID ADK41249 standard; DNA; 19 BP.
XX
XX ADK41249;
AC
XX 06-MAY-2004 (first entry)
DT
XX Human chromosome 19 DNA primer/probe SEQ ID No 7.
DE
XX

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KW sequence polymorphism analysis; human; chromosome 19q; cancer; RAI; ss;
KW single nucleotide polymorphism; SNP; probe; primer.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2275 GGTTCACCGTGTAGCCA 2293
DB 19 GGTTCACCGTGTAGCCA 1

RESULT 1954
ADK41375/c
ID ADK41375 standard; DNA; 19 BP.
XX
XX ADK41375;
AC
XX 06-MAY-2004 (first entry)
DT
XX Human chromosome 19 RAI il forward primer.
DE
XX sequence polymorphism analysis; human; chromosome 19q; cancer; RAI; ss;
KW single nucleotide polymorphism; SNP; primer.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2275 GGTTCACCGTGTAGCCA 2293
DB 19 GGTTCACCGTGTAGCCA 1

RESULT 1955
ADO23055
ID ADO23055 standard; cDNA; 19 BP.
XX
XX ADO23055;
AC
XX 01-JUL-2004 (first entry)
DT
XX Human p53-binding protein, mdm2, SDO target region #6.
DE
XX Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 AAAGGGAAGAAACCAAGA 1573
DB 1 AAAGGGAAGAAACCAAGA 19

RESULT 1956
ADO23052
ID ADO23052 standard; cDNA; 19 BP.
XX
XX ADO23052;
AC
XX 01-JUL-2004 (first entry)
DT
XX Human p53-binding protein, mdm2, SDO target region #3.
DE
XX Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1695 TTTACATGTGCAAGAAGC 1713  
 DB 1 TTTACATGTGCAAGAAGC 19

## RESULT 1957

ADO23051  
 ID ADO23051 standard; cDNA; 19 BP.

XX AC ADO23051;  
 XX DT 01-JUL-2004 (first entry)

XX DE Human p53-binding protein, mdm2, SDO target region #2.  
 XX KW Human; ss; SDO; short double stranded oligonucleotide; cleavage site;  
 KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match 0.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1765 TTGTGCTAACTATTTCCTC 1783

DB 1 TTGTGCTAACTATTTCCTC 19

## RESULT 1958

ADO23053  
 ID ADO23053 standard; cDNA; 19 BP.

XX AC ADO23053;  
 XX DT 01-JUL-2004 (first entry)

XX DE Human p53-binding protein, mdm2, SDO target region #4.  
 XX KW Human; ss; SDO; short double stranded oligonucleotide; cleavage site;  
 KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match 0.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 CCAACATGCTGTACCTAC 340

DB 1 CCAACATGCTGTACCTAC 19

## RESULT 1959

ADO22917  
 ID ADO22917 standard; cDNA; 19 BP.

XX AC ADO22917;  
 XX DT 01-JUL-2004 (first entry)

XX DE Human p53-binding protein, mdm2, SDO target region #1.  
 XX KW Human; ss; SDO; short double stranded oligonucleotide; cleavage site;  
 KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match 0.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 CCAGCTTCGGAACAAGAGA 387

DB 1 CCAGCTTCGGAACAAGAGA 19

## RESULT 1960

ADO23054

ID ADO23054 standard; cDNA; 19 BP.

XX AC ADO23054;  
 XX DT 01-JUL-2004 (first entry)

XX DE Human p53-binding protein, mdm2, SDO target region #5.  
 XX KW Human; ss; SDO; short double stranded oligonucleotide; cleavage site;  
 KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match 0.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1635 CAAGGTCGACCTAAAAATG 1653

DB 1 CAAGGTCGACCTAAAAATG 19

## RESULT 1961

ADO80008  
 ID ADO80008 standard; DNA; 19 BP.

XX AC ADO80008;  
 XX DT 26-AUG-2004 (first entry)

XX DE CENPC1 extend primer #59.  
 XX KW Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPF3;  
 KW CENPC1; SNP; single nucleotide polymorphism; centromere protein C1;

Query Match 0.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGG 2360

DB 1 AAAGTCTGGGATTACAGG 19

## RESULT 1962

ADO61537  
 ID ADO61537 standard; RNA; 19 BP.

XX AC ADO61537;  
 XX DT 09-SEP-2004 (first entry)

XX DE Anti-MDM2 siRNA related DNA sequence SEQ ID NO:1239.  
 XX KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;  
 KW RNA interference.

Query Match 0.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1128 GATGAGGTATATCAAGTTA 1146

DB 1 GATGAGGTATATCAAGTTA 19

## RESULT 1963

ADO61535  
 ID ADO61535 standard; RNA; 19 BP.

XX AC ADO61535;  
 XX DT 09-SEP-2004 (first entry)

XX DE Anti-MDM2 siRNA related DNA sequence SEQ ID NO:1237.

```
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 GGAGATATGTTGTGAAGA 938
Db 1 GGAGATATGTTGTGAAGA 19
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|||||

RESULT 1964
ADQ61536
ID ADQ61536 standard; RNA; 19 BP.
XX
AC ADQ61536;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-MDM2 siRNA related DNA sequence SEQ ID NO:1238.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 CCACAATCTGATGATT 878
Db 1 CCACAATCTGATGATT 19
|||||
|||||

RESULT 1965
ADQ61538
ID ADQ61538 standard; RNA; 19 BP.
XX
AC ADQ61538;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-MDM2 siRNA related DNA sequence SEQ ID NO:1240.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1559 GGAGAAACCCCAAGACAAA 1577
Db 1 GGAGAAACCCCAAGACAAA 19
|||||
|||||

RESULT 1966
ABS59253/c
ID ABS59253 standard; DNA; 20 BP.
XX
AC ABS59253;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CAS gene antisense oligonucleotide, ISIS 128206.
XX
KW Human; ss; antisense; cellular apoptosis susceptibility gene;
KW antiinflammatory; antitumour; cytostatic; CAS; CSB1; CSP;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTCTGGGA 2353
Db 1 GCCTCCCAAGTCTCTGGGA 1
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|||||

RESULT 1967
ABL60514/c
ID ABL60514 standard; DNA; 20 BP.
XX
AC ABL60514;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo primer 6.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 672 TCTGTGAGTGAGAACAGGTG 691
Db 20 TCTGTGAGTGAGAACAGGTG 1
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|||||

RESULT 1968
ABL60513/c
ID ABL60513 standard; DNA; 20 BP.
XX
AC ABL60513;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo primer 5.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 674 TGTGAGTGAGAACAGGTGTC 693
Db 20 TGTGAGTGAGAACAGGTGTC 1
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|||||

RESULT 1969
ABL60512/c
ID ABL60512 standard; DNA; 20 BP.
XX
AC ABL60512;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo primer 4.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 676 TGAGTGAGAACAGGTGTCAC 695
Db 20 TGAGTGAGAACAGGTGTCAC 1
|||||
|||||

RESULT 1970
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ABL60511/c
ID ABL60511 standard; DNA; 20 BP.
XX
AC ABL60511;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo primer 3.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match 0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 677 GAGTGAGACAGGTTGCACC 696
Db 20 GNGTGAGACAGGTTGCACC 1

RESULT 1971
ADD21777/c
ID ADD21777 standard; DNA; 20 BP.
XX
AC ADD21777;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mouse mdm2 antisense oligonucleotide #18.
XX
KW antisense oligonucleotide; mouse; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 TGGATCAGGATTCAGTTTC 1036
Db 20 TGGATCAGGATTCAGTTTC 2

RESULT 1972
ADF47745/c
ID ADF47745 standard; DNA; 20 BP.
XX
AC ADF47745;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human 5-HT7 receptor gene promoter related PCR primer.
XX
KW human; 5-HT7 receptor promoter; barbiturate-inducible element;
KW serotonin mediated response; gastrointestinal; neuroleptic;

Query Match 0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2352 GATTACAGGCATGAGCCAC 2370
Db 19 GATTACAGGCATGAGCCAC 1

RESULT 1973
ADM14508/c
ID ADM14508 standard; DNA; 20 BP.
XX
AC ADM14508;
XX
DT 01-JUL-2004 (first entry)
XX

DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:695.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;

Query Match 0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2336 CCTCCCAAAAGTCTGGGAT 2354
Db 20 CCTCCCAAAAGTCTGGGAT 2

RESULT 1974
ADM15268/c
ID ADM15268 standard; DNA; 20 BP.
XX
AC ADM15268;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1455.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;

Query Match 0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2330 CCTCGGCCTCCCAAGTGC 2348
Db 19 CCTCGGCCTCCCAAGTGC 1

RESULT 1975
AAH38422/c
ID AAH38422 standard; DNA; 22 BP.
XX
AC AAH38422;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific lower PCR primer SEQ ID 1218.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.8%; Score 19; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2234 CACCACACTGGCTAATTTT 2254
Db 22 CACCACACTGGCTAGTTTTT 2

RESULT 1976
ADO47348
ID ADO47348 standard; DNA; 23 BP.
XX
AC ADO47348;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human SORBS1 gene sequencing primer #54.
XX
KW Single nucleotide polymorphism; SNP; human;
KW sorbin and SH3-domain-containing-1 gene; SORBS1; sequence determination;

Query Match 0.8%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+03;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2353 ATTACAGGCATGAGCCACC 2371  
 Db 1 ATTACAGGCATGAGCCACC 19

RESULT 1977  
 AAI66603/c  
 ID AAI66603 standard; DNA; 24 BP.  
 XX  
 AC AAI66603;  
 DT 07-JAN-2002 (first entry)  
 XX  
 DE Human ubiquitin-like protein 13 cDNA specific RT-PCR primer 2.  
 KW Ubiquitin-like protein 13; cytostatic; virucidal; immunomodulatory;  
 KW antinflammatory; cancer; hemopathy; HIV infection; RT-PCR; primer; ss.

Query Match 0.8%; Score 19; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTTGCTCTG 2118  
 Db 23 GAGACCGAGTCTTGCTCTG 5

RESULT 1978  
 AAF24672/c  
 ID - AAF24672 standard; DNA; 25 BP.  
 XX  
 AC AAF24672;  
 DT 20-APR-2001 (first entry)  
 XX  
 DE PCR primer for exon 15 of the human HMG-CoA reductase gene.  
 KW 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene; dyslipidemia;  
 KW HMG-CoA reductase gene; genetic marker; cardiovascular disease;

Query Match 0.8%; Score 19; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2143 TGATCTTGGCTCACTGCAA 2161  
 Db 22 TGATCTTGGCTCACTGCAA 4

RESULT 1979  
 ADB04760  
 ID ADB04760 standard; DNA; 25 BP.  
 XX  
 AC ADB04760;  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human MD27 scanning oligonucleotide SEQ ID 5746.  
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MDZ12; chromosome 7q22.1;

Query Match 0.8%; Score 19; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCC 2292  
 Db 7 GGGTTTACCGTGTAGCC 25

RESULT 1980  
 AAQ82257/c  
 ID AAQ82257 standard; DNA; 22 BP.  
 XX  
 AC AAQ82257;  
 DT 25-MAR-2003 (revised)  
 DT 07-SEP-1995 (first entry)  
 XX  
 DE Chromosome 11 (locus D11S115) STS primer CSRL-4b6-tA.  
 KW sequence sampled mapping; genomic analysis; complex genome mapping;

Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2094 TTTTGTGAGACCGAGTCTTGCT 2115  
 Db 22 TTTTGTGAGACCGAGTCTTGCT 1

RESULT 1981  
 AAT71928/c  
 ID AAT71928 standard; DNA; 22 BP.  
 XX  
 AC AAT71928;  
 DT 18-AUG-1997 (first entry)  
 XX  
 DE Primer detects marker 4072-2 in HH region of chromosome 6p2.1.  
 KW Primer; polymerase chain reaction; amplify; hereditary haemochromatosis;  
 KW HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1;

Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2113 GCTCTGTATCCAGGCTGGAGT 2134  
 Db 22 GCTCTGTATCCAGGCTGGAGT 1

RESULT 1982  
 AAT71925/c  
 ID AAT71925 standard; DNA; 22 BP.  
 XX  
 AC AAT71925;  
 DT 18-AUG-1997 (first entry)  
 XX  
 DE Primer detects marker 3216-1 in HH region of chromosome 6p2.1.  
 KW Primer; polymerase chain reaction; amplify; hereditary haemochromatosis;  
 KW HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1;

Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2113 GCTCTGTATCCAGGCTGGAGT 2134  
 Db 22 GCTCTGTATCCAGGCTGGAGT 1

RESULT 1983  
 AAT72000/c  
 ID AAT72000 standard; DNA; 22 BP.  
 XX  
 AC AAT72000;  
 DT 18-AUG-1997 (first entry)

XX Primer detects marker 4072-2 in HH region of chromosome 6p2.1.  
 XX  
 KW Primer; polymerase chain reaction; amplify; hereditary haemochromatosis;  
 KW HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1,  
 KW  
 Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2113 GCTCTGTTACCCAGGCTGGAGT 2134  
 DB 22 GCTCTATGCCCCAGGCTGGAGT 1

RESULT 1984  
 AAT71997/c  
 ID AAT71997 standard; DNA; 22 BP.  
 XX  
 AC AAT71997;  
 XX  
 DT 18-AUG-1997 (first entry)  
 XX  
 DE Primer detects marker 3216-1 in HH region of chromosome 6p2.1.  
 XX  
 KW Primer; polymerase chain reaction; amplify; hereditary haemochromatosis;  
 KW HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1,  
 KW  
 Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2113 GCTCTGTTACCCAGGCTGGAGT 2134  
 DB 22 GCTCTATGCCCCAGGCTGGAGT 1

RESULT 1985  
 AAZ32938  
 ID AAZ32938 standard; DNA; 22 BP.  
 XX  
 AC AAZ32938;  
 XX  
 DT 09-FEB-2000 (first entry)  
 XX  
 DE Sequence tagged site (STS) 66111.T7 probe forward PCR primer.  
 XX  
 KW MKK4; mitogen activated protein kinase; MAPK; MAPK pathway; mutation;  
 KW somatic; signal transduction; apoptosis; stress; cytokine; induction;  
 KW  
 Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2261 TTTAGTAGACAGGGTTTCAC 2282  
 DB 1 TTTAGTAGAGATGGGGTTTCAC 22

RESULT 1986  
 AAH38401/c  
 ID AAH38401 standard; DNA; 22 BP.  
 XX  
 AC AAH38401;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE SNP specific upper PCR primer SEQ ID 1197.  
 XX  
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW  
 Query Match 0.8%; Score 18.8; DB 1; Length 22;

Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2301 CTCGATCTCTGACCTCGTGAT 2322  
 DB 22 CTCAAACTCTGACCTCGTGAT 1

RESULT 1987  
 AAF62067  
 ID AAF62067 standard; DNA; 22 BP.  
 XX  
 AC AAF62067;  
 XX  
 DT 04-MAY-2001 (first entry)  
 XX  
 DE Reverse PCR primer IL10SR for IL-10 promoter amplification.  
 XX  
 KW Human; immunoreponse; interleukin 10; IL-10; genotype; cancer;  
 KW systemic lupus erythematosus; systemic vasculitis; Fely's syndrome;  
 KW  
 Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2097 TTTGAGACCGAGTCTTGCTCTG 2118  
 DB 1 TTTGAGACAGAGTCTGCTCTG 22

RESULT 1988  
 AAL46346  
 ID AAL46346 standard; DNA; 22 BP.  
 XX  
 AC AAL46346;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human M30 protein coding sequence PCR primer hm30\_nn\_a5.  
 XX  
 KW Neurodegenerative disease; M30; M31; M32; M33; stroke;  
 KW fragile X syndrome; Huntington's disease; Parkinson's disease;  
 KW  
 Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2101 AGACCGAGTCTTGCTCTGTAC 2122  
 DB 1 AGACAGAGTCTTGCTCTGTTC 22

RESULT 1989  
 ACA88980/c  
 ID ACA88980 standard; DNA; 22 BP.  
 XX  
 AC ACA88980;  
 XX  
 DT 08-JUL-2003 (first entry)  
 XX  
 DE Selection and amplification of genetic markers PCR related primer #91.  
 XX  
 KW Genetic marker selection; multiplex PCR amplification;  
 KW prenatal diagnostic testing; foetal sex determination;  
 KW  
 Query Match 0.8%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2096 TTTTGAGACCGAGTCTTGCTCT 2117  
 DB 22 TGTGAGACAGAGTCTTGCTCT 1

```

RESULT 1990
AAH77082
ID AAH77082 standard; DNA; 24 BP.
XX
XX
AC AAH77082;
XX
XX
DT 15-DEC-2001 (first entry)
DE
DE Human vesicular transport-associated protein 9 RT-PCR primer, SEQ ID:4.
XX
XX
KW Human; vesicular transport-associated protein 9; recombinant production;
KW malignant tumour; cancer; blood disease; HIV infection;

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTACCCAGG 2127
Db 3 GAGTCTTGCTCTGTACCCAGG 24

RESULT 1991
AAH91382/c
ID AAH91382 standard; DNA; 24 BP.
XX
XX
AC AAH91382;
XX
XX
DT 09-OCT-2001 (first entry)
DE
DE Human inflammatory bowel disease associated polymorphic site #457.
XX
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGG 2296
Db 23 GGGTTTACCCANGTTGGCCAGG 1

RESULT 1992
ABK49351
ID ABK49351 standard; DNA; 24 BP.
XX
XX
AC ABK49351;
XX
XX
DT 15-JUL-2002 (first entry)
DE
DE RNA polymerase II associated protein 9.57 cDNA RT-PCR primer #2.
XX
XX
KW RNA polymerase II associated protein 9.57; ss; haemopathy; cancer;
KW human immunodeficiency virus; HIV; reverse transcriptase; RT-PCR; primer.

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2107 AGTCTTGCTCTGTACCCAGG 2128
Db 3 AGTCTTGCTCTGTACCCAGG 24

RESULT 1993
ABA04737
ID ABA04737 standard; DNA; 24 BP.
XX
XX
AC ABA04737;
XX
XX

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DT 22-FEB-2002 (first entry)
XX
XX
DE Human alkylation DNA protein cysteine methyltransferase 11 PCR primer #2.
XX
XX
KW Human; alkylation DNA protein cysteine methyltransferase 11; cytostatic;
KW haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy;

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTGTGCTCTGTAGTAGAGA 2271
Db 3 TTTTGTGCTCTGTAGTAGAGA 24

RESULT 1994
ABZ21179
ID ABZ21179 standard; DNA; 24 BP.
XX
XX
AC ABZ21179;
XX
XX
DT 25-MAR-2003 (first entry)
DE
DE Human transformer-2-beta protein 21.89 PCR primer #2.
XX
XX
KW Human; transformer-2-beta protein 21.89; tumour; haemopathy; PCR;
KW HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2107 AGTCTTGCTCTGTACCCAGG 2128
Db 3 AGTCTGCTCTGTGCCCAGG 24

RESULT 1995
ABZ79587
ID ABZ79587 standard; DNA; 24 BP.
XX
XX
AC ABZ79587;
XX
XX
DT 27-JUN-2003 (first entry)
DE
DE Hydrogenase 9.46 related PCR primer #SEQ ID 4.
XX
XX
KW Hydrogenase; 9.46; enzyme; hypertension; peptic ulcer; bronchial asthma;
KW nephrotic syndrome; Parkinson's disease; PCR; primer; ss.

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2267 AGACACAGGGTTTCCCGTGT 2288
Db 1 AGACACAGGGTTTCTCCATGTT 22

RESULT 1996
AAL55813/c
ID AAL55813 standard; DNA; 24 BP.
XX
XX
AC AAL55813;
XX
XX
DT 25-SEP-2003 (first entry)
DE
DE RT-PCR primer 1 to isolate cDNA encoding human fasciclin protein 9_46.
XX
XX
KW Human; fasciclin and elongation protein; 9.46; nervous system; agonist;
KW developmental malformation; primer; RT-PCR; PCR; ss.

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Query Match 0.8%; Score 18.8; DB 1; Length 24;  
Best Local Similarity 90.9%; Pred. No. 2.1e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCACCG 2372  
||||| ||||||| ||||||| |||||||  
Db 24 GGATAACAGGCATGAGCCACTG 3

RESULT 1997  
ADC56863/c  
ID ADC56863 standard; DNA; 24 BP.  
XX AC ADC56863;  
XX 18-DEC-2003 (first entry)  
DT RT-PCR primer Seq ID3 related to human protein 8-91.  
DE RT-PCR primer Seq ID3 related to human protein 8-91.  
XX human; protein 8-91; diabetes; cancer; PCR; primer; RT-PCR;  
KW reverse transcription PCR; ss.

Query Match 0.8%; Score 18.8; DB 1; Length 24;  
Best Local Similarity 90.9%; Pred. No. 2.1e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCACCG 2372  
||||| ||||||| ||||||| |||||||  
Db 24 GGATTACAGGCATGAGCCACTG 3

RESULT 1998  
AAC96023  
ID AAC96023 standard; DNA; 25 BP.  
XX AC AAC96023;  
XX 26-FEB-2001 (first entry)  
DT HLA HLA-C gene PCR primer #35.  
DE DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;

Query Match 0.8%; Score 18.8; DB 1; Length 25;  
Best Local Similarity 90.9%; Pred. No. 2.1e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2046 TTTTCTTCTTAATATGTAT 2067  
||||| ||||||| ||||||| |||||||  
Db 1 TTTTCTTCTTGAATATGTAT 22

RESULT 1999  
AAI65600  
ID AAI65600 standard; DNA; 25 BP.  
XX AC AAI65600;  
XX 03-JAN-2002 (first entry)  
DT Primer for microsatellite marker D16S299, used to localise IBD1.  
DE Human; inflammatory bowel disease 1 protein; IBD1; IBDiprox;  
KW intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;

Query Match 0.8%; Score 18.8; DB 1; Length 25;  
Best Local Similarity 90.9%; Pred. No. 2.1e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGATTACAGCA 2362  
||||| ||||||| ||||||| |||||||  
Db 2 CCAACTGCTGGATTACAGCA 23

RESULT 2000  
ADB04582  
ID ADB04582 standard; DNA; 25 BP.  
XX AC ADB04582;  
XX 20-NOV-2003 (first entry)  
DT Human MDZ7 scanning oligonucleotide SEQ ID 5568.  
DE Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW Query Match 0.8%; Score 18.8; DB 1; Length 25;  
Best Local Similarity 90.9%; Pred. No. 2.1e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2090 TATTTTGTGAGACCGAGTCT 2111  
||||| ||||||| ||||||| |||||||  
Db 1 TTTTGTGAGACCGAGTCT 22

Search completed: January 25, 2005, 16:22:12  
Job time : 113 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 25, 2005, 16:02:10 ; Search time 44 Seconds  
(without alignments)  
3.729 Million cell updates/sec

Title: US-09-966-724B-2-COPY

Perfect score: 2372

Sequence: 1 GCACCGCGGAGTGGCTG.....ATTACAGCATGAGCCACCG 2372

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 1271 seqs, 34589 residues

Total number of hits satisfying chosen parameters: 2542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1104 summaries

Database : rge.db.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86.4	3.6	100	1	AX901508
2	86.4	3.6	100	1	AX902820
3	86.4	3.6	100	1	BD037041
4	86.4	3.6	100	1	BD038353
5	85	3.6	94	1	AR421510
6	85	3.6	94	1	AX982204
7	85	3.6	94	1	BD177063
8	81.2	3.4	94	1	AX912163
9	81.2	3.4	94	1	BD047696
10	80.6	3.4	92	1	AX197468
11	80.6	3.4	94	1	AX197476
12	80.6	3.4	94	1	AX197483
13	80.6	3.4	95	1	AX916923
14	80.6	3.4	95	1	BD052456
15	80.2	3.4	89	1	AY003889
16	80.2	3.4	89	1	AY003892
17	80	3.4	100	1	AX899255
18	80	3.4	100	1	BD034788
19	79	3.3	94	1	AX197487
20	78.4	3.3	90	1	AX911782
21	78.4	3.3	90	1	BD047315
22	78	3.3	86	1	AX903206
23	78	3.3	86	1	BD038739
24	74.2	3.1	92	1	AX197472
25	73	3.1	73	1	BD074010
26	72.8	3.1	76	1	AX901901
27	72.8	3.1	76	1	BD037434
28	71.4	3.0	84	1	AX900729
29	71.4	3.0	84	1	BD036262
30	71	3.0	79	1	AX912245
31	71	3.0	79	1	BD047778
32	70.8	3.0	84	1	AX397063
33	70.2	3.0	92	1	AX899552

34	70.2	3.0	92	1	BD035085
35	66.6	2.8	85	1	AX421270
36	66.6	2.8	85	1	AX981964
37	66.6	2.8	85	1	BD116823
38	65.4	2.8	84	1	AR051521
39	65.4	2.8	84	1	AR072661
40	65.4	2.8	84	1	AR073206
41	62.2	2.6	81	1	AX900153
42	62.2	2.6	81	1	BD035686
43	60	2.5	60	1	CQ542955
44	60	2.5	68	1	AX523103
45	58.4	2.5	68	1	AX523168
46	56.8	2.4	68	1	AX522779
47	56.2	2.4	69	1	AX360697
48	54.4	2.3	65	1	AX901137
49	54.4	2.3	65	1	BD036670
50	52	2.2	60	1	AX523219
51	52	2.2	68	1	AR416502
52	52	2.2	68	1	AX977196
53	52	2.2	68	1	BD112055
54	51.6	2.2	66	1	AF087511
55	51	2.2	68	1	AX899244
56	51	2.2	68	1	BD034777
57	50.2	2.1	64	1	AX903935
58	50.2	2.1	64	1	BD039468
59	50	2.1	63	1	AX322319
60	49.4	2.1	51	1	CQ006684
61	48.4	2.0	51	1	AR444760
62	48	2.0	64	1	HUMUT5223A
63	47.8	2.0	51	1	AX161490
64	47.8	2.0	51	1	AX163313
65	47.8	2.0	51	1	AX163451
66	47.8	2.0	51	1	AX199317
67	47.2	2.0	52	1	AX522922
68	46.8	2.0	51	1	AR444761
69	46.8	2.0	59	1	AX396956
70	46.6	2.0	47	1	AR292147
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72	46.4	2.0	54	1	AX322189
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74	46.2	1.9	51	1	AX161489
75	46.2	1.9	51	1	AX163314
76	46.2	1.9	51	1	AX163452
77	46.2	1.9	51	1	AX164957
78	46.2	1.9	51	1	AX199318
79	45.8	1.9	51	1	AX116665
80	45.8	1.9	57	1	AX917839
81	45.8	1.9	50	1	BD053372
82	45.2	1.9	50	1	AY283614
83	45.2	1.9	51	1	AX160937
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86	44.6	1.9	51	1	AX199153
87	43.6	1.8	51	1	AX160938
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89	43.2	1.8	51	1	AX157145
90	43	1.8	51	1	AR444260
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94	43	1.8	51	1	AX163302
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103	42.2	1.8	51	1	AX163126
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C 192	37.4	1.6	41	1	AX520135	ACCESSION:AX520135
C 193	37.4	1.6	41	1	AX520215	ACCESSION:AX520215
C 194	37.4	1.6	41	1	AX520756	ACCESSION:AX520756
C 195	37.2	1.6	42	1	HUMALUANC	ACCESSION:L36838
C 196	37	1.6	47	1	AX291264	ACCESSION:AX291264
C 197	35.2	1.5	41	1	HUMALUANCA	ACCESSION:L36835
C 198	35.2	1.5	44	1	AX160004	ACCESSION:AX160004
C 199	35	1.5	43	1	HSLAS33	ACCESSION:X91548
C 200	34.8	1.5	41	1	AX516778	ACCESSION:AX516778
C 201	34.8	1.5	41	1	AX518941	ACCESSION:AX518941
C 202	34.2	1.4	35	1	A22672	ACCESSION:A22672
C 203	34.2	1.4	35	1	121796	ACCESSION:121796
C 204	34.2	1.4	39	1	AX709023	ACCESSION:AX709023
C 205	34.2	1.4	41	1	AX541485	ACCESSION:AX541485
C 206	34.2	1.4	41	1	AX520216	ACCESSION:AX520216
C 207	34	1.4	42	1	AX709009	ACCESSION:AX709009
C 208	34	1.4	45	1	CQ760643	ACCESSION:CQ760643
C 209	33.6	1.4	41	1	AX516379	ACCESSION:AX516379
C 210	33.6	1.4	44	1	AX160003	ACCESSION:AX160003
C 211	33.4	1.4	35	1	A25212	ACCESSION:A25212
C 212	33.4	1.4	35	1	E09140	ACCESSION:E09140
C 213	32.6	1.4	40	1	AX183780	ACCESSION:AX183780
C 214	32.6	1.4	41	1	AX514703	ACCESSION:AX514703
C 215	32.6	1.4	41	1	AX520711	ACCESSION:AX520711
C 216	32	1.3	41	1	AX327080	ACCESSION:AX327080
C 217	31.6	1.3	41	1	AX514160	ACCESSION:AX514160
C 218	31.6	1.3	40	1	AX520311	ACCESSION:AX520311
C 219	31	1.3	40	1	AX519117	ACCESSION:AX519117
C 220	31	1.3	41	1	AX513835	ACCESSION:AX513835
C 221	31	1.3	41	1	AX517711	ACCESSION:AX517711
C 222	31	1.3	41	1	AX519988	ACCESSION:AX519988
C 223	31	1.3	41	1	AX520856	ACCESSION:AX520856
C 224	29.8	1.3	33	1	AX709012	ACCESSION:AX709012
C 225	29	1.2	29	1	AX208404	ACCESSION:AX208404
C 226	28.4	1.2	30	1	BD169435	ACCESSION:BD169435
C 227	28.4	1.2	30	1	BD169436	ACCESSION:BD169436
C 228	28	1.2	28	1	AR089907	ACCESSION:AR089907
C 229	28	1.2	28	1	AR089908	ACCESSION:AR089908
C 230	28	1.2	28	1	AR196942	ACCESSION:AR196942
C 231	28	1.2	28	1	AR196943	ACCESSION:AR196943
C 232	28	1.2	28	1	AR208400	ACCESSION:AR208400
C 233	28	1.2	28	1	AR259096	ACCESSION:AR259096
C 234	28	1.2	28	1	AR259097	ACCESSION:AR259097
C 235	27.6	1.2	35	1	AX184110	ACCESSION:AX184110
C 236	27.4	1.2	32	1	A25214	ACCESSION:A25214
C 237	27.4	1.2	32	1	E09142	ACCESSION:E09142
C 238	26	1.1	26	1	AX208402	ACCESSION:AX208402
C 239	26	1.1	26	1	BD138344	ACCESSION:BD138344
C 240	25.8	1.1	30	1	AR214391	ACCESSION:AR214391
C 241	25.4	1.1	32	1	A72114	ACCESSION:A72114
C 242	25.4	1.1	32	1	BD003106	ACCESSION:BD003106
C 243	25	1.1	25	1	AR228262	ACCESSION:AR228262
C 244	25	1.1	25	1	AX116120	ACCESSION:AX116120
C 245	25	1.1	25	1	AX693020	ACCESSION:AX693020
C 246	25	1.1	25	1	AX693021	ACCESSION:AX693021
C 247	25	1.1	25	1	AX693022	ACCESSION:AX693022
C 248	25	1.1	25	1	AX693023	ACCESSION:AX693023
C 249	25	1.1	25	1	AX693024	ACCESSION:AX693024
C 250	25	1.1	25	1	AX693025	ACCESSION:AX693025
C 251	25	1.1	25	1	AX693026	ACCESSION:AX693026
C 252	25	1.1	25	1	AX693027	ACCESSION:AX693027

253	25	1.1	25	1	AX693028	ACCESSION:AX693028	326	21	0.9	21	1	AX800306	ACCESSION:AX800306
254	25	1.1	25	1	AX693029	ACCESSION:AX693029	327	21	0.9	21	1	BD073983	ACCESSION:BD073983
255	25	1.1	25	1	AX693030	ACCESSION:AX693030	328	21	0.9	21	1	BD074005	ACCESSION:BD074005
256	25	1.1	25	1	AX693031	ACCESSION:AX693031	329	21	0.9	21	1	BD138343	ACCESSION:BD138343
257	25	1.1	25	1	AX693032	ACCESSION:AX693032	330	21	0.9	22	1	AX092787	ACCESSION:AX092787
258	25	1.1	25	1	AX693033	ACCESSION:AX693033	331	21	0.9	25	1	AX693016	ACCESSION:AX693016
259	25	1.1	25	1	AX693034	ACCESSION:AX693034	332	20.8	0.9	24	1	CQ828992	ACCESSION:CQ828992
260	25	1.1	25	1	AX693035	ACCESSION:AX693035	333	20.8	0.9	24	1	AX092602	ACCESSION:AX092602
261	25	1.1	25	1	AX693036	ACCESSION:AX693036	334	20.8	0.9	24	1	AX092650	ACCESSION:AX092650
262	25	1.1	25	1	BD138345	ACCESSION:BD138345	335	20.8	0.9	24	1	AX662968	ACCESSION:AX662968
263	24.6	1.0	31	1	AX117259	ACCESSION:AX117259	336	20.8	0.9	24	1	AX975727	ACCESSION:AX975727
264	24.6	1.0	32	1	AX184256	ACCESSION:AX184256	337	20.8	0.9	24	1	AX817219	ACCESSION:AX817219
265	24.4	1.0	27	1	AX117744	ACCESSION:AX117744	338	20.8	0.9	25	1	AX115904	ACCESSION:AX115904
266	24.2	1.0	29	1	AR392160	ACCESSION:AR392160	339	20.8	0.9	25	1	AX116344	ACCESSION:AX116344
267	24.2	1.0	30	1	AR214384	ACCESSION:AR214384	340	20.8	0.9	25	1	AX692917	ACCESSION:AX692917
268	24.2	1.0	30	1	AX184136	ACCESSION:AX184136	341	20.8	0.9	25	1	AX692918	ACCESSION:AX692918
269	24	1.0	24	1	E40923	ACCESSION:E40923	342	20.8	0.9	25	1	AX692920	ACCESSION:AX692920
270	24	1.0	24	1	E40925	ACCESSION:E40925	343	20.8	0.9	25	1	AX692923	ACCESSION:AX692923
271	24	1.0	25	1	AX693019	ACCESSION:AX693019	344	20.8	0.9	25	1	AX692927	ACCESSION:AX692927
272	24	1.0	25	1	AX693037	ACCESSION:AX693037	345	20.8	0.9	25	1	AX692929	ACCESSION:AX692929
273	24	1.0	27	1	A72116	ACCESSION:A72116	346	20.8	0.9	25	1	AX692990	ACCESSION:AX692990
274	24	1.0	27	1	BD003108	ACCESSION:BD003108	347	20.8	0.9	25	1	AX692994	ACCESSION:AX692994
275	23.6	1.0	30	1	A68624	ACCESSION:A68624	348	20.8	0.9	25	1	AX692996	ACCESSION:AX692996
276	23.4	1.0	25	1	AX118472	ACCESSION:AX118472	349	20.8	0.9	25	1	AX692998	ACCESSION:AX692998
277	23.4	1.0	25	1	AX548255	ACCESSION:AX548255	350	20.8	0.9	27	1	AR381743	ACCESSION:AR381743
278	23.4	1.0	25	1	AX922581	ACCESSION:AX922581	351	20.8	0.9	27	1	AX116940	ACCESSION:AX116940
279	23.4	1.0	27	1	AX118000	ACCESSION:AX118000	352	20.8	0.9	27	1	AX183893	ACCESSION:AX183893
280	23.2	1.0	30	1	AX118407	ACCESSION:AX118407	353	20.6	0.9	21	1	AX095325	ACCESSION:AX095325
281	23	1.0	23	1	CQ766174	ACCESSION:CQ766174	354	20.6	0.9	27	1	AX709011	ACCESSION:AX709011
282	23	1.0	23	1	AR300897	ACCESSION:AR300897	355	20.4	0.9	22	1	E50641	ACCESSION:E50641
283	23	1.0	23	1	AR361046	ACCESSION:AR361046	356	20.4	0.9	22	1	AR242944	ACCESSION:AR242944
284	23	1.0	25	1	AX693018	ACCESSION:AX693018	357	20.4	0.9	22	1	AR242948	ACCESSION:AR242948
285	22.8	1.0	26	1	AR089946	ACCESSION:AR089946	358	20.4	0.9	22	1	AR393735	ACCESSION:AR393735
286	22.8	1.0	26	1	AR196981	ACCESSION:AR196981	359	20.4	0.9	22	1	AX384996	ACCESSION:AX384996
287	22.8	1.0	26	1	AR259135	ACCESSION:AR259135	360	20.4	0.9	22	1	AX385000	ACCESSION:AX385000
288	22.8	1.0	27	1	AX116952	ACCESSION:AX116952	361	20.4	0.9	22	1	AX674898	ACCESSION:AX674898
289	22.8	1.0	27	1	AX118160	ACCESSION:AX118160	362	20.4	0.9	22	1	AX674899	ACCESSION:AX674899
290	22.8	1.0	30	1	AX116662	ACCESSION:AX116662	363	20.2	0.9	25	1	AX115271	ACCESSION:AX115271
291	22.6	1.0	30	1	AR051440	ACCESSION:AR051440	364	20.2	0.9	25	1	AX115532	ACCESSION:AX115532
292	22.6	1.0	30	1	AR072580	ACCESSION:AR072580	365	20.2	0.9	25	1	AX116096	ACCESSION:AX116096
293	22.6	1.0	30	1	AR073125	ACCESSION:AR073125	366	20.2	0.9	25	1	AX116664	ACCESSION:AX116664
294	22.4	0.9	24	1	AX092647	ACCESSION:AX092647	367	20.2	0.9	25	1	AX117740	ACCESSION:AX117740
295	22.4	0.9	25	1	AR322085	ACCESSION:AR322085	368	20.2	0.9	25	1	AX118236	ACCESSION:AX118236
296	22.4	0.9	29	1	AX184030	ACCESSION:AX184030	369	20.2	0.9	25	1	AX692832	ACCESSION:AX692832
297	22	0.9	22	1	AR044033	ACCESSION:AR044033	370	20.2	0.9	25	1	AX692833	ACCESSION:AX692833
298	22	0.9	22	1	AR208403	ACCESSION:AR208403	371	20.2	0.9	25	1	AX692838	ACCESSION:AX692838
299	22	0.9	22	1	AR300896	ACCESSION:AR300896	372	20.2	0.9	25	1	AX692839	ACCESSION:AX692839
300	22	0.9	22	1	AR361045	ACCESSION:AR361045	373	20.2	0.9	25	1	AX692919	ACCESSION:AX692919
301	22	0.9	22	1	AR393736	ACCESSION:AR393736	374	20.2	0.9	25	1	AX692924	ACCESSION:AX692924
302	22	0.9	25	1	AX693017	ACCESSION:AX693017	375	20.2	0.9	25	1	AX692925	ACCESSION:AX692925
303	21.8	0.9	25	1	E50643	ACCESSION:E50643	376	20.2	0.9	25	1	AX692926	ACCESSION:AX692926
304	21.8	0.9	25	1	AX614112	ACCESSION:AX614112	377	20.2	0.9	25	1	AX692930	ACCESSION:AX692930
305	21.8	0.9	25	1	AX692921	ACCESSION:AX692921	378	20.2	0.9	25	1	AX692995	ACCESSION:AX692995
306	21.8	0.9	25	1	AX692922	ACCESSION:AX692922	379	20.2	0.9	25	1	AX692999	ACCESSION:AX692999
307	21.8	0.9	25	1	AX692928	ACCESSION:AX692928	380	20.2	0.9	25	1	AX693000	ACCESSION:AX693000
308	21.8	0.9	25	1	AX692991	ACCESSION:AX692991	381	20.2	0.9	26	1	AX183618	ACCESSION:AX183618
309	21.8	0.9	25	1	AX692992	ACCESSION:AX692992	382	20.2	0.9	26	1	AX183704	ACCESSION:AX183704
310	21.8	0.9	25	1	AX692993	ACCESSION:AX692993	383	20	0.8	20	1	AX154586	ACCESSION:AX154586
311	21.8	0.9	25	1	AX692997	ACCESSION:AX692997	384	20	0.8	20	1	AX154587	ACCESSION:AX154587
312	21.8	0.9	27	1	AX184125	ACCESSION:AX184125	385	20	0.8	20	1	AX154588	ACCESSION:AX154588
313	21.6	0.9	28	1	A49272	ACCESSION:A49272	386	20	0.8	20	1	AX154589	ACCESSION:AX154589
314	21.6	0.9	28	1	AR122136	ACCESSION:AR122136	387	20	0.8	20	1	AR154590	ACCESSION:AR154590
315	21.4	0.9	23	1	AR345149	ACCESSION:AR345149	388	20	0.8	20	1	AR154591	ACCESSION:AR154591
316	21.4	0.9	23	1	AX823487	ACCESSION:AX823487	389	20	0.8	20	1	AR154592	ACCESSION:AR154592
317	21.4	0.9	25	1	AR2465	ACCESSION:AR2465	390	20	0.8	20	1	AR154593	ACCESSION:AR154593
318	21.4	0.9	25	1	AX360029	ACCESSION:AX360029	391	20	0.8	20	1	AR154594	ACCESSION:AR154594
319	21.4	0.9	25	1	BD124526	ACCESSION:BD124526	392	20	0.8	20	1	AR154595	ACCESSION:AR154595
320	21.2	0.9	27	1	AX115732	ACCESSION:AX115732	393	20	0.8	20	1	AR154596	ACCESSION:AR154596
321	21.2	0.9	27	1	AX117196	ACCESSION:AX117196	394	20	0.8	20	1	AR154597	ACCESSION:AR154597
322	21.2	0.9	27	1	AX118476	ACCESSION:AX118476	395	20	0.8	20	1	AR154598	ACCESSION:AR154598
323	21	0.9	21	1	AR208405	ACCESSION:AR208405	396	20	0.8	20	1	AR154599	ACCESSION:AR154599
324	21	0.9	21	1	AX117999	ACCESSION:AX117999	397	20	0.8	20	1	AR154600	ACCESSION:AR154600
325	21	0.9	21	1	AX190635	ACCESSION:AX190635	398	20	0.8	20	1	AR154601	ACCESSION:AR154601

C 399	20	0.8	20	1	BD138083	ACCESSION: BD138083
C 400	20	0.8	20	1	BD138084	ACCESSION: BD138084
C 401	20	0.8	20	1	BD138085	ACCESSION: BD138085
C 402	20	0.8	20	1	BD138086	ACCESSION: BD138086
C 403	20	0.8	20	1	BD138087	ACCESSION: BD138087
C 404	20	0.8	20	1	BD138088	ACCESSION: BD138088
C 405	20	0.8	20	1	BD138089	ACCESSION: BD138089
C 406	20	0.8	20	1	BD138090	ACCESSION: BD138090
C 407	20	0.8	20	1	BD138091	ACCESSION: BD138091
C 408	20	0.8	20	1	BD138092	ACCESSION: BD138092
C 409	20	0.8	20	1	BD138093	ACCESSION: BD138093
C 410	20	0.8	20	1	BD138094	ACCESSION: BD138094
C 411	20	0.8	20	1	BD138095	ACCESSION: BD138095
C 412	20	0.8	20	1	BD138096	ACCESSION: BD138096
C 413	20	0.8	20	1	BD138097	ACCESSION: BD138097
C 414	20	0.8	20	1	BD138107	ACCESSION: BD138107
C 415	20	0.8	20	1	BD138108	ACCESSION: BD138108
C 416	20	0.8	20	1	BD138109	ACCESSION: BD138109
C 417	20	0.8	20	1	BD138110	ACCESSION: BD138110
C 418	20	0.8	20	1	BD138111	ACCESSION: BD138111
C 419	20	0.8	20	1	BD138112	ACCESSION: BD138112
C 420	20	0.8	20	1	BD138113	ACCESSION: BD138113
C 421	20	0.8	20	1	BD138114	ACCESSION: BD138114
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C 423	20	0.8	20	1	BD138116	ACCESSION: BD138116
C 424	20	0.8	20	1	BD138117	ACCESSION: BD138117
C 425	20	0.8	20	1	BD138118	ACCESSION: BD138118
C 426	20	0.8	20	1	BD138119	ACCESSION: BD138119
C 427	20	0.8	20	1	BD138120	ACCESSION: BD138120
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C 429	20	0.8	20	1	BD138122	ACCESSION: BD138122
C 430	20	0.8	20	1	BD138123	ACCESSION: BD138123
C 431	20	0.8	20	1	BD138124	ACCESSION: BD138124
C 432	20	0.8	20	1	BD138125	ACCESSION: BD138125
C 433	20	0.8	20	1	BD138126	ACCESSION: BD138126
C 434	20	0.8	20	1	BD138127	ACCESSION: BD138127
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C 437	20	0.8	20	1	BD138130	ACCESSION: BD138130
C 438	20	0.8	20	1	BD138131	ACCESSION: BD138131
C 439	20	0.8	20	1	BD138132	ACCESSION: BD138132
C 440	20	0.8	20	1	BD138133	ACCESSION: BD138133
C 441	20	0.8	20	1	BD138134	ACCESSION: BD138134
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C 444	20	0.8	20	1	BD138137	ACCESSION: BD138137
C 445	20	0.8	20	1	BD138138	ACCESSION: BD138138
C 446	20	0.8	20	1	BD138139	ACCESSION: BD138139
C 447	20	0.8	20	1	BD138140	ACCESSION: BD138140
C 448	20	0.8	20	1	BD138141	ACCESSION: BD138141
C 449	20	0.8	20	1	BD138142	ACCESSION: BD138142
C 450	20	0.8	20	1	BD138143	ACCESSION: BD138143
C 451	20	0.8	20	1	BD138144	ACCESSION: BD138144
C 452	20	0.8	20	1	BD138145	ACCESSION: BD138145
C 453	20	0.8	20	1	BD138146	ACCESSION: BD138146
C 454	20	0.8	20	1	BD138147	ACCESSION: BD138147
C 455	20	0.8	20	1	BD138148	ACCESSION: BD138148
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C 457	20	0.8	20	1	BD138150	ACCESSION: BD138150
C 458	20	0.8	20	1	BD138151	ACCESSION: BD138151
C 459	20	0.8	20	1	BD138152	ACCESSION: BD138152
C 460	20	0.8	20	1	BD138153	ACCESSION: BD138153
C 461	20	0.8	20	1	BD138154	ACCESSION: BD138154
C 462	20	0.8	20	1	BD138155	ACCESSION: BD138155
C 463	20	0.8	20	1	BD138156	ACCESSION: BD138156
C 464	20	0.8	20	1	BD138157	ACCESSION: BD138157
C 465	20	0.8	20	1	BD138158	ACCESSION: BD138158
C 466	20	0.8	20	1	BD138159	ACCESSION: BD138159
C 467	20	0.8	20	1	BD138160	ACCESSION: BD138160
C 468	20	0.8	20	1	BD138161	ACCESSION: BD138161
C 469	20	0.8	20	1	BD138162	ACCESSION: BD138162
C 470	20	0.8	20	1	BD138163	ACCESSION: BD138163
C 471	20	0.8	20	1	BD138164	ACCESSION: BD138164



C 691	20	0.8	20	1	BD138311	ACCESSION:BD138311	764	19.2	0.8	25	1	AX693001
C 692	20	0.8	20	1	BD138312	ACCESSION:BD138312	C 765	19	0.8	19	1	CQ760565
C 693	20	0.8	20	1	BD138313	ACCESSION:BD138313	C 766	19	0.8	19	1	CQ760691
C 694	20	0.8	20	1	BD138314	ACCESSION:BD138314	767	19	0.8	19	1	IS2002
C 695	20	0.8	20	1	BD138315	ACCESSION:BD138315	768	19	0.8	19	1	I72210
C 696	20	0.8	20	1	BD138316	ACCESSION:BD138316	769	19	0.8	19	1	AX115894
C 697	20	0.8	20	1	BD138317	ACCESSION:BD138317	770	19	0.8	19	1	AX116350
C 698	20	0.8	20	1	BD138318	ACCESSION:BD138318	C 771	19	0.8	19	1	BD089274
C 699	20	0.8	20	1	BD138319	ACCESSION:BD138319	C 772	19	0.8	20	1	AX116725
C 700	20	0.8	20	1	BD138320	ACCESSION:BD138320	C 773	19	0.8	20	1	I8275
C 701	20	0.8	20	1	BD138321	ACCESSION:BD138321	C 774	19	0.8	20	1	AR208407
C 702	20	0.8	20	1	BD138322	ACCESSION:BD138322	C 775	19	0.8	20	1	AR208408
C 703	20	0.8	20	1	BD138323	ACCESSION:BD138323	C 776	19	0.8	20	1	AR208409
C 704	20	0.8	20	1	BD138324	ACCESSION:BD138324	C 777	19	0.8	20	1	AR208410
C 705	20	0.8	20	1	BD138325	ACCESSION:BD138325	C 778	19	0.8	20	1	AR224472
C 706	20	0.8	20	1	BD138326	ACCESSION:BD138326	C 779	19	0.8	22	1	AX116095
C 707	20	0.8	20	1	BD138327	ACCESSION:BD138327	C 780	19	0.8	25	1	AX060516
C 708	20	0.8	20	1	BD138328	ACCESSION:BD138328	C 781	19	0.8	25	1	AX693014
C 709	20	0.8	20	1	BD138329	ACCESSION:BD138329	C 782	18.8	0.8	22	1	AR066909
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C 752	19.4	0.8	22	1	BD183598	ACCESSION:BD183598	826	18.4	0.8	22	1	E31636
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DEFINITION Sequence 18683 from Patent EP1033401.  
ACCESSION AX902820  
VERSION AX902820.1 GI:40057777  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
1  
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.  
TITLE Expressed sequence tags and encoded human proteins  
JOURNAL Patent: EP 1033401-A 18683 06-SEP-2000;  
Genset (FR)

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DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD037041  
VERSION BD037041.1 GI:22578783  
KEYWORDS JP 2001269182-A/13287.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
1  
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.  
TITLE Sequence tag and encoded human protein  
JOURNAL Patent: JP 2001269182-A 13287 02-OCT-2001;  
GENSET

OS Homo sapiens (human)  
PN JP 2001269182-A/13287  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES

PI JORDAN  
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC  
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CC

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Query Match  
Best Local Similarity 93.8%; Score 86.4; DB 1; Length 100;  
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 3 CCACATGCCCGCTAATTTTGTATTTTAGTAGACAGGGTTTCACAGTGTAGCC 62

QY 2293 AGGATGCTCTCGATCTCTGACCTCGTGATCCGCC 2328  
DB 63 AGGATGCTCTGATCTCTGACCTCGTGATCCGCC 98

RESULT 4  
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LOCUS BD038353 100 bp DNA linear PAT 27-AUG-2002  
DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD038353  
VERSION BD038353.1 GI:22580095  
KEYWORDS JP 2001269182-A/14599.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
1 (bases 1 to 100)  
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.  
TITLE Sequence tag and encoded human protein  
JOURNAL Patent: JP 2001269182-A 14599 02-OCT-2001;  
GENSET

OS Homo sapiens (human)  
PN JP 2001269182-A/14599  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES  
PI JORDAN  
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC  
G06F15/40  
CC

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match  
Best Local Similarity 93.8%; Score 86.4; DB 1; Length 100;  
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2233 CCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCC 2292  
DB 3 CCACATGCCCGCTAATTTTGTATTTTAGTAGACAGGGTTTCACAGTGTAGCC 62

QY 2293 AGGATGCTCTCGATCTCTGACCTCGTGATCCGCC 2328  
DB 63 AGGATGCTCTGATCTCTGACCTCGTGATCCGCC 98

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RESULT 5
AR421510/c
LOCUS AR421510 linear PAT 18-DEC-2003
DEFINITION Sequence 13007 from patent US 6639063.
ACCESSION AR421510
VERSION AR421510.1 GI:40176620
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 94)
AUTHORS Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 13007 28-OCT-2003;
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1..94
/organism="unknown"
/mol_type="genomic DNA"

Query Match 3.6%; Score 85; DB 1; Length 94;
Best Local Similarity 94.6%; Pred. No. 1.3;
Matches 88; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
94 TAGTAGAGACGGGTTTCATCGTGTAGCCAGGATGGTCTTGATCTCTGACCTCATGAT 35

QY 2323 CCGCCACCTCGGCTCCCAAGTCTGGGATT 2355
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
34 CCACCCACCTCGGCTCCCAAGTCTGGGATT 2

RESULT 6
AX982204/c
LOCUS AX982204 linear PAT 15-JAN-2004
DEFINITION Sequence 13007 from Patent EP1104808.
ACCESSION AX982204
VERSION AX982204.1 GI:40988344
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 94)
AUTHORS Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 13007 06-JUN-2001;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.6%; Score 85; DB 1; Length 94;
Best Local Similarity 94.6%; Pred. No. 1.3;
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Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
94 TAGTAGAGACGGGTTTCATCGTGTAGCCAGGATGGTCTTGATCTCTGACCTCATGAT 35

QY 2323 CCGCCACCTCGGCTCCCAAGTCTGGGATT 2355
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
34 CCACCCACCTCGGCTCCCAAGTCTGGGATT 2

RESULT 7
BD117063/c
LOCUS BD117063 linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD117063

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VERSION BD117063.1 GI:23211967
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 94)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 9140 15-JAN-2002;
COMMENT
OS Homo sapiens (human)
PN JP 2002010789-A/9140
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source 1..94
/organism="Homo sapiens (human)"
/organism="Homo sapiens"
/db_xref="taxon:9606"

Query Match 3.6%; Score 85; DB 1; Length 94;
Best Local Similarity 94.6%; Pred. No. 1.3;
Matches 88; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
94 TAGTAGAGACGGGTTTCATCGTGTAGCCAGGATGGTCTTGATCTCTGACCTCATGAT 35

QY 2323 CCGCCACCTCGGCTCCCAAGTCTGGGATT 2355
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
34 CCACCCACCTCGGCTCCCAAGTCTGGGATT 2

RESULT 8
AX912163
LOCUS AX912163 94 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 28026 from Patent EP1033401.
ACCESSION AX912163
VERSION AX912163.1 GI:40205952
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 28026 06-SEP-2000;
Genset (FR)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 81.2; DB 1; Length 94;
Best Local Similarity 91.5%; Pred. No. 2.1;
Matches 86; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322
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Db 1 TAGTAGAGACGAGGTTTCACCGAATTAGCCAGGATGCTCTCGATCTCTGACCTTGTGAT 60
QY 2323 CCGCCACCTCGGCCTCCCAAAGTCTGGGATTA 2356
Db 61 CTGCGCGCTTGGCCTCCCAAAGTCTGGGATTA 94

RESULT 9
BD047696
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/23942
PD 02-OCT-2001
PR 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
PC C12N1/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,PC
G06F15/40
CC
FH Key Location/Qualifiers.
FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 81.2; DB 1; Length 94;
Best Local Similarity 91.5%; Pred. No. 2.1;
Matches 86; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACGAGGTTTCACCGAATTAGCCAGGATGCTCTCGATCTCTGACCTTGTGAT 2322
Db 1 TAGTAGAGACGAGGTTTCACCGAATTAGCCAGGATGCTCTCGATCTCTGACCTTGTGAT 60

QY 2323 CCGCCACCTCGGCCTCCCAAAGTCTGGGATTA 2356
Db 61 CTGCGCGCTTGGCCTCCCAAAGTCTGGGATTA 94

RESULT 10
AX197468/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..94
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80.6; DB 1; Length 94;
Best Local Similarity 95.4%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 2345
Db 94 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 35

QY 2346 TGTCTGGATTACAGGCATGAGCCACCG 2372
Db 34 TGTCTGGATTACAGGCATGAGCCACCG 8

RESULT 12
AX197483
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..94
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80.6; DB 1; Length 94;
Best Local Similarity 95.4%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 2345
Db 94 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 35

QY 2346 TGTCTGGATTACAGGCATGAGCCACCG 2372
Db 34 TGTCTGGATTACAGGCATGAGCCACCG 8
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80.6; DB 1; Length 92;
Best Local Similarity 95.4%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 2345
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QY 2346 TGTCTGGATTACAGGCATGAGCCACCG 2372
Db 32 TGTCTGGATTACAGGCATGAGCCACCG 6

RESULT 11
AX197476/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..94
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80.6; DB 1; Length 94;
Best Local Similarity 95.4%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 2345
Db 94 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 35

QY 2346 TGTCTGGATTACAGGCATGAGCCACCG 2372
Db 34 TGTCTGGATTACAGGCATGAGCCACCG 8

RESULT 12
AX197483
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..94
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80.6; DB 1; Length 94;
Best Local Similarity 95.4%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 2345
Db 94 GTTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGCGCTCCCAAAG 35

QY 2346 TGTCTGGATTACAGGCATGAGCCACCG 2372
Db 34 TGTCTGGATTACAGGCATGAGCCACCG 8
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 3.4%; Score 80.6; DB 1; Length 94;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGCTCGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAAAG 2345
Db 1 GTTAGCCAGGATGCTCGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAAAG 60

QY 2346 TGCTGGATTACAGGCATGAGCCACCG 2372
Db 61 TGCTGGATTACAGGCATGAGCCACCG 87

RESULT 13
AX916923
LOCUS AX916923 95 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 32786 from Patent EP1033401.
ACCESSION AX916923
VERSION AX916923.1 GI:40210712
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 32786 06-SEP-2000;
Genet (FR)

FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 3.4%; Score 80.6; DB 1; Length 95;
Matches 86; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2264 AGTAGACACAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
Db 1 AGTAGACACAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTTGATC 60

QY 2324 CGCCACCTCGGCTCCCAAAGTCTGGGATTACA 2358
Db 61 CGCTGCTTGATCTCTGAGTCTGGGATTACA 95

RESULT 15
AY003889
LOCUS AY003889 89 bp DNA linear PRI 01-APR-2004
DEFINITION Homo sapiens clone C317, HTLV-1 integration site flanking region.
ACCESSION AY003889
VERSION AY003889.1 GI:9438211
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 89)
Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
Common human T cell leukemia virus type 1 (HTLV-1) integration
sites in cerebrospinal fluid and blood lymphocytes of patients with
HTLV-1-associated myelopathy/tropical spastic paraparesis indicate
that HTLV-1 crosses the blood-brain barrier via clonal
HTLV-1-infected cells
J. Infect. Dis. 182 (4), 1044-1050 (2000)

JOURNAL MEDLINE
20435894
REFERENCE PUBMED 10979898
AUTHORS 2 (bases 1 to 89)
Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
TITLE Direct Submission
Submitted (26-JUN-2000) Unite d'Oncogenese Virale, Centre Leon
Berard, Lyon, France

FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
misc_feature 1..89
/note="downstream of HTLV-1 integration site"

Query Match
Best Local Similarity 3.4%; Score 80.2; DB 1; Length 89;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2278 TTCCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCC 2337
Db 1 TTCCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCC 60

QY 2338 TCCCAAAGTCTGGGATTACAGGCA 2362
Db 61 TCCCAAAGTCTGGGATTACAGGCA 85

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PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
CC G06F15/40
FH Key Location/Qualifiers.
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source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 3.4%; Score 80.6; DB 1; Length 95;
Matches 86; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2264 AGTAGACACAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
Db 1 AGTAGACACAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTTGATC 60

QY 2324 CGCCACCTCGGCTCCCAAAGTCTGGGATTACA 2358
Db 61 CGCTGCTTGATCTCTGAGTCTGGGATTACA 95

RESULT 15
AY003889
LOCUS AY003889 89 bp DNA linear PRI 01-APR-2004
DEFINITION Homo sapiens clone C317, HTLV-1 integration site flanking region.
ACCESSION AY003889
VERSION AY003889.1 GI:9438211
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 89)
Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
Common human T cell leukemia virus type 1 (HTLV-1) integration
sites in cerebrospinal fluid and blood lymphocytes of patients with
HTLV-1-associated myelopathy/tropical spastic paraparesis indicate
that HTLV-1 crosses the blood-brain barrier via clonal
HTLV-1-infected cells
J. Infect. Dis. 182 (4), 1044-1050 (2000)

JOURNAL MEDLINE
20435894
REFERENCE PUBMED 10979898
AUTHORS 2 (bases 1 to 89)
Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
TITLE Direct Submission
Submitted (26-JUN-2000) Unite d'Oncogenese Virale, Centre Leon
Berard, Lyon, France

FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
misc_feature 1..89
/note="downstream of HTLV-1 integration site"

Query Match
Best Local Similarity 3.4%; Score 80.2; DB 1; Length 89;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2278 TTCCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCC 2337
Db 1 TTCCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCC 60

QY 2338 TCCCAAAGTCTGGGATTACAGGCA 2362
Db 61 TCCCAAAGTCTGGGATTACAGGCA 85

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RESULT 16
AY003892
LOCUS AY003892 89 bp DNA linear PRI 01-APR-2004
DEFINITION Homo sapiens clone C307, HTLV-1 integration site flanking region.
ACCESSION AY003892
VERSION AY003892.1 GI:9438214
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
TITLE Common human T cell leukemia virus type 1 (HTLV-1) integration
sites in cerebrospinal fluid and blood lymphocytes of patients with
HTLV-1-associated myelopathy/tropical spastic paraparesis indicate
that HTLV-1 crosses the blood-brain barrier via clonal
HTLV-1-infected cells
JOURNAL J. Infect. Dis. 182 (4), 1044-1050 (2000)
MEDLINE 20435894
PUBMED 10979898
REFERENCE
AUTHORS Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-2000) Unite d'Oncogenese Virale, Centre Leon
Berard, Lyon, France
FEATURES
source Location/Qualifiers
1..89
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="C307"
misc_feature 1..89
/notes="downstream of HTLV-1 integration site"

Query Match 3.4%; Score 80.2; DB 1; Length 89;
Best Local Similarity 96.5%; Pred. No. 2.2;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2278 TTCCCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTATCGGCCACTCGGCC 2337
Db 1 TTCCCGTGTAGCCAGGATGGTCTCTGATCTCTGACCTCGTATCGGCCACTCGGCC 60
QY 2338 TCCCAAAGTCTGGATTACAGCA 2362
Db 61 TCCCAAAGTCTGGATTACAGCA 85

RESULT 17
AX899255/c
LOCUS AX899255 100 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 15118 from Patent EP1033401.
ACCESSION AX899255
VERSION AX899255.1 GI:40054168
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 15118 06-SEP-2000;
Genset (FR)
FEATURES
source Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80; DB 1; Length 100;

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Best Local Similarity 89.6%; Pred. No. 2.4;
Matches 86; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2250 TTTTGTACTTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 2309
Db 96 TTTTGTACTTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 37
QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAG 2345
Db 36 CTGACCTCGTGATCCATCCACCTCGGCCTCCCAAAG 1

RESULT 18
BD034788/c
LOCUS BD034788 100 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD034788
VERSION BD034788.1 GI:22576530
KEYWORDS JP 2001269182-A/11034.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 11034 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/11034
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers
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source Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80; DB 1; Length 100;
Best Local Similarity 89.6%; Pred. No. 2.4;
Matches 86; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2250 TTTTGTACTTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 2309
Db 96 TTTTGTACTTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 37
QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAG 2345
Db 36 CTGACCTCGTGATCCATCCACCTCGGCCTCCCAAAG 1

RESULT 19
AX197487
LOCUS AX197487 94 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 52 from Patent WO0151632.
ACCESSION AX197487
VERSION AX197487.1 GI:15387847
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Padigar,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,

```

spytex,K.A. and Li,L.  
Odorant receptor polypeptides and nucleic acids encoding same  
Patent: WO 0151632-A S2 19-JUL-2001;  
Curagen Corporation (US)  
Location/Qualifiers  
source  
1. .94  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 3.3%; Score 79; DB 1; Length 94;  
Best Local Similarity 94.3%; Pred. No. 2.6;  
Matches 82; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAG 2345  
|||||  
Db 1 GTTAGCCAGGATGCTCAATCTCTGACCTCGTGATCCGCCCTGGCCTCCCAAAG 60  
|||||

QY 2346 TGCTGGGATTACAGCGATGAGCCACG 2372  
|||||  
Db 61 TGCTGGGATTACAGCGATGAGCCACTG 87  
|||||

RESULT 20  
AX911782/c  
LOCUS AX911782 90 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 27645 from Patent EP1033401.  
ACCESSION AX911782  
VERSION AX911782.1 GI:40205571  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.  
Expressed sequence tags and encoded human proteins  
Patent: EP 1033401-A 27645 06-SEP-2000;  
Genset (FR)

FEATURES  
source  
1. .90  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 3.3%; Score 78.4; DB 1; Length 90;  
Best Local Similarity 91.1%; Pred. No. 2.8;  
Matches 82; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2250 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 2309  
|||||  
Db 90 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 31  
|||||

QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
|||||  
Db 30 CTGACCTCGTGATCCGCCACCTCGGCCTC 1  
|||||

RESULT 21  
BD047315/c  
LOCUS BD047315 90 bp DNA linear PAT 27-AUG-2002  
DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD047315  
VERSION BD047315.1 GI:22589057  
KEYWORDS JP 2001269182-A/23561.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 90)  
Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.  
Sequence tag and encoded human protein  
Patent: JP 2001269182-A 23561 02-OCT-2001;

GENSET  
OS Homo sapiens (human)  
PN JP 2001269182-A/23561  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES  
PJ JORDAN  
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC  
C12N5/10,  
PC C12P21/02,C13P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC  
G06F15/40

CC  
FH Key Location/Qualifiers  
1. .90  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

FEATURES  
source  
1. .90  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 3.3%; Score 78.4; DB 1; Length 90;  
Best Local Similarity 91.1%; Pred. No. 2.8;  
Matches 82; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2250 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 2309  
|||||  
Db 90 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 31  
|||||

QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCTC 2339  
|||||  
Db 30 CTGACCTCGTGATCCGCCACCTCGGCCTC 1  
|||||

RESULT 22  
AX903206/c  
LOCUS AX903206 86 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 19069 from Patent EP1033401.  
ACCESSION AX903206  
VERSION AX903206.1 GI:40058163  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.  
Expressed sequence tags and encoded human proteins  
Patent: EP 1033401-A 19069 06-SEP-2000;  
Genset (FR)

FEATURES  
source  
1. .86  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 3.3%; Score 78; DB 1; Length 86;  
Best Local Similarity 94.2%; Pred. No. 2.8;  
Matches 81; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2260 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 2319  
|||||  
Db 86 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTC 27  
|||||

QY 2320 GATCGCCACCTCGGCCTCCCAAAG 2345  
|||||  
Db 26 GATCGCCACCTCGGCCTCCCAAAG 1  
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RESULT 23  
BD038739/c  
LOCUS BD038739 86 bp DNA linear PAT 27-AUG-2002  
DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD038739

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VERSION BD038739.1 GI:22580481
KEYWORDS JP 2001269182-A/14985.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 14985 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/14985
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers.
FEATURES
source 1..86 Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 3.3%; Score 78; DB 1; Length 86;
Best Local Similarity 94.2%; Pred. No. 2.8;
Matches 81; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2260 TTTTGTAGACAGAGGGTTTACCGTTGTAGCAGGATGGTCTCGATCTCCTGACCTCGT 2319
Db TTTTGTAGACAGAGGGTTTACCGTTGTAGCAGGATGGTCTCGATCTCCTGACCTCGT 27
QY 2320 GATCCGCCACCTCGGCTCCCAAAG 2345
Db TTTTGTAGACAGAGGGTTTACCGTTGTAGCAGGATGGTCTCGATCTCCTGACCTCGT 27
GATCCGCCACCTCGGCTCCCAAAG 1
RESULT 24
AX197472/c
LOCUS 92 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 37 from Patent WO0151632.
ACCESSION AX197472
VERSION AX197472.1 GI:15387842
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Padigaru,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,
Spytek,K.A. and Li,L.
TITLE Odorant receptor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0151632-A 37 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..92 Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 3.1%; Score 74.2; DB 1; Length 92;
Best Local Similarity 90.8%; Pred. No. 4.5;
Matches 79; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2286 GTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGTATCGGCCACCTCGGCTCCCAAAG 2345
Db GTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGTATCGGCCACCTCGGCTCCCAAAG 33

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QY 2346 TGTCTGGATTACAGGATGAGCCACCG 2372
Db TGTCTGGATTACAGGATGAGCCACCG 6
TGTCTGGATTACAGGATGAGCCACCG 6
RESULT 25
BD074010/c
LOCUS 73 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074010
VERSION BD074010.1 GI:23619613
KEYWORDS JP 2001513996-A/49.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 73)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 49 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/49
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JIANDONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
PC C12N15/09, A61K31/47, A61K31/7088, A61K48/00, A61P35/00, C07H21/00,
C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..73
/organism="Unidentified".
FEATURES
source 1..73 Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 3.1%; Score 73; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAGGTGGAGTGATCAAAAGACCT 724
Db AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAGGTGGAGTGATCAAAAGACCT 14
AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAGGTGGAGTGATCAAAAGACCT 14
QY 725 TGTACAAGAGCTT 737
Db TGTACAAGAGCTT 1
TGTACAAGAGCTT 1
RESULT 26
AX901901/c
LOCUS 76 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17764 from Patent EP1033401.
ACCESSION AX901901
VERSION AX901901.1 GI:40056815
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 17764 06-SEP-2000;
GENSET (FR)
FEATURES
source 1..76 Location/Qualifiers
/organism="Homo sapiens"

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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 3.1%; Score 72.8; DB 1; Length 76;  
Best Local Similarity 97.4%; Pred. No. 4.7;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGCTCTCGATCTCTGACCTCTGATCCGCGCCACCTCGGCTCCCAA 2344  
Db 76 TGTAGCCAGGATGCTCTCGATCTCTGACCTCTGATCCGCGCCACCTCGGCTCCCAA 17  
QY 2345 GTGCTGGGATTACAGG 2360  
Db 16 GTGCTGGGATTACAGG 1

RESULT 27  
BD037434/c  
LOCUS  
DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD037434  
VERSION BD037434.1 GI:22579176  
KEYWORDS JP 2001269182-A/13680.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1. (bases 1 to 76)  
Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.  
Sequence tag and encoded human protein  
Patent: JP 2001269182-A 13680 02-OCT-2001;  
GENSET  
OS Homo sapiens (human)  
PN JP 2001269182-A/13680  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JEAN BAPTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES  
PI JORDAN  
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC  
C12N5/10,  
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC  
G06F15/40  
CC  
FH Key Location/Qualifiers.  
FEATURES  
source  
1. .76  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 3.1%; Score 72.8; DB 1; Length 76;  
Best Local Similarity 97.4%; Pred. No. 4.7;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGCTCTCGATCTCTGACCTCTGATCCGCGCCACCTCGGCTCCCAA 2344  
Db 76 TGTAGCCAGGATGCTCTCGATCTCTGACCTCTGATCCGCGCCACCTCGGCTCCCAA 17  
QY 2345 GTGCTGGGATTACAGG 2360  
Db 16 GTGCTGGGATTACAGG 1

RESULT 28  
AX900729  
LOCUS  
DEFINITION Sequence 16592 from Patent EP1033401.  
ACCESSION AX900729  
VERSION AX900729.1 GI:40055643  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.  
Expressed sequence tags and encoded human proteins  
Patent: EP 1033401-A 16592 06-SEP-2000;  
GENSET (FR)  
FEATURES  
source  
1. .84  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 3.0%; Score 71.4; DB 1; Length 84;  
Best Local Similarity 92.6%; Pred. No. 5.9;  
Matches 75; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2248 AATTTTGTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307  
Db 2 AATTTTGTATTTTAGTAGAGATGGGGTTTCACCATGGTAGCCAGATGCTCTCGATC 61  
QY 2308 TCCTGACCTCGTGATCCGCC 2328  
Db 62 TCCTGACCTCGTGATCCGCC 82

RESULT 29  
BD036262  
LOCUS  
DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD036262  
VERSION BD036262.1 GI:22578004  
KEYWORDS JP 2001269182-A/12508.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 84)  
Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.  
Sequence tag and encoded human protein  
Patent: JP 2001269182-A 12508 02-OCT-2001;  
GENSET  
OS Homo sapiens (human)  
PN JP 2001269182-A/12508  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JEAN BAPTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES  
PI JORDAN  
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC  
C12N5/10,  
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC  
G06F15/40  
CC  
FH Key Location/Qualifiers.  
FEATURES  
source  
1. .84  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 3.0%; Score 71.4; DB 1; Length 84;  
Best Local Similarity 92.6%; Pred. No. 5.9;  
Matches 75; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2248 AATTTTGTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307  
Db 2 AATTTTGTATTTTAGTAGAGATGGGGTTTCACCATGGTAGCCAGATGCTCTCGATC 61  
QY 2308 TCCTGACCTCGTGATCCGCC 2328  
Db 62 TCCTGACCTCGTGATCCGCC 82



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RESULT 30
AX912245
LOCUS
DEFINITION Sequence 28108 from Patent EP1033401.
ACCESSION AX912245
VERSION AX912245.1 GI:40206034
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: Ep 1033401-A 28108 06-SEP-2000;
GENSET Genset (FR)
FEATURES
source Location/Qualifiers
1. .79
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 3.0%; Score 71; DB 1; Length 79;
Best Local Similarity 93.7%; Pred. No. 5.9;
Matches 74; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2252 TTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCT 2311
Db 1 TTTTGTATTTTATAGTAGACACCGGGTTTCACCATGTATACCCAGATGGTCTCGATCTCCT 60
QY 2312 GACCTCGTGATCGCCAC 2330
Db 61 GACCTCGTGATCGCCGC 79
RESULT 31
AX912245
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD047778
VERSION BD047778.1 GI:22589520
KEYWORDS JP 2001269182-A/24024.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 24024 02-OCT-2001;
GENSET Genset
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/24024
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,PC
G06F15/40
CC
FH Key Location/Qualifiers.
source Location/Qualifiers
1. .79
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 3.0%; Score 71; DB 1; Length 79;
Best Local Similarity 93.7%; Pred. No. 5.9;
Matches 74; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2252 TTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCT 2311
Db 1 TTTTGTATTTTATAGTAGACACCGGGTTTCACCATGTATACCCAGATGGTCTCGATCTCCT 60
QY 2312 GACCTCGTGATCGCCAC 2330
Db 61 GACCTCGTGATCGCCGC 79
RESULT 32
AX9397063
LOCUS
DEFINITION Sequence 1278 from Patent WO212328.
ACCESSION AX9397063
VERSION AX9397063.1 GI:21067810
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS King,G.E., Meagher,M.J., Xu,J. and Secrist,H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0212328-A 1278 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1. .84
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 3.0%; Score 70.8; DB 1; Length 84;
Best Local Similarity 91.5%; Pred. No. 6.3;
Matches 75; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2291 CCAGGATGGTCTCGATCTCTGACCTCGTGATCGCCACCTCGGCTCCCAAAGTCTG 2350
Db 1 CCAGATGGTCTGGATCTCTGACCTCGTGATCTGCCGCTCGGCTCCCAAAGTCTG 60
QY 2351 GGATTACAGGCATGAGCCACCG 2372
Db 61 GGATTACCGGTGTGAGCCACCG 82
RESULT 33
AX899552
LOCUS
DEFINITION Sequence 15415 from Patent EP1033401.
ACCESSION AX899552
VERSION AX899552.1 GI:40054466
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 15415 06-SEP-2000;
GENSET Genset (FR)
FEATURES
source Location/Qualifiers
1. .92
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 3.0%; Score 70.2; DB 1; Length 92;
Best Local Similarity 85.7%; Pred. No. 7.1;
Matches 78; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 2251 TTTTGTGACTTTTAGTAGAGACAGGGTTTACCGTGTTAGCCAGGATGGTCTGATCTCC 2310  
Db 1 TTTTGTGATTTTGTAGAGACGGGGTTTACCATGTGTGGTCAGGGTGGTCTTGAACCTCC 60			

**Qy**            2311 TGACCTGTGATCGGCCACCTGGGCCTCCC 2341  
               |||||  
**Dδ**            61 TGACCTGTGATCCACCTGCCTGGGCCTCCC 91  
               |||||

RESULT 34	BD035085	92 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD035085				
DEFINITION	Sequence tag and encoded human protein.				
ACCESSION	BD035085				
VERSION	BD035085.1	Gr:22576827			
KEYWORDS	JP 2001269182-A/11331.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1. (bases 1 to 92)				
AUTHORS	Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.				
TITLE	Sequence tag and encoded human protein				
JOURNAL	Patent: JP 2001269182-A 11331 02-OCT-2001;				
	GENSET				

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FEATURES
  PH Key
    Location/Qualifiers
      1..92
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"

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Query Match 3.0%; Score 70.2; DB 1; Length 92;  
Best Local Similarity 85.7%; Pred. No. 7.1;  
Matches 78; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy	2311	TGACCTGTGATCGGCCACCCTGGGCTCCC	2341
Db	61	TGACCTGTGATCCACTGCCTGGGCTCCC	91

RESULT	35
AR4211270	
LOCUS	85 bp DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 12767 from patent US 6639063.
ACCESSION	AR4211270
VERSION	AR4211270.1 GI:40176380
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 85)
AUTHORS	Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE	EST's and encoded human proteins
JOURNAL	Patent : US 6639063-A 12767 28-OCT-2003;
FEATURES	Location/Qualifiers source 1..85

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/organism="unknown"
/mol_type="genomic DNA"

Query Match      2.8%; Score 66.6; DB 1; Length 85;
Best Local Similarity 84.7%; Pred. No. 10;
Matches 72; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 2258 ACATTTAGTAGACAGCGTTTACCGTGTTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
      |||||
Db 1 ATTTTTCATAGACATGGTTTACCACATGTAGCCATGATGGTCTCGATCTCTGACCTC 60

QY 2318 GTGATCGGCCACCTCGGCCTCCCA 2342
      |||||
Db 61 GTGATCCACATGCGTTGGCCTCCYW 85
      |||||

```

Qy		2318	GTGATCGGGCCACCTCGGCCCTCCCCA	2342
Db		61	GTGCATCACATGCCTTGGCCTCCCYW	85

RESULT	36
LOCUS	AX981964
DEFINITION	Sequence 12767 from Patent EP1104808.
ACCESSION	AX981964
VERSION	AX981964.1 GI:40988104
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y. ESTs and encoded human proteins Patent: EP 1104808-A 12767 06-JUN-2001; Genset (FR)
AUTHORS	Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
TITLE	ESTs and encoded human proteins
JOURNAL	Patent: EP 1104808-A 12767 06-JUN-2001;

Query Match	2.8%;	Score 66.6;	DB 1;	Length 85;
Best Local Similarity	84.7%;	Pred. NO. 1.0;		
Matches 72;	Conservative	2;	Mismatches 11;	Indels 0;
				Caps 0;

Qy		2318	GTGATCGGGCCACCTCGGCCTCCCCA	2342
Dδ		61	GTGATCCACATGCCCTTGGCCTCCYW	85

RESULT	37
BD116823	
LOCUS	85 bp DNA linear PAT 18-SEP-2002
DEFINITION	EST and encoded human protein.
ACCESSION	BD116823
VERSION	BD116823.1 GI:23211727
KEYWORDS	JP 2002010789-A/8900.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 85)
AUTHORS	Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE	EST and encoded human protein
JOURNAL	Patent: JP 2002010789-A 8900 15-JAN-2002;
	GENSET CORP
COMMENT	OS Homo sapiens (human)

COMMENT	GENDRI	CORR
OS Homo sapiens (human)		
PN JP 2002010789-A/8900		
PD 15-JAN-2002		
PF 07-AUG-2000 JP 2000280989		
PR 05-AUG-1999 US 60/147499		
DT JEAN RADISTAT DIMAS MTINE EDWARDS SEVELIN TOBERT JEAN EVER DT		

TITLE Neural thread protein gene expression and detection of Alzheimer's disease

JOURNAL Patent: US 5948634-A 91 07-SEP-1999;

FEATURES Location/Qualifiers

source 1..84

/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 2.8%; Score 65.4; DB 1; Length 84;

Best Local Similarity 86.7%; Pred. No. 12;

Matches 72; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2282 CCCTGTTAGCCAGGATGGTCTCGATCTCTCGACCTCGTGCATCGCCACCTCGGCCTCCC 2341

Db 1 CCATGTTTCATCAGCGTGGTGTGGAACCTCTGACCTCGTGCATCGCCCGGCTCAGCCTCCC 60

QY 2342 AAAGTGCTGGGATTACAGGCATG 2364

Db 61 AAAGTGCTGGGATTACAGCGTG 83

RESULT 40

AR073206

LOCUS AR073206 84 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 91 from patent US 5948888.

ACCESSION AR073206

VERSION AR073206.1 GI:9999969

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 84)

AUTHORS de la Monte, S. and Wands, J.R.

TITLE Neural thread protein gene expression and detection of Alzheimer's disease

JOURNAL Patent: US 5948888-A 91 07-SEP-1999;

FEATURES Location/Qualifiers

source 1..84

/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 2.8%; Score 65.4; DB 1; Length 84;

Best Local Similarity 86.7%; Pred. No. 12;

Matches 72; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2282 CCCTGTTAGCCAGGATGGTCTCGATCTCTCGACCTCGTGCATCGCCACCTCGGCCTCCC 2341

Db 1 CCATGTTTCATCAGCGTGGTGTGGAACCTCTGACCTCGTGCATCGCCCGGCTCAGCCTCCC 60

QY 2342 AAAGTGCTGGGATTACAGGCATG 2364

Db 61 AAAGTGCTGGGATTACAGCGTG 83

RESULT 41

AX900153

LOCUS AX900153 81 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 16016 from Patent EP1033401.

ACCESSION AX900153

VERSION AX900153.1 GI:40055067

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.

TITLE Expressed sequence tags and encoded human proteins

JOURNAL Patent: EP 1033401-A 16016 06-SEP-2000;

FEATURES Genset (FR)

source Location/Qualifiers

1..81

/organism="Homo sapiens"

REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE		Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL		Patent: WO 0210449-A 12590 07-FEB-2002;
COMPEN		CompuGen Inc. (US)
FEATURES		Location/Qualifiers
source		1..60
Query Match		2.5%; Score 60; DB 1; Length 60;
Best Local Similarity		100.0%; Pred. No.18;
Matches		60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	98	TGACCGAGATCCTGCTGCTTTCCGACGCCAGGAGCACCGTCCCTCCCGGATTAGTCGTA 157
Db	1	TGACCGAGATCCTGCTGCTTTCCGACGCCAGGAGCACCGTCCCTCCCGGATTAGTCGTA 60
RESULT 44		
AX523103/c		
LOCUS		AX523103 68 bp DNA linear PAT 24-OCT-2002
DEFINITION		Sequence 773 from Patent WO02064731.
ACCESSION		AX523103
VERSION		AX523103.1 GI:24412057
KEYWORDS		
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		Telerman,A., Amson,R., Tuijnder,M. and Susini,L.
TITLE		Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL		Patent: WO 02064731-A 773 22-AUG-2002;
COMPEN		Molecular Engines Laboratories (FR)
FEATURES		Location/Qualifiers
source		1..68
Query Match		2.5%; Score 60; DB 1; Length 68;
Best Local Similarity		92.6%; Pred. No.19;
Matches		63; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy	2256	GTAACCTTTTAGTAGACACAGGGTTTACCGCTGTAGCCAGATGGTCTCGATCTCCTGACC 2315
Db	68	GTAATTTTAGTAGACACGGGGTTTCCACCTATTAGCTAGGATGGTCTCGATTTCTCTGACC 9
Qy	2316	TCGTGATC 2323
Db	8	TCGTGATC 1
RESULT 45		
AX523168/c		
LOCUS		AX523168 68 bp DNA linear PAT 24-OCT-2002
DEFINITION		Sequence 838 from Patent WO02064731.
ACCESSION		AX523168
VERSION		AX523168.1 GI:24412122
KEYWORDS		
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		Telerman,A., Amson,R., Tuijnder,M. and Susini,L.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 02064731-A 838 22-AUG-2002;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
Location/Qualifiers  
1..68  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 2.5%; Score 58.4; DB 1; Length 68;  
Best Local Similarity 91.2%; Pred. No. 23;  
Matches 62; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTATTTTGTAGTACAGAGGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCCTGACC 2315  
|||||  
Db 68 GTATTTTGTAGTACAGAGGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCCTGACC 9

QY 2316 TCGTGATC 2323  
|||||  
Db 8 TCGTGATC 1

RESULT 46  
AX522779  
LOCUS AX522779 68 bp DNA linear PAT 24-OCT-2002  
DEFINITION Sequence 449 from Patent WO02064731.  
ACCESSION AX522779  
VERSION AX522779.1 GI:24411733  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Telerman, A., Amson, R., Tuijnder, M. and Susinl, L.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 02064731-A 449 22-AUG-2002;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
Location/Qualifiers  
1..68  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 2.4%; Score 56.8; DB 1; Length 68;  
Best Local Similarity 85.3%; Pred. No. 27;  
Matches 58; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTATTTTGTAGTACAGAGGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCCTGACC 2315  
|||||  
Db 1 GTATTTTGTAGTACAGAGGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCCTGACC 60

QY 2316 TCGTGATC 2323  
|||||  
Db 61 TCGTGATC 68

RESULT 47  
AX260697  
LOCUS AX260697 69 bp DNA linear PAT 26-OCT-2001  
DEFINITION Sequence 348 from Patent WO0173027.  
ACCESSION AX260697  
VERSION AX260697.1 GI:16509664  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Meagher, M.J., Xu, J. and King, G.E.  
TITLE Compositions and methods for therapy and diagnosis of colon cancer  
JOURNAL Patent: WO 0173027-A 348 04-OCT-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source  
Location/Qualifiers  
1..69  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 2.4%; Score 56.2; DB 1; Length 69;  
Best Local Similarity 88.4%; Pred. No. 29;  
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2291 CCAGGATGCTTCGATCTCCTGACCTCGTGATCGGCCACCTCGGCTCCCAAAGTCTG 2350  
|||||  
Db 1 CCAGGCCGGTCTCGAACTCCAGACCTCATGATCCACCGCTTGGCTCCCAAAGTCTG 60

QY 2351 GGATTACAG 2359  
|||||  
Db 61 GGATTACAG 69

RESULT 48  
AX901137  
LOCUS AX901137 65 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 17000 from Patent EP1033401.  
ACCESSION AX901137  
VERSION AX901137.1 GI:40056051  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.  
TITLE Expressed sequence tags and encoded human proteins  
JOURNAL Patent: EP 1033401-A 17000 06-SEP-2000;  
Genset (FR)  
FEATURES  
source  
Location/Qualifiers  
1..65  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 2.3%; Score 54.4; DB 1; Length 65;  
Best Local Similarity 90.6%; Pred. No. 34;  
Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2270 GACAGGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCTGACCTCGTATCCGCCCA 2329  
|||||  
Db 1 GACGGGGTTTCCTCGTGTAGCCAGGATGCTTCGATCTCCTGACCTCGTATCCGCCCA 60

QY 2330 CCTC 2333  
|||||  
Db 61 CCGC 64

RESULT 49  
BD036670  
LOCUS BD036670 65 bp DNA linear PAT 27-AUG-2002  
DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD036670  
VERSION BD036670.1 GI:22578412  
KEYWORDS JP 2001269182-A/12916.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 65)  
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.  
TITLE Sequence tag and encoded human protein  
JOURNAL Patent: JP 2001269182-A 12916 02-OCT-2001;

COMMENT

GENSET

OS Homo sapiens (human)

PN JP 2001269182-A/12916

PD 02-OCT-2001

PF 24-FEB-2000 JP 2000118773

PR 26-FEB-1999 US 60/122487

PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES

PI JORDAN

PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC

C12N5/10,

PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC

G06F15/40

CC

Key Location/Qualifiers

FEATURES

source

1..65

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

Query Match 2.3%; Score 54.4; DB 1; Length 65;

Best Local Similarity 90.6%; Pred. No. 34;

Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2270 GACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCCA 2329

Db 1 GACGGGGTTTCTCTGTTAGCCAGGATGGTCTCGATCTCTGACCTGTGATCCGCCCA 60

QY 2330 CCTC 2333

Db 61 CGCG 64

RESULT 50

AX523219/c

LOCUS

DEFINITION Sequence 889 from Patent WO02064731.

ACCESSION AX523219

VERSION AX523219.1 GI:24412173

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Telerman, A., Amson, R., Tuijnder, M. and Susini, L.

TITLE Sequences involved in phenomena of tumour suppression, tumour

reversion, apoptosis and/or virus resistance and their use as

medicines

JOURNAL Patent: WO 02064731-A 889 22-AUG-2002;

FEATURES

source

1..60

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 2.2%; Score 52; DB 1; Length 60;

Best Local Similarity 91.7%; Pred. No. 43;

Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323

Db 60 AGTAGAGATGGGGTTTCACTGTGTAGCCAGGATGTCTCCATCTCTGACCTCGTGATC 1

RESULT 51

AR416502/c

LOCUS

DEFINITION Sequence 7999 from patent US 6639063.

ACCESSION AR416502

VERSION AR416502.1 GI:40171612

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 68)

AUTHORS

Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.

TITLE EST's and encoded human proteins

JOURNAL Patent: US 6639063-A 7999 28-OCT-2003;

FEATURES

source

1..68

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 2.2%; Score 52; DB 1; Length 68;

Best Local Similarity 85.3%; Pred. No. 46;

Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2189 TCTCTGCTCAGCCTCCCAATTAGCTTGCGCTACAGTCATCTGCCACACACCTGGCTA 2248

Db 68 TCTCTGCTCAGCCTCCCGAGTAGCTGGACTACAGGACCCGCCCGCGGCTA 9

QY 2249 ATTTTGTG 2256

Db 8 ATTTTGTG 1

RESULT 52

AX977196/c

LOCUS

DEFINITION Sequence 7999 from Patent EP1104808.

ACCESSION AX977196

VERSION AX977196.1 GI:40983336

KEYWORDS

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.

TITLE ESTs and encoded human proteins

JOURNAL Patent: EP 1104808-A 7999 06-JUN-2001;

FEATURES

source

1..68

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 2.2%; Score 52; DB 1; Length 68;

Best Local Similarity 85.3%; Pred. No. 46;

Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2189 TCTCTGCTCAGCCTCCCAATTAGCTTGCGCTACAGTCATCTGCCACACACCTGGCTA 2248

Db 68 TCTCTGCTCAGCCTCCCGAGTAGCTGGACTACAGGACCCGCCCGCGGCTA 9

QY 2249 ATTTTGTG 2256

Db 8 ATTTTGTG 1

RESULT 53

BD112055/c

LOCUS

DEFINITION EST and encoded human protein.

ACCESSION BD112055

VERSION BD112055.1 GI:23206873

KEYWORDS

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

```

TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 4132 15-JAN-2002;
COMMENT GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/4132
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source 1..68
FT /organism="Homo sapiens (human)".

FEATURES
source
1..68
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 2.2%; Score 52; DB 1; Length 68;
Best Local Similarity 85.3%; Pred. No. 46;
Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2189 TCCTCCCTCCAGCCCTCCGATTCAGTTCGCTACAGTCACTGCCACACACCTGGCTA 2248
Db |||||||
68 TCCTCCCTCCAGCCCTCCGATTCAGTTCGCTACAGTCACTGCCACACACCTGGCTA 9

QY 2249 ATTTTGTG 2256
Db |||||||
8 ATTTTGTG 1

RESULT 54
AF087511/c
LOCUS 66 bp mRNA linear PRI 04-SEP-2001
DEFINITION Homo sapiens clone ENAc+22 epithelial sodium channel alpha subunit
ACCESSION AF087511
VERSION AF087511.1 GI:5870626
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Oh, Y. S., Lee, S., Won, C. and Warnock, D. G.
TITLE An Alu cassette in the human epithelial sodium channel
JOURNAL Biochim. Biophys. Acta 1520 (1), 94-98 (2001)
MEDLINE 21363042
PUBMED 11470165
REFERENCE 2 (bases 1 to 66)
AUTHORS Oh, Y. and Warnock, D. G.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1998) Medicine, UAB, 1720 7th Ave. So.,
Birmingham, AL 35294, USA
FEATURES
source
1..66
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
/clone="ENAc+22"
<1..->66
/gene="SCNN1A"
<1..->66
/gene="SCNN1A"
/notes="alternatively spliced epithelial sodium channel
alpha subunit containing intronic Alu sequence"

gene
misc_feature

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Query Match 2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 93.1%; Pred. No. 47;
Matches 54; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2315 CTCGTGATCGCCACCTCGGCTCCCAAAGTCTGGATTACAGGATGAGCCACCG 2372
Db |||||||
66 CTCGTGATCGCCCGCTCGGCTCCCAAAGTCTGGATTACAGGATGAGCCACCG 9

RESULT 55
AX899244/c
LOCUS 68 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 15107 from Patent EP1033401.
ACCESSION AX899244
VERSION AX899244.1 GI:40054157
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 15107 06-SEP-2000;
GENSET (FR)
FEATURES
source
1..68
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 2.2%; Score 51; DB 1; Length 68;
Best Local Similarity 85.1%; Pred. No. 52;
Matches 57; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
Db |||||||
67 TTTTGTATTTTAGCAGAGACGGGTTTCACCATATTGTCAGGCTGGTCTCGAACTCC 8

QY 2311 TGACCTC 2317
Db |||||||
7 TGACCTC 1

RESULT 56
BD034777/c
LOCUS 68 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD034777
VERSION BD034777.1 GI:22576519
KEYWORDS JP 2001269182-A/11023.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 11023 02-OCT-2001;
GENSET
COMMENT
1..68
/organism="Homo sapiens (human)"
PN JP 2001269182-A/11023
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC

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FH KEY Location/Qualifiers.
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    /organism="Homo sapiens"
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    85.1%; Pred. No. 52;
  Matches
    57; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGACAGCGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
Db |||||
67 TTTTGTATTTTAGCAGACAGCGGTTTACCAATATTGCCAGGTGGTCTCGAATCTC 8
QY 2311 TGACCTC 2317
Db |||||
7 TGACCCC 1

RESULT 57
AX903935
LOCUS
DEFINITION
ACCESSION AX903935
VERSION
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)
REFERENCE
  1
  Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
  Expressed sequence tags and encoded human proteins
  Patent: EP 1033401-A 19798 06-SEP-2000;
  Genset (FR)
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    1..64
    /organism="Homo sapiens"
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    55; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2255 TGTACTTTTAGTAGACAGCGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGAC 2314
Db |||||
2 TGTATTTTAGTAGACAGCGTTTCGCCATGTTGTCGGGCTGGTCTCGAATCTCTGAC 61
QY 2315 CTC 2317
Db |||||
62 CTC 64

RESULT 58
BX039468
LOCUS
DEFINITION
ACCESSION BX039468
VERSION
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
  Expressed sequence tags and encoded human proteins
  Patent: EP 1033401-A 19798 06-SEP-2000;
  Genset (FR)
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  Best Local Similarity
    87.3%; Pred. No. 55;
  Matches
    55; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2255 TGTACTTTTAGTAGACAGCGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGAC 2314
Db |||||
2 TGTATTTTAGTAGACAGCGTTTCGCCATGTTGTCGGGCTGGTCTCGAATCTCTGAC 61
QY 2315 CTC 2317
Db |||||
62 CTC 64

RESULT 59
AX322319
LOCUS
DEFINITION
ACCESSION AX322319
VERSION
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Kramer,M.D., Winter,H. and Reinartz,J.
  Mrna molecules to be used as indicators of the functional and
  activation state of t-lymphocytes
  Patent: EP 1162276-A 192 12-DEC-2001;
  Lynx Therapeutics GmbH (DE)
FEATURES
  source
    1..63
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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  Best Local Similarity
    91.4%; Pred. No. 55;
  Matches
    53; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2250 TTTTGTACTTTTAGTAGACAGCGTTTCACCGTGTAGCCAGGATGGTCTCGATC 2307
Db |||||
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RESULT 60
CQ006684/c
LOCUS
DEFINITION
ACCESSION CQ006684
VERSION
KEYWORDS
SOURCE
ORGANISM
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  Sequence tag and encoded human protein
  Patent: JP 2001269182-A 15714 02-OCT-2001;
  Genset
COMMENT
  OS Homo sapiens (human)
  PN JP 2001269182-A/15714

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REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: WO 0147944-A 5324 05-JUL-2001;
        Curagen Corporation (US)
FEATURES
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                /db_xref="taxon:9606"
                /note="Accession number cg43287619"
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Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGGCTCCCA 2342
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Db 51 CAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGGCTCCCA 1

RESULT 61
AR444760
LOCUS AR444760 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1171 from patent US 6670464.
ACCESSION AR444760
VERSION AR444760.1 GI:42672539
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: US 6670464-A 1171 30-DEC-2003;
        Curagen Corporation (US)
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        Location/Qualifiers
            1..51
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                /mol_type="genomic DNA"
Query Match 2.0%; Score 48.4; DB 1; Length 51;
Best Local Similarity 98.0%; Pred. No. 59;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTATCGCCACCTCGGCTCCCAAGTCTG 2350
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Db 2 CTCGATCTCTGACCTCGTATCGCCACCTCGGCTCCCAAGTCTG 51

RESULT 62
HUMUT5223A/C
LOCUS HUMUT5223A 64 bp DNA linear STS 28-DEC-1994
DEFINITION Human STS UT5223, 5' primer bind, sequence tagged site.
ACCESSION L31134
VERSION L31134.1 GI:604619
KEYWORDS STS; PCR primer; STS sequence; dinucleotide repeat; microsatellite
        DNA; microsatellite marker; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 64)
AUTHORS Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L.,
        Melis,R., Lawrence,M., Moore,M., Holik,P.R., Carlson,M., Zhao,X.,
        Robertson,M., Bradley,P., Elener,T., Tingey,A., Lalouel,J.-M. and
        White,R.
TITLE Genetic and physical mapping of simple sequence repeat containing
        sequence tagged sites from the human genome
JOURNAL Unpublished (1994)
COMMENT Original source text: Homo sapiens DNA.
        Submitted by: Utah Center for Human Genome Research University of

```

```

Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: CACTGCACCTCCAGGCTGGG
Primer B: AGGTGAGGCTGCAGTGAGC
End to Label: Primer B
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing Extension 5 94
C 10 sec. 50 C 10 sec. 72 C 20 sec. 30
50 C 10 sec. 72 C 20 sec. Mg++: 0.00 mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 0.
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                /evidence=experimental
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            Matches 51; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2086 TTATTATTTTGTGAGACCGAGCTTGTCTCTTACCCAGGCTGGAGTGCAGTGGG 2142
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Db 59 TTTTATTTTGTGAGACCGAGCTTGTCTCTTACCCAGGCTGGAGTGCAGTGGG 3

RESULT 63
AX161490
LOCUS AX161490 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4818 from Patent WO0140521.
ACCESSION AX161490
VERSION AX161490.1 GI:14542821
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: WO 0140521-A 4818 07-JUN-2001;
        Curagen Corporation (US)
FEATURES
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
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                /note="2 of 2 allelic variants (4817 is other entry)"
            Accession number cg43971764"
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            2.0%; Score 47.8; DB 1; Length 51;
            Best Local Similarity 96.1%; Pred. No. 63;
            Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGGCTCCCA 2342
      |||||||
Db 1 CAGGATGGTCTCGATCTCTGACCTCGTATCGCCACCTCGGCTCCCA 51

RESULT 64
AX163313/c
LOCUS AX163313 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6641 from Patent WO0140521.
ACCESSION AX163313
VERSION AX163313.1 GI:14544644
KEYWORDS

```

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Shimkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0140521-A 6641 07-JUN-2001;
            Curagen Corporation (US)
FEATURES    Location/Qualifiers
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Query Match      2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 63;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2319 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCCA 2369
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Db 51 TGATCCGCCATCTCGGCTCCCAATGCTGGGATTACAGGCATGAGCCA 1

RESULT 65
AX163451/c
LOCUS       AX163451 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6779 from Patent WO0140521.
ACCESSION  AX163451
VERSION     AX163451.1 GI:14544782
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Shimkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0140521-A 6779 07-JUN-2001;
            Curagen Corporation (US)
FEATURES    Location/Qualifiers
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            misc_feature
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            /note="1 of 2 allelic variants (6780 is other entry)"
            Accession number cg42657675"

Query Match      2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 63;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2318 GTGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCC 2368
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Db 51 GTGATCCGCCATCTCGGCTCCCAATGCTGGGATTACAGGCATGAGCC 1

RESULT 66
AX199317/c
LOCUS       AX199317 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 247 from Patent WO0151670.
ACCESSION  AX199317
VERSION     AX199317.1 GI:15389696
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Shimkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: US 6670464-A 1172 30-DEC-2003;
            Curagen Corporation (US)

```

```

REFERENCE   1
AUTHORS     Shimkets,R.A. and Leach,M.D.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0151670-A 247 19-JUL-2001;
            Curagen Corporation (US)
FEATURES    Location/Qualifiers
            source
            1..51
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            /db_xref="taxon:9606"
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            Accession number cg39662754"

Query Match      2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 63;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2300 TCTGATCTCTGACCTCGATCGGCTCCGACCTCGGCTCCCAAGTCTG 2350
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Db 51 TCTGATCTCTGACCTCGATCGGCTCCGACCTCGGCTCCCAAGTCTG 1

RESULT 67
AX522922
LOCUS       AX522922 52 bp DNA linear PAT 24-OCT-2002
DEFINITION Sequence 592 from Patent WO02064731.
ACCESSION  AX522922
VERSION     AX522922.1 GI:24411876
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Anson,R., Tuijnder,M. and Susini,L.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 02064731-A 592 22-AUG-2002;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
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            1..52
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      2.0%; Score 47.2; DB 1; Length 52;
Best Local Similarity 94.2%; Pred. No. 68;
Matches 49; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2256 GTACTTTTACTAGACAGGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
      |||||
Db 1 GCATTTTATAGACAGGGTTTCACCATGTTAGCCAGGATGCTCTCGATC 52

RESULT 68
AR444761
LOCUS       AR444761 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1172 from patent US 6670464.
ACCESSION  AR444761
VERSION     AR444761.1 GI:42672540
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 51)
AUTHORS     Shimkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: US 6670464-A 1172 30-DEC-2003;
            Curagen Corporation (US)

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Best Local Similarity								
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Db	2	CTCGATCTCTGACCTCGTGATCCGCCACCTCGCGCTCCCAAGTGCTG	51					
RESULT 69	AX396956/c							
LOCUS	AX396956	Sequence 1171 from Patent WO0212328.	59 bp	DNA	linear	PAT 18-MAY-2002		
DEFINITION	AX396956							
ACCESSION	AX396956							
VERSION	AX396956.1	GI:21067703						
KEYWORDS								
ORGANISM		Homo sapiens (human)						
REFERENCE								
AUTHORS		Homo sapiens						
TITLE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
JOURNAL		Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.						
FEATURES								
source								
Query Match								
Best Local Similarity								
Matches	51; Conservative	0; Mismatches	7; Indels	0; Gaps	0;			
QY	2233	CCACACACCTGGCTAATTTTGTGATCTTTAGTAGACACAGGTTTCACCGTGTAG	2290					
Db	58	CCACACACACCTGGCTAATTTTGTGATCTTTAGTAGACACAGGTTTCACCATGTGG	1					
RESULT 70	AR292147							
LOCUS	AR292147	Sequence 3882 from patent US 6537751.	47 bp	DNA	linear	PAT 12-JUN-2003		
DEFINITION	AR292147							
ACCESSION	AR292147							
VERSION	AR292147.1	GI:31679431						
KEYWORDS								
SOURCE		Unknown.						
ORGANISM		Unknown.						
REFERENCE								
AUTHORS		Cohen, D., Chumakov, I. and Blumenfeld, M.						
TITLE		Biallelic markers for use in constructing a high density						
JOURNAL		disequilibrium map of the human genome						
FEATURES								
source								
Query Match								
Best Local Similarity								
Matches	46; Conservative	1; Mismatches	0; Indels	0; Gaps	0;			
QY	2271	ACAGGTTTCACCGTTAGCCAGGATGTTCTCGATCTCTGACCTC	2317					
Db	1	ACAGGTTTCACCGTTAGCCAGGATGTTCTCGATCTCTGACCTC	47					

KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Picoult-Newburg,L. and Pohl,M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 012962-A 3124 26-APR-2001;  
Orchid Biosciences, Inc. (US)  
FEATURES Location/Qualifiers  
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Best Local Similarity 94.1%; Pred. No. 75;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2304 GATCTCTGACCTCGTGTGATCCGCCACCTCGGCTCCCAAGTCTGGAT 2354  
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Db 51 GATCTCTGACCTCGTGTGATCCGCCCTCGGCTCCCAAGTCCGGAT 1  
RESULT 74  
AX161489  
LOCUS AX161489 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 4817 from Patent WO0140521.  
ACCESSION AX161489  
VERSION AX161489.1 GI:14542820  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 4817 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
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Best Local Similarity 94.1%; Pred. No. 75;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2292 CAGGATGCTCGATCTCTGATCCGCTGATCCGCCACCTCGGCTCCCA 2342  
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Db 1 CAGGATGCTCGATCTCTGATCCGCTGATCCGCCCGCTCAGCTCCCA 51  
RESULT 75  
AX163314/c  
LOCUS AX163314 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6642 from Patent WO0140521.  
ACCESSION AX163314  
VERSION AX163314.1 GI:14544645  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0138586-A 152 31-MAY-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/note="2 of 2 allelic variants (6641 is other entry)  
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Best Local Similarity 94.1%; Pred. No. 75;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2319 TGATCCGCCACCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCCA 2369  
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Db 51 TGATCCGCCACCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCCA 1  
RESULT 76  
AX163452/c  
LOCUS AX163452 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6780 from Patent WO0140521.  
ACCESSION AX163452  
VERSION AX163452.1 GI:14544783  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 6780 07-JUN-2001;  
Curagen Corporation (US)  
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/note="2 of 2 allelic variants (6779 is other entry)  
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Best Local Similarity 94.1%; Pred. No. 75;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2318 GTGATCCGCCACCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCC 2368  
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Db 51 GTGATCCGCCACCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCC 1  
RESULT 77  
AX164957  
LOCUS AX164957 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 152 from Patent WO0138586.  
ACCESSION AX164957  
VERSION AX164957.1 GI:14545786  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0138586-A 152 31-MAY-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/note="2 of 2 allelic variants (6779 is other entry)  
Accession number CG42657675"

TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 6642 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
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26  
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Accession number CG42657675"  
Query Match 1.9%; Score 46.2; DB 1; Length 51;  
Best Local Similarity 94.1%; Pred. No. 75;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2319 TGATCCGCCACCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCCA 2369  
|||||  
Db 51 TGATCCGCCACCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCCA 1  
RESULT 76  
AX163452/c  
LOCUS AX163452 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6780 from Patent WO0140521.  
ACCESSION AX163452  
VERSION AX163452.1 GI:14544783  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 6780 07-JUN-2001;  
Curagen Corporation (US)  
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Db 51 GTGATCCGCCACCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCC 1  
RESULT 77  
AX164957  
LOCUS AX164957 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 152 from Patent WO0138586.  
ACCESSION AX164957  
VERSION AX164957.1 GI:14545786  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0138586-A 152 31-MAY-2001;  
Curagen Corporation (US)  
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Best Local Similarity 94.1%; Pred. No. 75;
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  1 ATTTTAGTAGACAGGGTTTCACTGTGTAGCCAGGATGGTCTCGATCT 51
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RESULT 78
LOCUS
  AX199318/c
  51 bp DNA linear PAT 29-AUG-2001
DEFINITION
  Sequence 248 from Patent WO0151670.
ACCESSION
  AX199318
VERSION
  AX199318.1 GI:15389697
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Shimkets, R.A. and Leach, M.D.
  Nucleic acids containing single nucleotide polymorphisms and
  methods of use thereof
  Patent: WO 0151670-A 248 19-JUL-2001;
  Curagen Corporation (US)
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Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 79
AX116665
LOCUS
  AX116665
  51 bp DNA linear PAT 11-MAY-2001
DEFINITION
  Sequence 1788 from Patent WO0129262.
ACCESSION
  AX116665
VERSION
  AX116665.1 GI:14033607
SOURCE
  Homo sapiens (human)
ORGANISM
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Picoult-Newburg, L. and Pohl, M.
  Genotyping reagents, kits and methods of use thereof
  Patent: WO 0129262-A 1788 26-APR-2001;
  Orchid Biosciences, Inc. (US)
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Best Local Similarity 87.7%; Pred. No. 83;
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  57 TTTTGTATTTTAGTAGACAGGGTTTCCCGGTGTTCACCGGTGTTCGAACT 1
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RESULT 81
BD053372/c
LOCUS
  BD053372
  57 bp DNA linear PAT 27-AUG-2002
DEFINITION
  Sequence tag and encoded human protein.
ACCESSION
  BD053372
VERSION
  BD053372.1 GI:22598978
KEYWORDS
  JP 2001269182-A/29618.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 57)
  Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
  Sequence tag and encoded human protein
  Patent: JP 2001269182-A 29618 02-OCT-2001;
  GENSET
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  PN JP 2001269182-A/29618
  PD 02-OCT-2001
  PF 24-FEB-2000 JP 2000118773
  PR 26-FEB-1999 US 60/122487
  PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
  JC JORDAN
  PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
  C12N5/10,
  PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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Db 57 TTTTGTATTTTAGTAGAGAGCGTGTTCACCGGTGTTCACCGGATGCTCTCGA 1

RESULT 82
AY283614 50 bp DNA linear PRI 17-JUL-2003
LOCUS Homo sapiens KLK3 gene promoter region, partial sequence.
DEFINITION
ACCESSION AY283614
VERSION AY283614.1 GI:32879294
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Cramer,S.D., Chang,B.-L., Rao,A., Hawkins,G.A., Chang,S.,
Wade,W.N., Cooke,R.T., Thomas,L.N., Bleecker,E.R., Catalona,W.J.,
Sterling,D.A., Meyers,D.A., Ohar,J. and Xu,J.
Association between Genetic Polymorphisms in the Prostate-specific
Antigen Gene Promoter and Serum Prostate-specific Antigen Levels
J. Natl. Cancer Inst. Monographs (2003) In press
REFERENCE 2 (bases 1 to 50)
AUTHORS Cramer,S.D., Xu,J. and Hawkins,G.A.
Direct Submission
TITLE Submitted (25-APR-2003) Cancer Biology, Wake Forest University
JOURNAL School of Medicine, Medical Center Blvd, Winston-Salem, NC 27157,
USA
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QY 2283 CGTGTAGCCAGGATGCTCGATCTCTCGACCTCGTGATCCGCCACCT 2332
|||||
Db 1 CGTGTAGCCAGGATGCTCGATCTCTCGACCTCGTGATCTGCCACCT 50

RESULT 83
AX160937 51 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION
ACCESSION AX160937
VERSION AX160937.1 GI:14542268
KEYWORDS
SOURCE Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4265 07-JUN-2001;
Curagen Corporation (US)
FEATURES
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Accession number cg3941567"

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Best Local Similarity 1.9%; Score 45.2; DB 1; Length 51;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2323 CGCCCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
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Db 1 CCTCCCGCCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 50

RESULT 84
AX163202 51 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION
ACCESSION AX163202
VERSION AX163202.1 GI:14544533
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6530 07-JUN-2001;
Curagen Corporation (US)
FEATURES
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Location/Qualifiers
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Best Local Similarity 1.9%; Score 45.2; DB 1; Length 51;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2323 CGCCCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
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RESULT 85
AX117745/c 51 bp DNA linear PAT 11-MAY-2001
LOCUS
DEFINITION
ACCESSION AX117745
VERSION AX117745.1 GI:14034696
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2868 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
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Best Local Similarity 92.2%; Pred. No. 90;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2306 TCTCCTGACCTCGTATCCGCCACCTCGGCCCTCCCAAGTGTGGGATTA 2356
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Db 51 TCTCCTGACCTCGTATCCACCCACCCGCCCTCCCAAGGGGTGGATTA 1
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RESULT 86
LOCUS AX199153 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 83 from Patent WO0151670.
ACCESSION AX199153
VERSION AX199153.1 GI:15389504
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0151670-A 83 19-JUL-2001;
Curagen Corporation (US)
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Best Local Similarity 92.2%; Pred. No. 90;
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RESULT 87
LOCUS AX160938 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4266 from Patent WO0140521.
ACCESSION AX160938
VERSION AX160938.1 GI:14542269
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4266 07-JUN-2001;
Curagen Corporation (US)
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Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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LOCUS AX163201 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6529 from Patent WO0140521.
ACCESSION AX163201
VERSION AX163201.1 GI:14544532
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6529 07-JUN-2001;
Curagen Corporation (US)
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RESULT 89
LOCUS AX157145/c 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 473 from Patent WO0140521.
ACCESSION AX157145
VERSION AX157145.1 GI:14538476
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 473 07-JUN-2001;
Curagen Corporation (US)
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DEFINITION	AX159798	Sequence 3126 from Patent WO0140521.	51 bp DNA	linear	PAT 22-JUN-2001
ACCESSION	AX159798	Sequence 3126 from Patent WO0140521.	51 bp DNA	linear	PAT 22-JUN-2001
VERSION	AX159798.1	GI:14541129	51 bp DNA	linear	PAT 22-JUN-2001
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VERSION	AX159805.1	GI:14541136	51 bp DNA	linear	PAT 22-JUN-2001
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LOCUS	AX163302	Sequence 6630 from Patent WO0140521.	51 bp DNA	linear	PAT 22-JUN-2001
DEFINITION	AX163302	Sequence 6630 from Patent WO0140521.	51 bp DNA	linear	PAT 22-JUN-2001
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VERSION	AX163302.1	GI:14541129	51 bp DNA	linear	PAT 22-JUN-2001
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FEATURES					
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misc_feature					
Query Match					
Best Local Similarity					
Matches					
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Db					





REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.D.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0151670-A 265 19-JUL-2001;  
AUTHORS Curagen Corporation (US)  
TITLE Location/Qualifiers  
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RESULT 99  
LOCUS AX199357 51 bp DNA linear PAT 29-AUG-2001  
DEFINITION Sequence 287 from Patent WO0151670.  
ACCESSION AX199357  
VERSION AX199357.1 GI:15389742  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.D.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0151670-A 287 19-JUL-2001;  
AUTHORS Curagen Corporation (US)  
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Db 1 AGTAGACAGGGTTTACCGTTGTTAGCCAGGATGCTCGATCTCCTGAC 51  
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LOCUS AY283615 50 bp DNA linear PRI 17-JUL-2003  
DEFINITION Homo sapiens KLK3 gene promoter region, partial sequence.  
ACCESSION AY283615  
VERSION AY283615.1 GI:32879295  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Cramer, S.D., Chang, B.-L., Rao, A., Hawkins, G.A., Chang, S., Wade, W.N., Cooke, R.T., Thomas, L.N., Bleecker, E.R., Catalona, W.J.,

Sterling, D.A., Meyers, D.A., Ohar, J. and Xu, J.  
TITLE Association between Genetic Polymorphisms in the Prostate-specific Antigen Gene Promoter and Serum Prostate-specific Antigen Levels  
J. Natl. Cancer Inst. Monographs (2003) In press  
REFERENCE 2 (bases 1 to 50)  
AUTHORS Cramer, S.D., Xu, J. and Hawkins, G.A.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2003) Cancer Biology, Wake Forest University School of Medicine, Medical Center Blvd, Winston-Salem, NC 27157, USA  
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Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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Db 2 TGATCGCCACCTCGCGCTCCCAAGTGTGGATTACAGGATGAGC 50  
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RESULT 101  
LOCUS AR288911/c 47 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 646 from patent US 6537751.  
ACCESSION AR288911  
VERSION AR288911.1 GI:31676195  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 47)  
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.  
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 646 25-MAR-2003;  
FEATURES  
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Best Local Similarity 93.5%; Pred. No. 1.1e+02;  
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2261 TTATAGAGACAGGGTTTACCGTTGTTAGCCAGGATGCTCGAT 2306  
|||||  
Db 47 TTATAGAGACAGGGTTTACCGTTGTTAGCCAGGATGCTCGAT 2  
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RESULT 102  
LOCUS AX114379/c 47 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 48 from Patent WO0129257.  
ACCESSION AX114379  
VERSION AX114379.1 GI:14031343  
KEYWORDS

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Schork, N. and Skierczynski, B.  
 TITLE Methods of genetic cluster analysis and use thereof  
 JOURNAL Patent: WO 0129257-A 48 26-APR-2001;  
 GENSET (FR)  
 FEATURES  
 source Location/Qualifiers  
 1. .47  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 variation 24  
 /notes="99-1602-200 : polymorphic base G or C"  
 Query Match 1.8%; Score 42.4; DB 1; Length 47;  
 Best Local Similarity 93.5%; Pred. No. 1.1e+02;  
 Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2261 TTATGATAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGAT 2306  
 |||||  
 Db 47 TTATGATAGACCGGGTTTCACTGTGTAGCCAGGATGGTCTCGAT 2  
 |||||  
 RESULT 103  
 AX156682/c  
 LOCUS AX156682 51 bp DNA linear PAT 22-JUN-2001  
 DEFINITION Sequence 6454 from Patent WO0140521.  
 ACCESSION AX156682  
 VERSION AX163126.1 GI:14544457  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shinkets, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and  
 methods of use thereof  
 JOURNAL Patent: WO 0140521-A 6454 07-JUN-2001;  
 Curagen Corporation (US)  
 FEATURES  
 source Location/Qualifiers  
 1. .51  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 misc\_feature 26  
 /notes="2 of 2 allelic variants (6453 is other entry)"  
 Accession number cg34287601"  
 Query Match 1.8%; Score 42.2; DB 1; Length 51;  
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
 Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2271 ACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317  
 |||||  
 Db 1 ACAGGGTTTCACCGTGTAGCCAGGATGGTCTGAACTCTGACCTC 47  
 |||||  
 RESULT 104  
 AX156682/c  
 LOCUS AX156682 51 bp DNA linear PAT 22-JUN-2001  
 DEFINITION Sequence 10 from Patent WO0140521.  
 ACCESSION AX156682  
 VERSION AX156682.1 GI:14537802  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1

AUTHORS Shinkets, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and  
 methods of use thereof  
 JOURNAL Patent: WO 0140521-A 10 07-JUN-2001;  
 Curagen Corporation (US)  
 FEATURES  
 source Location/Qualifiers  
 1. .51  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 misc\_feature 26  
 /notes="2 of 2 allelic variants (9 is other entry)"  
 Accession number cg42918213"  
 Query Match 1.8%; Score 42; DB 1; Length 51;  
 Best Local Similarity 90.0%; Pred. No. 1.2e+02;  
 Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 2089 TTATTTTTCAGACCGAGTCTTGTCTGTATACCAGGCTGGAGTGCGAG 2138  
 |||||  
 Db 50 TTCTTTTTCAGACAGAGTCTCGCTCTGTGCCCCAGGCTGGAGTGCGAG 1  
 |||||  
 RESULT 105  
 AX159128  
 LOCUS AX159128 51 bp DNA linear PAT 22-JUN-2001  
 DEFINITION Sequence 2456 from Patent WO0140521.  
 ACCESSION AX159128  
 VERSION AX159128.1 GI:14540459  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shinkets, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and  
 methods of use thereof  
 JOURNAL Patent: WO 0140521-A 2456 07-JUN-2001;  
 Curagen Corporation (US)  
 FEATURES  
 source Location/Qualifiers  
 1. .51  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 misc\_feature 26  
 /notes="2 of 2 allelic variants (2455 is other entry)"  
 Accession number cg39602254"  
 Query Match 1.8%; Score 42; DB 1; Length 51;  
 Best Local Similarity 90.0%; Pred. No. 1.2e+02;  
 Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 2268 GAGACAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317  
 |||||  
 Db 1 GAGACAGGTTTCACCATGTTGACCAGGCTGGTCTCGAACTCTGACCTC 50  
 |||||  
 RESULT 106  
 AX163383  
 LOCUS AX163383 51 bp DNA linear PAT 22-JUN-2001  
 DEFINITION Sequence 6711 from Patent WO0140521.  
 ACCESSION AX163383  
 VERSION AX163383.1 GI:14544714  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shinkets, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and  
 methods of use thereof

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JOURNAL Patent: WO 0140521-A 6711 07-JUN-2001;
FEATURES Curagen Corporation (US)
source Location/Qualifiers
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature
26
/note="1 of 2 allelic variants (6712 is other entry)"
Accession number c943989360"

Query Match 1.8%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2246 CTAATTTTGTACTTTAGTAGAGACAGGTTTCACCGTGTAGCCAGG 2295
|||||
Db 1 CTAATTTTGTATTTTATTTAGTAGAGACGGGTTTCGCCATGTTGGCCAGG 50

RESULT 107
AX157146/c
LOCUS AX157146 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 474 from Patent WO0140521.
ACCESSION AX157146
VERSION AX157146.1 GI:14538477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 474 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature
26
/note="2 of 2 allelic variants (473 is other entry)"
Accession number c944928115"

Query Match 1.8%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2324 CGCCACCTCGGCTCCCAAGTCTGGATTACAGCATGAGCCACC 2371
|||||
Db 51 CGCCCGCTCGGCTCCCAAGTCCCGGATTACAGGCTTGAGTCACC 4

RESULT 108
AX163259/c
LOCUS AX163259 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6587 from Patent WO0140521.
ACCESSION AX163259
VERSION AX163259.1 GI:14544590
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6587 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature
26
/note="1 of 2 allelic variants (6588 is other entry)"
Accession number c943273813"

Query Match 1.8%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2241 CTTGGCTAATTTTCTACTTTTCTAGTAGACAGGGTTTCACCGTGT 2288
|||||
Db 48 CTTGGCTAATTTTCTATTTTATTTTCTAGTAGACGGGTTTCACCAATGT 1

RESULT 109
AX910629
LOCUS AX910629 52 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 26492 from Patent EP1033401.
ACCESSION AX910629
VERSION AX910629.1 GI:40066709
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 26492 06-SEP-2000;
Genset (FR)
FEATURES
source Location/Qualifiers
1. .52
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.8%; Score 41.6; DB 1; Length 52;
Best Local Similarity 86.5%; Pred. No. 1.3e+02;
Matches 45; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2255 TGTACTTTTGTAGTAGACAGGGTTTCACCGTGTAGCCAGATGTCGAT 2306
|||||
Db 1 TGTATTTTGTGBAGACAGCGGGTTTCGCCATGTTGGCCAGATGTCGAT 52

RESULT 110
BD046162
LOCUS BD046162 52 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD046162
VERSION BD046162.1 GI:22587904
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 22408 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/22408
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
C12N5/10,

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QY 2262 TTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2398 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/morganism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (2397 is other entry)"
Accession number cg939574041

Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred.No.1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2292 CAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCCA 2342
|||||
Db 51 CAGGCTGGTCTCAAACTCCTGATCTCGTCATCCGCCGCCGCTCGGCTCCCCA 1

RESULT 118
AXI59266/c
LOCUS AXI59266 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2594 from Patent WO0140521.
ACCESSION AXI59266
VERSION AXI59266.1 GI:14540597
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2594 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/morganism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (2593 is other entry)"
Accession number cg40949022

Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred.No.1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2242 CTGGCTAATTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCC 2292
|||||
Db 51 CTGGCTGAATTTTGTATTATTTTAGTAGAGACGGGGTTTCGCCCATGTGGCC 1

RESULT 119
AXI59797/c
LOCUS AXI59797 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3125 from Patent WO0140521.
ACCESSION AXI59797
VERSION AXI59797.1 GI:14541128
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 3125 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
source Location/Qualifiers  
1..51  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 26  
/note="1 of 2 allelic variants (3126 is other entry)"  
Accession number cg42920603"  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2255 TGTACTTTTAGTAGACAGGGTTTCCCGTTAGCCAGGATGGTCTCGA 2305  
|||||  
Db 51 TGTATTTTAGTAGACAGGGTTTACCATGTTGGCCAGGCTGGTCTCGA 1  
RESULT 120  
AX159806/c  
LOCUS AX159806 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 3134 from Patent WO0140521.  
ACCESSION AX159806  
VERSION AX159806.1 GI:14541137  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 3134 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 26  
/note="2 of 2 allelic variants (3133 is other entry)"  
Accession number cg42924993"  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2262 TTAGTAGACAGGGTTTCCCGTTAGCCAGGATGGTCTCGATCTCTG 2312  
|||||  
Db 51 TTAGTAGACAGGGTTTCCCATGCTGGCCAGGCTGGTCTCGAATCTCTG 1  
RESULT 121  
AX160263/c  
LOCUS AX160263 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 3591 from Patent WO0140521.  
ACCESSION AX160263  
VERSION AX160263.1 GI:14541594  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 3591 07-JUN-2001;  
Curagen Corporation (US)

methods of use thereof  
Patent: WO 0140521-A 3591 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 26  
/note="1 of 2 allelic variants (3592 is other entry)"  
Accession number cg43318557"  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2225 GTCATCTGCCACACACCTGGCTAAATTTTGTACTTTTAGTAGACAGG 2275  
|||||  
Db 51 GGCACCTGCCACCATCTCGCTAAATTTTGTATTTTAGTAGACAGG 1  
RESULT 122  
AX163301  
LOCUS AX163301 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6629 from Patent WO0140521.  
ACCESSION AX163301  
VERSION AX163301.1 GI:14544632  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 6629 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 26  
/note="1 of 2 allelic variants (6630 is other entry)"  
Accession number cg43090974"  
Query Match 1.7%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2300 TCTCGATCTCCTGACCTCGTGATCCGCCACCTCGCGCTCCCAAGTGCTG 2350  
|||||  
Db 1 TCTCGAATCTCCTGACCTCAAGATCCACCTCGCTCGCGCTCCCAAGTGCTG 51  
RESULT 123  
AX163479/c  
LOCUS AX163479 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6807 from Patent WO0140521.  
ACCESSION AX163479  
VERSION AX163479.1 GI:14544810  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 6807 07-JUN-2001;  
Curagen Corporation (US)

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FEATURES
  source
    Location/Qualifiers
      1..51
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
  misc_feature
    26
    /note="1 of 2 allelic variants (6808 is other entry)"
    Accession number CG42487874"

Query Match
  Best Local Similarity 1.7%; Score 41.4; DB 1; Length 51;
  Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2264 AGTAGAGACGGGCTTCACCGCTGTACCGAGGATGGTCTCGATCTCTGAC 2314
Db 51 AGTAGAGACGGGCTTCACCGCTGTACCGAGGATGGTCTCAAACTCTGAC 1

RESULT 124
LOCUS AX164872 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 67 from Patent WO0138586.
ACCESSION AX164872
VERSION AX164872.1 GI:14545701
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Shimkets, R.A. and Leach, M.
  TITLE Nucleic acids containing single nucleotide polymorphisms and
  JOURNAL Patent: WO 0138586-A 67 31-MAY-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..51
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
  variation
    26
    /note="single nucleotide polymorphism"
    Accession number CG43957170"

Query Match
  Best Local Similarity 1.7%; Score 41.4; DB 1; Length 51;
  Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2218 GCTACAGTCATCTGCCACACACCTGGCTAAATTTTGTACTTTTAGTAG 2268
Db 51 GACTACAGGCAAGCGCCACACCGCTGGCTAAATTTTGTATTTTTAGTAG 1

RESULT 125
LOCUS AX189876/c 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 55 from Patent WO0147942.
ACCESSION AX189876
VERSION AX189876.1 GI:15143247
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Shimkets, R.A. and Leach, M.
  TITLE Nucleic acids containing single nucleotide polymorphisms and
  JOURNAL Patent: WO 0147942-A 55 05-JUL-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
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      /organism="Homo sapiens"

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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
      /note="1 of 2 allelic variants (56 is other entry)"
      Accession number CG42869755"

Query Match
  Best Local Similarity 1.7%; Score 41.4; DB 1; Length 51;
  Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2308 TCTGACCTCGTATCGCCACCTCGGCTCCCAAAAGTGTGGGATTACA 2358
Db 51 TACTGACCTCGTATCGCCACCTCGGCTCCCAAAAGTGTGGGATTACA 1

RESULT 126
LOCUS AX190286/c 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 465 from Patent WO0147942.
ACCESSION AX190286
VERSION AX190286.1 GI:15143665
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Shimkets, R.A. and Leach, M.
  TITLE Nucleic acids containing single nucleotide polymorphisms and
  JOURNAL Patent: WO 0147942-A 465 05-JUL-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..51
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
      /note="1 of 2 allelic variants (466 is other entry)"
      Accession number CG43080072"

Query Match
  Best Local Similarity 1.7%; Score 41.4; DB 1; Length 51;
  Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2319 TGATCGCCACCTCGGCTCCCAAAAGTGTGGGATTACAGGATGAGCCA 2369
Db 51 TGATCCACTGCTTCGGCTCCCAAAAGTGTGGGATTATAGCGTGAGCCA 1

RESULT 127
LOCUS AX199155 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 85 from Patent WO0151670.
ACCESSION AX199155
VERSION AX199155.1 GI:15389506
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Shimkets, R.A. and Leach, M.D.
  TITLE Nucleic acids containing single nucleotide polymorphisms and
  JOURNAL Patent: WO 0151670-A 85 19-JUL-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..51
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
      /note="1 of 2 allelic variants (86 is other entry)"
      Accession number CG43130275"
  misc_feature
    26

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Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2245 GCTAAATTTTGTACTTTTAGTAGACAGAGGTTTTCACCGTGTAGCCAGG 2295
Db 1 GCTAAATTTTGTATTTTAAATAGAGACGGGATTCACCATGTGGCCAGG 51

RESULT 128
AX199159/c
LOCUS AX199159 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 89 from Patent WO0151670.
ACCESSION AX199159
VERSION AX199159.1 GI:15389510
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS of use thereof
JOURNAL Patent: WO 0151670-A 89 19-JUL-2001;
Curagen Corporation (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (90 is other entry)"
Accession number c942657675"

Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2279 TCACCGTGTAGCAGGATGTTCTCGATCTCCGTGACCTCGATCCGCCCA 2329
Db 51 TCATCATGTGTCGCCAGGATGCTTGTGATTTCTCGACCTCGTGCATCCGCCCA 1

RESULT 129
AX199336/c
LOCUS AX199336 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 266 from Patent WO0151670.
ACCESSION AX199336
VERSION AX199336.1 GI:15389717
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS of use thereof
JOURNAL Patent: WO 0151670-A 266 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (265 is other entry)"
Accession number c943011316"

Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACAGAGGTTTTCACCGTGTAGCCAGGATGGTCTGATCTCCT 2311
Db 51 TTTAGTAGACAGAGGTTTTCACCATATTTGCCAGGCTGGTCTCAAACTCCT 1

RESULT 130
AX199358
LOCUS AX199358 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 288 from Patent WO0151670.
ACCESSION AX199358
VERSION AX199358.1 GI:15389743
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS of use thereof
JOURNAL Patent: WO 0151670-A 288 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (287 is other entry)"
Accession number c941584420"

Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2264 AGTAGACAGAGGTTTTCACCGTGTAGCCAGGATGGTCTGATCTCCTGAC 2314
Db 1 AGTAGACAGAGGTTTTCACCATGTTGCCAGGCTGGTCTCAAACTCCTGAC 51

RESULT 131
AX199370/c
LOCUS AX199370 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 300 from Patent WO0151670.
ACCESSION AX199370
VERSION AX199370.1 GI:15389761
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS of use thereof
JOURNAL Patent: WO 0151670-A 300 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (299 is other entry)"
Accession number c943973526"

Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTGTCTGGGATTACAGGCATGAGCC 2368

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||||| 51 GTGATCATCGCCTGGCTCCCAAGTCTGGATTACAGCGGGAGCC 1
|||||
Db
RESULT 132
CQ006027
LOCUS CQ006027 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 4667 from Patent WO0147944.
ACCESSION CQ006027
VERSION CQ006027.1 GI:41012659
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
JOURNAL Patent: WO 0147944-A 4667 05-JUL-2001;
FEATURES
source
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Accession number c939524115"
Query Match 1.7%; Score 41.2; DB 1; Length 51;
Best Local Similarity 93.5%; Pred. No. 1.3e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2326 CCACCTCGGCTCCCAAGTCTGGATTACAGCGATGAGCCACC 2371
|||||
Db 1 CCCGCTTGGCTCCCAAGTCTGGATTACAGCGATGAGCCACC 46
|||||

RESULT 133
AX163312/c
LOCUS AX163312 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6640 from Patent WO0140521.
ACCESSION AX163312
VERSION AX163312.1 GI:14544643
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
JOURNAL Patent: WO 0140521-A 6640 07-JUN-2001;
FEATURES
source
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="2 of 2 allelic variants (6639 is other entry)
Accession number c938021538"
misc_feature
26
Query Match 1.7%; Score 41.2; DB 1; Length 51;
Best Local Similarity 93.5%; Pred. No. 1.3e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2096 TTTTGAGACCGAGTCTGCTGTACCCAGGCTGGAGTCAGTGG 2141
|||||
Db 51 TTTAGACAGAGTCTGCTGTACCCAGGCTGGAGTCAGTGG 6
|||||

RESULT 134
AX115473/c
LOCUS AX115473 51 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 596 from Patent WO0129262.
ACCESSION AX115473
VERSION AX115473.1 GI:14032415
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 596 26-APR-2001;
FEATURES
source
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.7%; Score 41; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.3e+02;
Matches 44; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2096 TTTTGAGACCGAGTCTGCTGTACCCAGGCTGGAGTCAGTGGTGTAT 2146
|||||
Db 51 TTTTGAGACCGAGTCTGCTGTACCCAGGCTGGAGTCAGTGGTGTAT 1
|||||

RESULT 135
AX161913
LOCUS AX161913 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 5241 from Patent WO0140521.
ACCESSION AX161913
VERSION AX161913.1 GI:14543244
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
JOURNAL Patent: WO 0140521-A 5241 07-JUN-2001;
FEATURES
source
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature
26
/notes="1 of 2 allelic variants (5242 is other entry)
Accession number c943988015"
Query Match 1.7%; Score 40.8; DB 1; Length 51;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2329 ACCTCGGCTCCCAAGTCTGGATTACAGCGATGAGCCACC 2372
|||||
Db 1 ACCTTGGCTCCCAAGTCTGGATTACAGCGATGAGCCACC 44
|||||

RESULT 136
AX522514/c
LOCUS AX522514 52 bp DNA linear PAT 24-OCT-2002
DEFINITION Sequence 184 from Patent WO02064731.
ACCESSION AX522514
VERSION AX522514.1 GI:24411468
KEYWORDS
SOURCE Homo sapiens (human)

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source
1. .41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.7%; Score 40.6; DB 1; Length 41;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCT 2338
|||||
|1| GGTCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCT 1
|||||

RESULT 139
AX161652/c
LOCUS AX161652 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4980 from Patent WO0140521.
ACCESSION AX161652
VERSION AX161652.1 GI:14542983
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4980 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="2 of 2 allelic variants (4979 is other entry)"
Accession number cg43979411"

Query Match
Best Local Similarity 1.7%; Score 40.6; DB 1; Length 51;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2326 CCCACTCGGCCCTCCCAAAGTCTGGATTACAGGCATGAGCCACCG 2372
|||||
|50 CCTGCTCAGCCTCCCAAAGTCTGGATTACAGGCATGAGCCACTG 4
|||||

RESULT 140
AX163125
LOCUS AX163125 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6453 from Patent WO0140521.
ACCESSION AX163125
VERSION AX163125.1 GI:14544456
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6453 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="1 of 2 allelic variants (6454 is other entry)"

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2330 CCTCGGCCTCCCAAAGTGTCTGGATTACAGGCATGAGCCACC 2371

7

7

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RESULT 145
AX163384
LOCUS AX163384 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6712 from Patent WO0140521.
ACCESSION AX163384
VERSION AX163384.1 GI:14544715
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6712 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="2 of 2 allelic variants (6711 is other entry)"
Accession number cg43989360"
Query Match 1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2246 CTAATTTTGTACTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGG 2295
|||||
Db 1 CTAATTTTGTATTTTGTAGTAGAGGGGGTTTCGCCATGTTGCCAGG 50
|||||

RESULT 146
AX117197
LOCUS AX117197 51 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2320 from Patent WO0129262.
ACCESSION AX117197
VERSION AX117197.1 GI:14034148
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2320 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 1.5e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 2307
|||||
Db 2 TTTTAGTAGAGATGGGGTTTCACCGTGTGGCCAGGCTGCTCTGATC 49
|||||

RESULT 147
AX156918
LOCUS AX156918 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 246 from Patent WO0140521.
ACCESSION AX156918
VERSION AX156918.1 GI:14538249

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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 246 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="2 of 2 allelic variants (245 is other entry)"
Accession number cg17872027"
Query Match 1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 1.5e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTCTCGGATTACAGCATCA 2365
|||||
Db 4 GTGATCCTCTGCTCGGCTCCCAAAGTCTCGGATTACAGATATGA 51
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RESULT 148
AX163260/c
LOCUS AX163260 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6588 from Patent WO0140521.
ACCESSION AX163260
VERSION AX163260.1 GI:14544591
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6588 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="2 of 2 allelic variants (6587 is other entry)"
Accession number cg43273813"
Query Match 1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 1.5e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2241 CCTGGCTAATTTTCTACTTTAGTAGACAGAGGTTTCACCGTGT 2288
|||||
Db 48 CCTGGCTAATTTTCTATTTTTCAGTAGAGACGGGGTTTCACCATGTT 1
|||||

RESULT 149
AX523088
LOCUS AX523088 51 bp DNA linear PAT 24-OCT-2002
DEFINITION Sequence 758 from Patent WO02064731.
ACCESSION AX523088
VERSION AX523088.1 GI:24412042
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Telerman, A., Amson, R., Tuijnder, M. and Susini, L.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines

JOURNAL Patent: WO 02064731-A 758 22-AUG-2002;

FEATURES Molecular Engines Laboratories (FR)

Location/Qualifiers

source 1..51

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 1.7%; Score 40; DB 1; Length 51;  
Best Local Similarity 89.6%; Pred. No. 1.5e+02;  
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2260 TTTTGTAGACAGGGTTTACCGTGTATGCCAGGATGCTCGATC 2307

Db 4 TTTTGTAGACAGGGTTTACCAATGTTGCCAGGATGCTCGATC 51

## RESULT 150

AR444503

LOCUS

Sequence 914 from patent US 6670464. linear PAT 20-FEB-2004

ACCESSION AR444503

VERSION AR444503.1 GI:42672282

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 51)

AUTHORS Shimkets, R.A. and Leach, M.

TITLE Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof

JOURNAL Patent: US 6670464-A 914 30-DEC-2003;

FEATURES Location/Qualifiers

source 1..51

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 1.7%; Score 39.8; DB 1; Length 51;  
Best Local Similarity 86.3%; Pred. No. 1.5e+02;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2262 TTATGATAGACAGGGTTTACCGTGTATGCCAGGATGCTCGATCCTG 2312

Db 1 TTATGATAGACAGGGTTTACCATGCTGTCAGGCTGCTCGAACTCCTG 51

## RESULT 151

AX156683/c

LOCUS

Sequence 11 from Patent WO0140521. linear PAT 22-JUN-2001

DEFINITION

AX156683

ACCESSION

AX156683.1

VERSION

AX156683.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Shimkets, R.A. and Leach, M.

TITLE Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof

JOURNAL Patent: WO 0140521-A 11 07-JUN-2001;

FEATURES Curagen Corporation (US)

Location/Qualifiers

source 1..51

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

misc\_feature 26

/notes="1 of 2 allelic variants (12 is other entry)"

Accession number cg42918213"

Query Match 1.7%; Score 39.8; DB 1; Length 51;  
Best Local Similarity 86.3%; Pred. No. 1.5e+02;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTGAGACCGAGTCTTCTGTGTACCGAGCTGGAGTGCA 2137

Db 51 TTTTCTTTTGTGAGACAGAGTCTCACTCTGTGCGCCAGGCTGGAGTGCA 1

## RESULT 152

AX158064/c

LOCUS

Sequence 1392 from Patent WO0140521. linear PAT 22-JUN-2001

DEFINITION

AX158064

ACCESSION

AX158064.1

VERSION

AX158064.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Shimkets, R.A. and Leach, M.

TITLE Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof

JOURNAL Patent: WO 0140521-A 1392 07-JUN-2001;

FEATURES Curagen Corporation (US)

Location/Qualifiers

source 1..51

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

misc\_feature 26

/notes="2 of 2 allelic variants (1391 is other entry)"

Accession number cg29337682"

Query Match 1.7%; Score 39.8; DB 1; Length 51;  
Best Local Similarity 86.3%; Pred. No. 1.5e+02;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

## RESULT 153

AX158592/c

LOCUS

Sequence 1920 from Patent WO0140521. linear PAT 22-JUN-2001

DEFINITION

AX158592

ACCESSION

AX158592.1

VERSION

AX158592.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Shimkets, R.A. and Leach, M.

TITLE Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof

JOURNAL Patent: WO 0140521-A 1920 07-JUN-2001;

FEATURES Curagen Corporation (US)

Location/Qualifiers

source 1..51

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

misc\_feature 26

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/note="2 of 2 allelic variants (1919 is other entry)
Accession number cg36753762"

Query Match      1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGAGGTTTCACGGTTTCAGCGTTAGCCAGGATGGTCTCGATCTCCCTG 2312
DB 51 TTAGTAGACAGAGGTTTCATCATGCTGCGCAGGCTGGTCTTGAACCTCG 1

RESULT 154
AX159067/c
LOCUS AX159067 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2395 from Patent WO0140521.
ACCESSION AX159067
VERSION AX159067.1 GI:14540398
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2395 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (2396 is other entry)
Accession number cg39574041"

Query Match      1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2294 GGATGGTCTCGATCTCTGACCTCGTGATCGCCACCTCGGCTCCCAA 2344
DB 51 GGCTGGTCTCAACTCTTGATCTTGTATCGCCCGCTCGGCTCCCAA 1

RESULT 155
AX159069/c
LOCUS AX159069 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2397 from Patent WO0140521.
ACCESSION AX159069
VERSION AX159069.1 GI:14540400
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2397 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
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/note="1 of 2 allelic variants (2398 is other entry)
Accession number cg39574041"

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QY 2320 GATCGCCACCTGGGCTCCCAAGTCTGGATTACAGCATGAGCCAC 2370  
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Db 51 GATCTCTGCTTTGGCTCCCAAGTCTGGATTATAGGCATGAGCCGC 1

RESULT 158  
AX161023/c  
LOCUS AX161023 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 4351 from Patent WO0140521.  
ACCESSION AX161023  
VERSION AX161023.1 GI:14542354  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Shimkets, R.A. and Leach, M.  
AUTHORS Nucleic acids containing single nucleotide polymorphisms and  
TITLE Methods of use thereof  
JOURNAL Patent: WO 0140521-A 4351 07-JUN-2001;  
Curagen Corporation (US)  
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misc\_feature  
26  
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Accession number CG43948257"

Query Match 1.7%; Score 39.8; DB 1; Length 51;  
Best Local Similarity 86.3%; Pred. No. 1.5e+02;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2202 CCTCCCAATTAGTTGGCTACGTCTGCCACACACCTGGCTAATTT 2252  
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Db 51 CCTCCCAATTAGTTGGCTACGTCTGCCACACACCTGGCTAATTT 1

RESULT 159  
AX164908/c  
LOCUS AX164908 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 103 from Patent WO0138586.  
ACCESSION AX164908  
VERSION AX164908.1 GI:14545737  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Shimkets, R.A. and Leach, M.  
AUTHORS Nucleic acids containing single nucleotide polymorphisms and  
TITLE Methods of use thereof  
JOURNAL Patent: WO 0138586-A 103 31-MAY-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
variation  
26  
/note="single nucleotide polymorphism  
Accession number CG43265754"

Query Match 1.7%; Score 39.8; DB 1; Length 51;  
Best Local Similarity 86.3%; Pred. No. 1.5e+02;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2254 TTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCG 2304  
|||||

Db 51 TTGTATTTTAGTAGAGATGGGTTGCACCATGTTGGCCAGGCTGGTCTCG 1

RESULT 160  
AX190287/c  
LOCUS AX190287 51 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 466 from Patent WO0147942.  
ACCESSION AX190287  
VERSION AX190287.1 GI:15143666  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Shimkets, R.A. and Leach, M.  
AUTHORS Nucleic acids containing single nucleotide polymorphisms and  
TITLE Methods of use thereof  
JOURNAL Patent: WO 0147942-A 466 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
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Query Match 1.7%; Score 39.8; DB 1; Length 51;  
Best Local Similarity 86.3%; Pred. No. 1.5e+02;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTCCCAAGTGTGGATTACAGGCATGAGCCA 2369  
|||||  
Db 51 TGATCCACTCGCTCGGCTCCCAAGTGTGGATTATAGGCGTGAGCCA 1

RESULT 161  
AX199156/c  
LOCUS AX199156 51 bp DNA linear PAT 29-AUG-2001  
DEFINITION Sequence 86 from Patent WO0151670.  
ACCESSION AX199156  
VERSION AX199156.1 GI:15389507  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Shimkets, R.A. and Leach, M.D.  
AUTHORS Nucleic acids containing single nucleotide polymorphisms and  
TITLE Methods of use thereof  
JOURNAL Patent: WO 0151670-A 86 19-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
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misc\_feature  
26  
/note="2 of 2 allelic variants (85 is other entry)  
Accession number CG43130275"

Query Match 1.7%; Score 39.8; DB 1; Length 51;  
Best Local Similarity 86.3%; Pred. No. 1.5e+02;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2245 GCTAATTTTGTACTTTTAGTAGACAGACAGCGTTTACCGTGTAGCCAGG 2295  
|||||  
Db 1 GCTAATTTTGTATTTTAAATAGAAACGGGGATTCCACCATGTGTGGCCAGG 51

RESULT 162



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AX199160/c
LOCUS AX199160 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 90 from Patent WO0151670.
ACCESSION AX199160
VERSION AX199160.1 GI:15389511
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL Patent: WO 0151670-A 90 19-JUL-2001;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
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misc_feature 26
/notes="2 of 2 allelic variants (89 is other entry)"
Accession number cg42657675"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2279 TCACCGGTGTAGCCAGGATGCTCGATCTCCGACCTCGTATCGGCCCA 2329
|||||
DB 51 TCATCATGTGTGCCAGGATGCTCTTAATTTCTCGACCTCGTATCGGCCCA 1

RESULT 163
AX199168/c
LOCUS AX199168 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 98 from Patent WO0151670.
ACCESSION AX199168
VERSION AX199168.1 GI:15389520
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL Patent: WO 0151670-A 98 19-JUL-2001;
FEATURES
source Location/Qualifiers
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misc_feature 26
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Accession number cg43273813"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2214 CTTGGCCTACGATCATCTGCCACACACCTGGCTAATTTTGTACTTTTA 2264
|||||
DB 51 CTGGGACTACAGGCATATGCCACACCGCTGGCTAATTTTATATTTTA 1

RESULT 164
AX199369/c
LOCUS AX199369 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 299 from Patent WO0151670.

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ACCESSION AX199369
VERSION AX199369.1 GI:15389759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL Patent: WO 0151670-A 299 19-JUL-2001;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="1 of 2 allelic variants (300 is other entry)"
Accession number cg43973526"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCC 2368
|||||
DB 51 GTGATCCATCCGCTTGGCTCCAGAGTCTGGGATTACAGCGGAGCC 1

RESULT 165
AX199404/c
LOCUS AX199404 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 334 from Patent WO0151670.
ACCESSION AX199404
VERSION AX199404.1 GI:15389799
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL Patent: WO 0151670-A 334 19-JUL-2001;
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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misc_feature 26
/notes="2 of 2 allelic variants (333 is other entry)"
Accession number cg43926000"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2267 AGAGACAGGTTTCCACCGTGTAGCCAGGATGCTCGATCTCCTGACCTC 2317
|||||
DB 51 AGAGACGGGTTTCCACCATTTTGGCCAGGCTGGTCTTGAACTCCTGACCTC 1

RESULT 166
AX199417/c
LOCUS AX199417 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 347 from Patent WO0151670.
ACCESSION AX199417
VERSION AX199417.1 GI:15389814
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shinkets, R.A. and Leach, M.D.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0151670-A 347 19-JUL-2001;
            Curguen Corporation (US)
FEATURES    Location/Qualifiers
            1..51
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             /db_xref="taxon:9606"
misc_feature 26
             /note="1 of 2 allelic variants (348 is other entry)"
             accession number cg43273813"

Query Match      1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy  2218 GCCTACAGTCATCTGCCACACACACCTGGCTTAATTTTTTCTACTTTTAGTAG 2268
      |||||
      51 GACTACAGGCATATGCCACCATGCTGGCTTAATTTTTTATATTATTATTAGTAG 1

RESULT 167
AX903134/c
LOCUS       AX903134
DEFINITION Sequence 18997 from Patent EP1033401.
ACCESSION  AX903134
VERSION     AX903134.1 GI:40058091
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE       Expressed sequence tags and encoded human proteins
JOURNAL     Patent: EP 1033401-A 18997 06-SEP-2000;
            Genset (FR)
FEATURES    Location/Qualifiers
            1..51
             /organism="Homo sapiens"
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Query Match      1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy  2086 TTATTATTTTTTTGACACGAGTCTTGCTCTCTTACCCAGGCTGGAGTGC 2136
      |||||
      51 TTTTATTTTTTTTGAGATGGAGTCTCACTCTCTGTCGCCAGGCTGGAGTGC 1

RESULT 168
BD038667/c
LOCUS       BD038667
DEFINITION Sequence tag and encoded human protein.
ACCESSION  BD038667
VERSION     BD038667.1 GI:22580409
KEYWORDS    JP 2001269182-A/14913.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 51)
AUTHORS     Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE       Sequence tag and encoded human protein

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Patent: JP 2001269182-A 14913 02-OCT-2001;

GENSET  
OS Homo sapiens (human)  
PN JP 2001269182-A/14913  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PI 26-FEB-1999 US 60/122487  
PR JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES  
PJ JORDAN  
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC  
G06F15/40

CC

FH Key Location/Qualifiers.  
1. .51  
Location/Qualifiers

FEATURES  
source

Query Match 1.7%; Score 39.8; DB 1; Length 51;  
Best Local Similarity 86.3%; Pred. No. 1.5e+02;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2086 TTATTATTTTTTGGAGCCGAGCTCTGCTCTGTACCCAGGCTGGAGTGCC 2136  
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Db 51 TTTTATTTTTTTGGAGTGGAGTCTCACTCTGTTGCCAGGCTGGAGTGCC 1

RESULT 169  
AX163311/c  
LOCUS AX163311 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6639 from Patent WO0140521.  
ACCESSION AX163311  
VERSION AX163311.1 GI:14544642  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Shinkets, R.A. and Leach, M.  
Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 6639 07-JUN-2001;  
Curagen Corporation (US)

FEATURES  
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Location/Qualifiers  
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/db\_xref="taxon:9606"  
26  
misc\_feature  
/note="1 of 2 allelic variants (6640 is other entry)  
Accession number cg38821538"

Query Match 1.7%; Score 39.6; DB 1; Length 51;  
Best Local Similarity 91.3%; Pred. No. 1.5e+02;  
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2096 TTTTGAGACCGAGCTCTGCTCTGTACCCAGGCTGGAGTGCGAGTGG 2141  
|||||  
|||||

Db 51 TTTTGAGACAGAGCTCTGCTCTGTGTTGCCAGGCTGGAGTACAGTGG 6

RESULT 170  
AX163193/c  
LOCUS AX163193 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6521 from Patent WO0140521.  
ACCESSION AX163193  
VERSION AX163193.1 GI:14544524  
KEYWORDS  
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5221 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="1 of 2 allelic variants (6522 is other entry)"
Accession number cg39667665"

Query Match 1.7%; Score 39.4; DB 1; Length 51;
Best Local Similarity 97.6%; Pred. No. 1.6e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 GTGATCGCCGCTCGGCTCCCAAGTCTGGGATTACA 2358
|||||
Db 41 GTGATCGCCGCTCGGCTCCCAAGTCTGGGATTACA 1

RESULT 171
AX199669 AX199669 51 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 599 from Patent WO0151670.
DEFINITION AX199669
ACCESSION AX199669
VERSION AX199669.1 GI:15390109
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0151670-A 599 19-JUL-2001;
Curagen Corporation (US)
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/db_xref="taxon:9606"
misc_feature 26
/notes="1 of 2 allelic variants (600 is other entry)"
Accession number cg43130275"

Query Match 1.7%; Score 39.4; DB 1; Length 51;
Best Local Similarity 87.8%; Pred. No. 1.6e+02;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2232 GCCACACACCTGGCTTAATTTTGTACTTTTGTAGACAGCGTTTC 2280
|||||
Db 3 GCCACACACCCGCTAATTTTGTATTTTGTATTTTGTATAGACGGGGATTC 51

RESULT 172
AX161914 AX161914 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 5242 from Patent WO0140521.
DEFINITION AX161914
ACCESSION AX161914
VERSION AX161914.1 GI:14543245
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5242 07-JUN-2001;
Curagen Corporation (US)
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source 1..51
/organism="Homo sapiens"
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/db_xref="taxon:9606"
misc_feature 26
/notes="2 of 2 allelic variants (5241 is other entry)"
Accession number cg43988015"

Query Match 1.7%; Score 39.2; DB 1; Length 51;
Best Local Similarity 93.2%; Pred. No. 1.6e+02;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2329 ACCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCCACCG 2372
|||||
Db 1 ACCTTGGCTCCCAAGTCTGGACTACAGGCATGAGCCACCG 44

RESULT 173
AX161651/c AX161651 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 4979 from Patent WO0140521.
DEFINITION AX161651
ACCESSION AX161651
VERSION AX161651.1 GI:14542982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4979 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="1 of 2 allelic variants (4980 is other entry)"
Accession number cg43979411"

Query Match 1.6%; Score 39; DB 1; Length 51;
Best Local Similarity 89.4%; Pred. No. 1.6e+02;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2326 CCCATCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCCACCG 2372
|||||
Db 50 CCTGCTCAGCTCCCAAGTCTGAGATTACAGGCATGAGCCACTG 4

RESULT 174
AX161487 AX161487 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 4815 from Patent WO0140521.
DEFINITION AX161487
ACCESSION AX161487
VERSION AX161487.1 GI:14542818
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and

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methods of use thereof
Patent: WO 0140521-A 4815 07-JUN-2001;
Curagen Corporation (US)
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
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    misc_feature
        /note="1 of 2 allelic variants (4816 is other entry)"
        Accession number cg43971764"

Query Match
Best Local Similarity 1.6%; Score 38.9; DB 1; Length 51;
Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2248 AATTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGG 2299
|||||
Db 1 AATTTTGTATTTTGTAGTAGAC-GGGTTTCACCGTGTAGCCAGGATGG 51

RESULT 175
AX161488
LOCUS
DEFINITION
Sequence 4816 from Patent WO0140521.
ACCESSION
AX161488
VERSION
AX161488.1 GI:14542819
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shinkets, R.A. and Leach, M.
TITLE
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: WO 0140521-A 4816 07-JUN-2001;
Curagen Corporation (US)
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        26
    misc_feature
        /note="2 of 2 allelic variants (4815 is other entry)"
        Accession number cg43971764"

Query Match
Best Local Similarity 1.6%; Score 38.9; DB 1; Length 51;
Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2248 AATTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGG 2299
|||||
Db 1 AATTTTGTATTTTGTAGTAGACA-GGTTTCACCGTGTAGCCAGGATGG 51

RESULT 176
AR444501
LOCUS
DEFINITION
Sequence 912 from patent US 6670464.
ACCESSION
AR444501
VERSION
AR444501.1 GI:42672280
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 51)
AUTHORS
Shinkets, R.A. and Leach, M.
TITLE
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: US 6670464-A 912 30-DEC-2003;
Curagen Corporation (US)
FEATURES
    source
        1..51

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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.6%; Score 38.8; DB 1; Length 51;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2330 CCTGGCCTCCCAAGTGTGGGATTACAGGCATGAGCCACC 2371
|||||
Db 1 CCTCAGCCTCCCAAGTGTGGGATCAGAGGCATGAGCCACC 42

RESULT 177
AX158432
LOCUS
DEFINITION
Sequence 1760 from Patent WO0140521.
ACCESSION
AX158432
VERSION
AX158432.1 GI:14539763
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shinkets, R.A. and Leach, M.
TITLE
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: WO 0140521-A 1760 07-JUN-2001;
Curagen Corporation (US)
FEATURES
    source
        1..51
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
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    misc_feature
        /note="2 of 2 allelic variants (1759 is other entry)"
        Accession number cg34750113"

Query Match
Best Local Similarity 1.6%; Score 38.8; DB 1; Length 51;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2089 TTATTTTGTGACACGAGTCTGCTCTGTTACCCAGGCTGGAGTGCG 2138
|||||
Db 2 TTTTATTTGTTGACACAGAGTCTGCTCTGTTGCTAGGCTGGAGTGCG 51

RESULT 178
AX158497
LOCUS
DEFINITION
Sequence 1825 from Patent WO0140521.
ACCESSION
AX158497
VERSION
AX158497.1 GI:14539828
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shinkets, R.A. and Leach, M.
TITLE
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: WO 0140521-A 1825 07-JUN-2001;
Curagen Corporation (US)
FEATURES
    source
        1..51
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        26
    misc_feature
        /note="1 of 2 allelic variants (1826 is other entry)"
        Accession number cg35097892"

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Query Match	1.6%	Score 38.8	DB 1	Length 51	
Best Local Similarity	86.0%	Pred. No. 1.7e+02			
Matches	43	Conservative 0	Mismatches 7	Indels 0	Gaps 0
QY	2256	GTACTTTTAGTAGACAGAGGTTTCACCGTGTTAGCCAGGATGCTCTCGA	2305		
Db	1	GTATTTTCAGTAGACAGCGGGTTTACCAATGTGCCAGGCTGCTCTCGA	50		
RESULT 179					
AX158578/6					
LOCUS	AX158578	51 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 1906 from Patent WO0140521.				
ACCESSION	AX158578				
VERSION	AX158578.1	GI:14539909			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Shimkets, R.A. and Leach, M.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
JOURNAL	Patent: WO 0140521-A 1906 07-JUN-2001;				
FEATURES	Curagen Corporation (US)				
source	1..51	Location/Qualifiers			
misc_feature	26	/organism="Homo sapiens"			
		/mol_type="unassigned DNA"			
		/db_xref="taxon:9606"			
		/note="2 of 2 allelic variants (1905 is other entry)"			
		Accession number cg36603177"			
Query Match	1.6%	Score 38.8	DB 1	Length 51	
Best Local Similarity	86.0%	Pred. No. 1.7e+02			
Matches	43	Conservative 0	Mismatches 7	Indels 0	Gaps 0
QY	2268	GAGACAGGTTTCACCGTGTTAGCCAGGATGCTCTCGATCTCCGACCTC	2317		
Db	51	GAGACAGGTTTCATATGTTGGTAGGCTGCTCGAATCCATGATCTC	2		
RESULT 180					
AX159264/6					
LOCUS	AX159264	51 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 2592 from Patent WO0140521.				
ACCESSION	AX159264				
VERSION	AX159264.1	GI:14540595			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Shimkets, R.A. and Leach, M.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
JOURNAL	Patent: WO 0140521-A 2592 07-JUN-2001;				
FEATURES	Curagen Corporation (US)				
source	1..51	Location/Qualifiers			
misc_feature	26	/organism="Homo sapiens"			
		/mol_type="unassigned DNA"			
		/db_xref="taxon:9606"			
		/note="2 of 2 allelic variants (2591 is other entry)"			
		Accession number cg40949022"			
Query Match	1.6%	Score 38.8	DB 1	Length 51	
Best Local Similarity	86.0%	Pred. No. 1.7e+02			
Matches	43	Conservative 0	Mismatches 7	Indels 0	Gaps 0

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Db      2 CTACAGGCACGGCCACACCGCGCTAATTTTGTGTAATTTTAGTAGA 51

RESULT 183
LOCUS   AX159155
DEFINITION Sequence 2483 from Patent WO0140521.
ACCESSION AX159155
VERSION  AX159155.1 GI:14540486
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Shimkets, R.A. and Leach, M.
TITLE    Nucleic acids containing single nucleotide polymorphisms and
         methods of use thereof
JOURNAL  Patent: WO 0140521-A 2483 07-JUN-2001;
         Curagen Corporation (US)
FEATURES
         source
         Location/Qualifiers
             1..51
                 /organism="Homo sapiens"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:9606"
         misc_feature
             26
                 /note="1 of 2 allelic variants (2484 is other entry)"
                 Accession number CG93704218"

Query Match      1.6%; Score 38.6; DB 1; Length 51;
Best Local Similarity 91.1%; Pred. No. 1.7e+02;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  2318 GFGATCCGCCACCTCGCGCTCCCAAAGTCTGGGATTACAGGCA 2362
      |||||
Db   7 GCGATCTCCCAACCGCGCGCTCCCAAAGTCTGGGATTACAGGCA 51

RESULT 184
LOCUS   A68621/c
DEFINITION Sequence 1 from Patent WO9801573.
ACCESSION A68621
VERSION  A68621.1 GI:4759648
KEYWORDS
SOURCE  unidentified
         unclassified.
REFERENCE
AUTHORS  Resnick, M.A., Larionov, V.L., Koupriina, N.Y. and Perkins, E.L.
TITLE    TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING
JOURNAL  Patent: WO 9801573-A 1 15-JAN-1998;
         US HEALTH (US)
FEATURES
         source
         Location/Qualifiers
             1..40
                 /organism="unidentified"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:32644"

Query Match      1.6%; Score 38.4; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 1.6e+02;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2332 TCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 2371
      |||||
Db   40 TCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 1

RESULT 185
LOCUS   AR208401
DEFINITION Sequence 17 from patent US 6383752.
ACCESSION AR208401

Db      2 CTACAGGCACGGCCACACCGCGCTAATTTTGTGTAATTTTAGTAGA 51

VERSION AR208401.1 GI:21509546
KEYWORDS Unknown.
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS  Agrawal, S. and Kandimala, E.R.
TITLE    Pseudo-cyclic oligonucleobases
JOURNAL  Patent: US 6383752-A 17 07-MAY-2002;
         Location/Qualifiers
FEATURES
         source
         Location/Qualifiers
             1..40
                 /organism="unknown"
                 /mol_type="unassigned DNA"

Query Match      1.6%; Score 38.4; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 1.6e+02;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  659 GGACTCAGGTACATCTGTGAGTGAGAACACAGGTGTCACTT 698
      |||||
Db   1 GGACCCAGGTACATCTGTGAGTGAGAACACAGGTGTCACTT 40

RESULT 186
LOCUS   AX160116
DEFINITION Sequence 3444 from Patent WO0140521.
ACCESSION AX160116
VERSION  AX160116.1 GI:14541447
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Shimkets, R.A. and Leach, M.
TITLE    Nucleic acids containing single nucleotide polymorphisms and
         methods of use thereof
JOURNAL  Patent: WO 0140521-A 3444 07-JUN-2001;
         Curagen Corporation (US)
FEATURES
         source
         Location/Qualifiers
             1..50
                 /organism="Homo sapiens"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:9606"
         misc_feature
             25..26
                 /note="Nucleotide deleted between bases 25 and 26"
                 Accession number CG43271020"

Query Match      1.6%; Score 38.4; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY  2241 CTGGCTAATTTTGTGTAATTTTAGTAGAGAGGGTTTCACTGT 2288
      |||||
Db   3 CCCAGCTAATTTTGTGTAATTTTAGTAGAGAGGGTTTCACTGT 50

RESULT 187
LOCUS   AX156917
DEFINITION Sequence 245 from Patent WO0140521.
ACCESSION AX156917
VERSION  AX156917.1 GI:14538248
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Shimkets, R.A. and Leach, M.

```

TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 245 07-JUN-2001;  
Curagen Corporation (US)

FEATURES  
source Location/Qualifiers  
1..51  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

misc\_feature  
26  
/note="1 of 2 allelic variants (246 is other entry)"  
Accession number CG1782027

Query Match 1.6%; Score 38.4; DB 1; Length 51;  
Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2318 GTGATCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGATGA 2365  
Db 4 GTGATCCTCTGCTCGGCTCTCAAAGTCTGGGATTACAGATATGA 51

RESULT 188  
AX160427  
LOCUS AX160427 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 3755 from Patent WO0140521.  
ACCESSION AX160427  
VERSION AX160427.1 GI:14541758

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 Shimkets, R.A. and Leach, M.  
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
Patent: WO 0140521-A 3755 07-JUN-2001;  
Curagen Corporation (US)

FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

misc\_feature  
26  
/note="1 of 2 allelic variants (3756 is other entry)"  
Accession number CG43919529

Query Match 1.6%; Score 38.4; DB 1; Length 51;  
Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGGTTTCACGGTTTAGCCAGGATGCTCGATC 2307  
Db 4 TTTTAGTAGACAGAGGGTTTCACCATGTTGCCAGGCTGCTTGAAC 51

RESULT 189  
AX514184/C  
LOCUS AX514184 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 382 from Patent WO02052044.  
ACCESSION AX514184  
VERSION AX514184.1 GI:23560548

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
Detection of genetic polymorphisms  
Patent: WO 02052044-A 382 04-JUL-2002;  
Riken (JP)

FEATURES  
source Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.6%; Score 37.4; DB 1; Length 41;  
Best Local Similarity 92.7%; Pred. No. 1.8e+02;  
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2328 CACCTCGGCTCCCAAGTCTGGGATTACAGGATGAGCC 2368  
Db 41 CGCCTCGGCTCCCAAGTGTGGGATTACAGCGTGAGCC 1

RESULT 190  
AX514544  
LOCUS AX514544 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 742 from Patent WO02052044.  
ACCESSION AX514544  
VERSION AX514544.1 GI:23561073

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
Detection of genetic polymorphisms  
Patent: WO 02052044-A 742 04-JUL-2002;  
Riken (JP)

FEATURES  
source Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.6%; Score 37.4; DB 1; Length 41;  
Best Local Similarity 92.7%; Pred. No. 1.8e+02;  
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2314 CCTCGTGATCCGCCACCTCGGCTCCCAAGTGTGGAT 2354  
Db 1 CCTCGTGATTTGCCACCTCRGCTCCCAAGTGTGGAT 41

RESULT 191  
AX514746  
LOCUS AX514746 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 944 from Patent WO02052044.  
ACCESSION AX514746  
VERSION AX514746.1 GI:23561396

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
Detection of genetic polymorphisms  
Patent: WO 02052044-A 944 04-JUL-2002;  
Riken (JP)

FEATURES  
source Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.6%; Score 37.4; DB 1; Length 41;  
Best Local Similarity 92.7%; Pred. No. 1.8e+02;  
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2264 AGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGCTCG 2304

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Db      1 AGTAGAGCGGGTTTACCTGTTAGCCACGATGCTCG 41
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RESULT 192
AX520135
LOCUS      41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6333 from Patent WO02052044.
ACCESSION AX520135
VERSION    AX520135.1 GI:23570620
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE      Detection of genetic polymorphisms
JOURNAL    Patent: WO 02052044-A 6333 04-JUL-2002;
            Riken (JP)
FEATURES   Location/Qualifiers
            source
            1..41
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      2314 CCTGTGATCGCCACCTCGCTCCCAAGTCTGGGAT 2354
|||||
Db      1 CCTGTGATTTGCCACCTCGCTCCCAAGTCTGGGAT 41
|||||
RESULT 193
AX520215/c
LOCUS      41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6413 from Patent WO02052044.
ACCESSION AX520215
VERSION    AX520215.1 GI:23570721
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE      Detection of genetic polymorphisms
JOURNAL    Patent: WO 02052044-A 6413 04-JUL-2002;
            Riken (JP)
FEATURES   Location/Qualifiers
            source
            1..41
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      2328 CACCTCGCCCTCCCAAGTCTGGGATTCAGGCATGAGCC 2368
|||||
Db      41 GCCTCGCCCTCCCAAGTGTGGGATTACAGGCGTGAGCC 1
|||||
RESULT 194
AX520756
LOCUS      41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6954 from Patent WO02052044.
ACCESSION AX520756
VERSION    AX520756.1 GI:23571411
KEYWORDS

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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE      Detection of genetic polymorphisms
JOURNAL    Patent: WO 02052044-A 6954 04-JUL-2002;
            Riken (JP)
FEATURES   Location/Qualifiers
            source
            1..41
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      2264 AGTAGAGACAGGGTTTACCGTGTAGCCAGGATGCTCG 2304
|||||
Db      1 AGTAGAGCGGGTTTACCTGTTAGCCACGATGCTCG 41
|||||
RESULT 195
HUMALUANC/c
LOCUS      42 bp DNA linear PRI 08-OCT-1994
DEFINITION Homo sapiens 4000 year old remains from Nekht-anhk Alu repeat
            fragment 12.4.
ACCESSION L36838
VERSION    L36838.1 GI:556195
KEYWORDS   Alu repeat.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (sites)
AUTHORS    Paabo, S.
TITLE      Ancient DNA: extraction, characterization, molecular cloning, and
            enzymatic amplification
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
MEDLINE    89184542
PUBMED     2928314
COMMENT     Original source text: Homo sapiens (individual isolate 4000 year
            old remains from Nekht-anhk) liver DNA.
FEATURES   Location/Qualifiers
            source
            1..42
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /isolate="4000 year old remains from Nekht-anhk"
            /db_xref="taxon:9606"
            /tissue type="liver"
            repeat_region <1..>42
            /rpt_family="Alu"
Query Match      1.6%; Score 37.2; DB 1; Length 42;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      2311 TGACCTCGTGATCGCCACCTCGCTCCCAAGTCTGGG 2352
|||||
Db      42 TGACCTCGTGATCCACCGCTCGGCTCCCAAGTCTGGG 1
|||||
RESULT 196
AR291264
LOCUS      47 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2999 from patent US 6537751.
ACCESSION AR291264
VERSION    AR291264.1 GI:31678548
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
        disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 2999 25-MAR-2003;
FEATURES
    source      Location/Qualifiers
        1..47
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.6%; Score 37; DB 1; Length 47;
Best Local Similarity 85.1%; Pred. No. 2e+02;
Matches 40; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2322 TCGCCACCTCGGCTCCCAAGTGTGGATTACAGGATGAGCC 2368
      |||||
Db 1 TCGCCCTGCTCAGCTCCCAAGTGTGGATTATAGGCTGAGCC 47

RESULT 197
LOCUS HUMALUANCA
DEFINITION Homo sapiens 4000 year old remains from Nekht-anKh Alu repeat
        fragment 11:2.
ACCESSION L36835
VERSION L36835.1 GI:556193
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Paabo,S.
TITLE Ancient DNA: extraction, characterization, molecular cloning, and
        enzymatic amplification
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
MEDLINE 89184542
PUBMED 2928314
COMMENT Original source text: Homo sapiens (individual isolate 4000 year
        old remains from Nekht-anKh) .liver DNA.
FEATURES
    source      Location/Qualifiers
        1..41
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /isolate="4000 year old remains from Nekht-anKh"
            /db_xref="taxon:9606"
            /tissue_type="liver"
            <1..>41
            /rpt_family="Alu"

        repeat_region

Query Match      1.5%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 2.2e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2312 GACCTCGTGTGCTCGCCACCTCGGCTCCCAAGTGTCTGG 2351
      |||||
Db 41 GACCTCGTGTGCTCGCTCGGCTCCCAAGTGTCTGG 2

RESULT 198
LOCUS AX160004
DEFINITION Sequence 3332 from Patent WO0140521.
ACCESSION AX160004
VERSION AX160004.1 GI:14541335
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.

TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: WO 0140521-A 3332 07-JUN-2001;
        Curagen Corporation (US)
FEATURES
    source      Location/Qualifiers
        1..44
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

        misc_feature
            19
                /notes="2 of 2 allelic variants (3331 is other entry)"
                Accession number CG43247846"

Query Match      1.5%; Score 35.2; DB 1; Length 44;
Best Local Similarity 92.5%; Pred. No. 2.3e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2316 TCGTGTGCTCGCCACCTCGGCTCCCAAGTGTCTGGATT 2355
      |||||
Db 5 TCATGATCGCGCGCTCGGCTCTCAAAAGTGTCTGGATT 44

RESULT 199
LOCUS HSLAS33
DEFINITION H. sapiens DNA for loop attachment sequence (clone LAS33).
ACCESSION X91548
VERSION X91548.1 GI:987907
KEYWORDS loop attachment sequence.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS Jackson,D.A., Bartlett,J. and Cook,P.R.
TITLE Sequences attaching loops of nuclear and mitochondrial DNA to
        underlying structures in human cells: the role of transcription
        unite
JOURNAL Nucleic Acids Res. 24 (7), 1212-1219 (1996)
MEDLINE 96188852
PUBMED 8614621
REFERENCE 2 (bases 1 to 43)
AUTHORS Cook,P.R.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1995) P.R. Cook, Sir William Dunn School of
        Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE,
        UK
COMMENT Related sequence: Proc.Natl.Acad.Sci. USA 85:4775-4778(1988) .
FEATURES
    source      Location/Qualifiers
        1..43
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="LAS33"
            /cell_line="HeLa"
            /clone_lib="DNA loop attachment sequences (LAS)"
            /notes="DNA loop attachment site (LAS)"

        misc_feature
            1..43
                /rpt_family="Alu"

        repeat_region

Query Match      1.5%; Score 35; DB 1; Length 43;
Best Local Similarity 88.4%; Pred. No. 2.3e+02;
Matches 38; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTGATCTCTGACCTCGTACCTCGGCGCCACCTCG 2334
      |||||
Db 1 CCGGATGGTCTTGATCTCTTGACCTTGATCGCGCGCTCG 43

RESULT 200
LOCUS AX516778
DEFINITION Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.

```

DEFINITION Sequence 2976 from Patent WO02052044.  
ACCESSION AX516778  
VERSION AX516778.1 GI:23564830  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 2976 04-JUL-2002;  
Riken (JP)  
FEATURES  
source Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1..5%; Score 34.8; DB 1; Length 41;  
Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
Matches 36; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2092 TTTTTCGAGCCGAGCTTGCTCTGTACCCAGGCTGG 2131  
|||||  
Db 1 TTTTTCGAGATGGAGCTGCTCTGTGCCAGGCTGG 40  
|||||  
RESULT 201  
AX518941  
LOCUS AX518941  
DEFINITION Sequence 5139 from Patent WO02052044.  
ACCESSION AX518941  
VERSION AX518941.1 GI:23568913  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 5139 04-JUL-2002;  
Riken (JP)  
FEATURES  
source Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1..5%; Score 34.8; DB 1; Length 41;  
Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
Matches 36; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2092 TTTTTCGAGCCGAGCTTGCTCTGTACCCAGGCTGG 2131  
|||||  
Db 1 TTTTTCGAGATGGAGCTGCTCTGTGCCAGGCTGG 40  
|||||  
RESULT 202  
A22672  
LOCUS A22672  
DEFINITION Oligonucleotide.  
ACCESSION A22672  
VERSION A22672.1 GI:1247933  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Anand, R.  
TITLE Nucleotide sequences  
JOURNAL Patent: EP 0518583-A 10 16-DEC-1992;  
Riken (JP)

FEATURES  
source Location/Qualifiers  
1..35  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
Query Match 1..4%; Score 34.2; DB 1; Length 35;  
Best Local Similarity 94.3%; Pred. No. 2.3e+02;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2335 GCCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 2369  
|||||  
Db 1 GCCTCCCAAAGTCTGGGATTACAGGYRTGAGCCA 35  
|||||  
RESULT 203  
I21796  
LOCUS I21796  
DEFINITION Sequence 10 from patent US 5525467.  
ACCESSION I21796  
VERSION I21796.1 GI:1602150  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Anand, R.  
TITLE Nucleotide sequences  
JOURNAL Patent: US 5525467-A 10 11-JUN-1996;  
Riken (JP)  
FEATURES  
source Location/Qualifiers  
1..35  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1..4%; Score 34.2; DB 1; Length 35;  
Best Local Similarity 94.3%; Pred. No. 2.3e+02;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2335 GCCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 2369  
|||||  
Db 1 GCCTCCCAAAGTCTGGGATTACAGGYRTGAGCCA 35  
|||||  
RESULT 204  
AX709023  
LOCUS AX709023  
DEFINITION Sequence 47 from Patent WO03008443.  
ACCESSION AX709023  
VERSION AX709023.1 GI:29564696  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Averback, P.A.  
TITLE Peptides effective in the treatment of tumors and other conditions  
JOURNAL requiring the removal or destruction of cells  
Patent: WO 03008443-A 47 30-JAN-2003;  
Nymox Corporation (CA)  
FEATURES  
source Location/Qualifiers  
1..39  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/notes="Synthetic oligonucleotide"  
Query Match 1..4%; Score 34.2; DB 1; Length 39;  
Best Local Similarity 92.3%; Pred. No. 2.4e+02;  
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2326 CCCACCTCGGCTCCCAAGTCTGGGATTACAGGCATG 2364  
|||||

Db 1 CCTCCCTCGGCCTCCCAAAGTGTGGGATTACAGGCGTG 39

RESULT 205  
AX514185/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AX514185 41 bp DNA linear PAT 05-OCT-2002  
Sequence 383 from Patent WO02052044.  
AX514185  
AX514185.1 GI:23560550  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

1  
Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
Detection of genetic polymorphisms  
Patent: WO 02052044-A 383 04-JUL-2002;  
Riken (JP)  
Location/Qualifiers  
source  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.4%; Score 34.2; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 2.5e+02;  
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCGGCCACCTCGGCTCCCAAAGTG 2347  
Db 41 CTCCTGACTTTGTGATGCACGCGCTCGGCTCCCAAAGTG 1

RESULT 206  
AX520216/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AX520216 41 bp DNA linear PAT 05-OCT-2002  
Sequence 6414 from Patent WO02052044.  
AX520216  
AX520216.1 GI:23570722  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

1  
Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
Detection of genetic polymorphisms  
Patent: WO 02052044-A 6414 04-JUL-2002;  
Riken (JP)  
Location/Qualifiers  
source  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.4%; Score 34.2; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 2.5e+02;  
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCGGCCACCTCGGCTCCCAAAGTG 2347  
Db 41 CTCCTGACTTTGTGATGCACGCGCTCGGCTCCCAAAGTG 1

RESULT 207  
AX709009  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AX709009 42 bp DNA linear PAT 04-APR-2003  
Sequence 33 from Patent WO03008443.  
AX709009  
AX709009.1 GI:29564682  
synthetic construct

ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

synthetic construct  
artificial sequences.  
1  
Averback, P.A.  
Peptides effective in the treatment of tumors and other conditions  
requiring the removal or destruction of cells  
Patent: WO 03008443-A 33 30-JAN-2003;  
Nymox Corporation (CA)  
Location/Qualifiers  
source  
1..42  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/notes="Synthetic oligonucleotide"

Query Match 1.4%; Score 34; DB 1; Length 42;  
Best Local Similarity 88.1%; Pred. No. 2.6e+02;  
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2322 TCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCGAT 2363  
Db 1 TCCACCTGCTCAGCTCCCAAAGTGTGGGATTACAGGCGT 42

RESULT 208  
CO760643  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CO760643 45 bp DNA linear PAT 03-MAR-2004  
Sequence 85 from Patent WO2004003229.  
CO760643  
CO760643.1 GI:44904146  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

1  
Nex, B.R., Vogel, U., Rockenbauer, E. and Bukowy, Z.K.  
Disease risk estimating method using sequence polymorphisms in a  
specific region of chromosome 19  
Patent: WO 2004003229-A 85 08-JAN-2004;  
Aarhus University (DK); Arbejdsmiljø Institut (National  
Institute of Occupational Health) (DK)  
Location/Qualifiers  
source  
1..45  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/notes="Probe"

Query Match 1.4%; Score 34; DB 1; Length 45;  
Best Local Similarity 84.1%; Pred. No. 2.6e+02;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGCTTCCACCGTTAGCCAGG 2295  
Db 1 TTTTGTATCTTTTAGTAGACAGGCTTCTCCATGTTGGTCAGG 44

RESULT 209  
AX516379/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AX516379 41 bp DNA linear PAT 05-OCT-2002  
Sequence 2577 from Patent WO02052044.  
AX516379  
AX516379.1 GI:23564062  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

1  
Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
Detection of genetic polymorphisms  
Patent: WO 02052044-A 2577 04-JUL-2002;  
Riken (JP)

```

FEATURES
  source
    Location/Qualifiers
      1..41
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 1.4%; Score 33.6; DB 1; Length 41;
  Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2326 CCACCTGGCTCCCAAGTCTGGGATTACAGGCATGA 2365
  |||||
Db 40 CCACCTGGCTCCCAAGTCTGGGATTACAGGCATGA 1

RESULT 210
LOCUS AX160003 44 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3331 from Patent WO0140521.
ACCESSION AX160003
VERSION AX160003.1 GI:14541334
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
Patent: WO 0140521-A 3331 07-JUN-2001;
Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..44
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      19
        /note="1 of 2 allelic variants (3332 is other entry)"
        Accession number CG43247846"

Query Match
  Best Local Similarity 1.4%; Score 33.6; DB 1; Length 44;
  Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2316 TCGTATCGCCACCTCGGCTCCCAAGTCTGGGATT 2355
  |||||
Db 5 TCATGATCGCCGCTCGGCTCTCAAAAGTCTGGGATT 44

RESULT 211
LOCUS A25212 35 bp DNA linear PAT 11-APR-1995
DEFINITION inter-Alu specific primer DNA (pdj33) from patent WO9213101.
ACCESSION A25212
VERSION A25212.1 GI:904592
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 35)
AUTHORS
TITLE METHOD OF DETECTING DNA SEQUENCE VARIATION
JOURNAL Patent: WO 9213101-A 3 06-AUG-1992;
FEATURES
  source
    Location/Qualifiers
      1..35
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 1.4%; Score 33.4; DB 1; Length 35;
  Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 2369
  |||||
Db 1 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 35

RESULT 212
LOCUS E09140 35 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for Alu specific primer.
ACCESSION E09140
VERSION E09140.1 GI:22025766
KEYWORDS JP 1995115999-A/3.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 35)
AUTHORS Andureau, H.A. and Yan, F.
TITLE DETECTING METHOD FOR DNA ARRANGEMENT VARIATION
JOURNAL Patent: JP 1995115999-A 3 09-MAY-1995;
INGENII BV
COMMENT OS None
OC Artificial sequences.
PN JP 1995115999-A/3
PD 09-MAY-1995
PF 22-MAY-1992 JP 1992130668
PI ANDOREASU HERARUDOUSU AITSUTERURINDEN, YAN FUEIKU PC
CI2Q1/68, CI2N15/00, GOIN27/447, GOIN27/447;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH
FT source 1..35
FT misc_feature 1..35 /organism='Artificial sequences' FT
FT /note='Alu specific primer'.
FEATURES
  source
    Location/Qualifiers
      1..35
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 1.4%; Score 33.4; DB 1; Length 35;
  Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 2369
  |||||
Db 1 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 35

RESULT 213
LOCUS AX183780 40 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1533 from Patent WO0142511.
ACCESSION AX183780
VERSION AX183780.1 GI:15135106
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1533 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipse
Biotherapeutics Corporation (CA)
FEATURES
  source
    Location/Qualifiers
      1..40
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

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Query Match      1.4%; Score 32.6; DB 1; Length 40;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2277 TTTCCACGCTGTAGCCAGGATGGTCTCGATCTCTGACCT 2316
Db 40 TTTCCACGATGTAGTCAGCGTGGTCTCNAACTCTGACCT 1

RESULT 214
AX520711/c
LOCUS AX514703 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 901 from Patent WO02052044.
ACCESSION AX514703
VERSION AX514703.1 GI:23561309
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 901 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.4%; Score 32.6; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 2.9e+02;
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGCGGTTTCACCGTTAGCC 2292
Db 41 TTTTGTATTTTAGTAGAGAYGGGTTTCGCCATGTTGGCC 1

RESULT 215
AX520711/c
LOCUS AX520711 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6909 from Patent WO02052044.
ACCESSION AX520711
VERSION AX520711.1 GI:23571362
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6909 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.4%; Score 32.6; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 2.9e+02;
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGCGGTTTCACCGTTAGCC 2292
Db 41 TTTTGTATTTTAGTAGAGAYGGGTTTCGCCATGTTGGCC 1

RESULT 216
AX520711/c
LOCUS AX520711 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6909 from Patent WO02052044.
ACCESSION AX520711
VERSION AX520711.1 GI:23571362
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6909 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.4%; Score 32.6; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 2.9e+02;
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGCGGTTTCACCGTTAGCC 2292
Db 41 TTTTGTATTTTAGTAGAGAYGGGTTTCGCCATGTTGGCC 1

RESULT 217
AX514160/c
LOCUS AX514160 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 358 from Patent WO02052044.
ACCESSION AX514160
VERSION AX514160.1 GI:23560520
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 358 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2315 CTGCTGATCGCCACCTCGGCCTCCAAAGTCTGGGAT 2354
Db 40 CTGCTGATCTCTCTACCCGCTTCCAAAGTCTGGGAT 1

RESULT 218
AX520311/c
LOCUS AX520311 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6509 from Patent WO02052044.
ACCESSION AX520311
VERSION AX520311.1 GI:23570855
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6509 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.3%; Score 31.6; DB 1; Length 41;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 34; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGACAGCGGTTTCACCGTTAGCCAGGATGGTCT 2302
Db 41 TAGTAGAGACGGGGTTTCACYGTGTTGGTCAGCGCTGCT 2

RESULT 219
AX520311/c
LOCUS AX520311 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6509 from Patent WO02052044.
ACCESSION AX520311
VERSION AX520311.1 GI:23570855
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6509 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.3%; Score 31.6; DB 1; Length 41;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 34; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGACAGCGGTTTCACCGTTAGCCAGGATGGTCT 2302
Db 41 TAGTAGAGACGGGGTTTCACYGTGTTGGTCAGCGCTGCT 2
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REFERENCE 1  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 6509 04-JUL-2002;  
Riken (JP)  
FEATURES  
source  
Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.3%; Score 31.6; DB 1; Length 41;  
Best Local Similarity 85.0%; Pred. No. 3.2e+02;  
Matches 34; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2263 TAGTAGACAGCGGTTTACCGTGTACCCAGGATGGTCT 2302  
|||||  
Db 41 TAGTAGACAGCGGTTTACCGTGTACCCAGGATGGTCT 2  
|||||  
RESULT 219  
AX519117  
LOCUS AX519117 40 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 5315 from Patent WO02052044.  
ACCESSION AX519117  
VERSION AX519117.1 GI:23569187  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 5315 04-JUL-2002;  
Riken (JP)  
FEATURES  
source  
Location/Qualifiers  
1..40  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.3%; Score 31; DB 1; Length 40;  
Best Local Similarity 87.2%; Pred. No. 3.4e+02;  
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2257 TACTTTTAGTAGACAGCGGTTTACCGTGTACCCAGG 2295  
|||||  
Db 1 TACTTTTAGTAGACAGCGGTTTACCCATATTGCCAGG 39  
|||||  
RESULT 220  
AX513835/c  
LOCUS AX513835 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 33 from Patent WO02052044.  
ACCESSION AX513835  
VERSION AX513835.1 GI:23560039  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 33 04-JUL-2002;  
Riken (JP)  
FEATURES  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.3%; Score 31; DB 1; Length 41;  
Best Local Similarity 82.9%; Pred. No. 3.4e+02;  
Matches 34; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 2092 TTTTGTGAGACCGAGTCTTGTCTGTACCCAGGCTGGA 2132  
|||||  
Db 41 TTTTGTGAGATGAAGTCTTACTGTCTACCCCAAGCTGGA 1  
|||||  
RESULT 221  
AX517711/c  
LOCUS AX517711 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 3909 from Patent WO02052044.  
ACCESSION AX517711  
VERSION AX517711.1 GI:23566615  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 3909 04-JUL-2002;  
Riken (JP)  
FEATURES  
source  
Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.3%; Score 31; DB 1; Length 41;  
Best Local Similarity 82.9%; Pred. No. 3.4e+02;  
Matches 34; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 2092 TTTTGTGAGACCGAGTCTTGTCTGTACCCAGGCTGGA 2132  
|||||  
Db 41 TTTTGTGAGATGAAGTCTTACTGTCTACCCCAAGCTGGA 1  
|||||  
RESULT 222  
AX519988  
LOCUS AX519988 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 6186 from Patent WO02052044.  
ACCESSION AX519988  
VERSION AX519988.1 GI:23570430  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 6186 04-JUL-2002;  
Riken (JP)  
FEATURES  
source  
Location/Qualifiers  
1..41  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.3%; Score 31; DB 1; Length 41;  
Best Local Similarity 82.9%; Pred. No. 3.4e+02;  
Matches 34; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 2272 CAGGGTTTACCGTGTACCCAGGATGGTCTCGATCTCCTG 2312  
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Db 1 CAGAGTTTACCATGTTGGCYAGGCTGTCTTGAACCTCTG 41  
|||||  
RESULT 223  
AX520856

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LOCUS AX520856 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 7054 from Patent WO02052044.
ACCESSION AX520856
VERSION AX520856.1 GI:23571532
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of Genetic Polymorphisms
JOURNAL Patent: WO 02052044-A 7054 04-JUL-2002;
Riken (JP)
FEATURES
source 1..41
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 82.9%; Pred. No. 3.4e+02;
Matches 34; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2195 GCCTCAGCCTCCCAATTAGTTCGCTACAGTACATCTGCCA 2235
Db 1 GCCTCAGCCTCCCAAGTAGCGGAGCTACAGGCGCTGCCA 41
RESULT 224
AX709012
LOCUS AX709012 33 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 36 from Patent WO03008443.
ACCESSION AX709012
VERSION AX709012.1 GI:29564685
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Averbach,P.A.
TITLE Peptides effective in the treatment of tumors and other conditions
requiring the removal or destruction of cells
JOURNAL Patent: WO 03008443-A 36 30-JAN-2003;
Nymox Corporation (CA)
FEATURES
source 1..33
/mol_type="synthetic construct"
/mol_types="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
Query Match 1.3%; Score 29.8; DB 1; Length 33;
Best Local Similarity 93.9%; Pred. No. 3.6e+02;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2331 CTCGGCCTCCCAAGTCTGGATTACAGGCAT 2363
Db 1 CTCAGCCTCCCAAGTCTGGATTACAGCGT 33
RESULT 225
AR208404/c
LOCUS AR208404 29 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 20 from patent US 6383752.
ACCESSION AR208404
VERSION AR208404.1 GI:21509549
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Agrawal,S. and Kandimalla,E.R.
TITLE Pseudo-cyclic oligonucleobases
JOURNAL Patent: US 6383752-A 20 07-MAY-2002;
FEATURES
source 1..29
/mol_type="unassigned DNA"
Query Match 1.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 649 AGGAATCATCGGACTCAGGTACATCTGTG 677
Db 29 AGGAATCATCGGACTCAGGTACATCTGTG 1
RESULT 226
BD169435
LOCUS BD169435 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Genomes participating in rheumatoid arthritis, method of diagnosing
the same, method of judging the onset risk thereof, kit for
detecting and diagnosing the same, method of treating rheumatoid
arthritis and remedies therefor.
ACCESSION BD169435
VERSION BD169435.1 GI:27875247
KEYWORDS WO 0234912-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Shiozawa,S. and Konishi,Y.
TITLE Genomes participating in rheumatoid arthritis, method of diagnosing
the same, method of judging the onset risk thereof, kit for
detecting and diagnosing the same, method of treating rheumatoid
arthritis and remedies therefor
JOURNAL Patent: WO 0234912-A 12 02-MAY-2002;
SHUNICHI SHIOZAWA,YOSHITAKE KONISHI
COMMENT OS Artificial Sequence
PN WO 0234912-A/12
PD 02-MAY-2002
PF 24-OCT-2001 WO 2001JP009313
PR 24-OCT-2000 JP 00P 324296,27-MAR-2001 JP 01P 090546 PR
30-MAR-2001 JP 01P 099990
PI SHUNICHI SHIOZAWA,YOSHITAKE KONISHI
PC C12N15/12,C07K14/47,C12Q1/68,G01N33/50,A61K38/17,A61K48/00 CC
FH Key Location/Qualifiers
FT source 1..30
FT /organism='Artificial Sequence'.
FEATURES
source 1..30
/mol_type="synthetic construct"
/mol_types="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.2%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2295 GATGGTCTCGATCTCTGACCTCGTGATCC 2324
Db 1 GATGGTCTTGATCTCTGACCTCGTGATCC 30
RESULT 227
BD169436/c
LOCUS BD169436 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Genomes participating in rheumatoid arthritis, method of diagnosing
the same, method of judging the onset risk thereof, kit for
detecting and diagnosing the same, method of treating rheumatoid
arthritis and remedies therefor.
ACCESSION BD169436
VERSION BD169436.1 GI:27875248
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KEYWORDS      WO 0234912-A/13.
SOURCE         synthetic construct
ORGANISM       artificial construct
REFERENCE      1 (bases 1 to 30)
AUTHORS        Shiozawa,S. and Konishi,Y.
TITLE          Genomes participating in rheumatoid arthritis, method of diagnosing
                the same, method of judging the onset risk thereof, kit for
                detecting and diagnosing the same, method of treating rheumatoid
                arthritis and remedies therefor
JOURNAL        Patent: WO 0234912-A 13 02-MAY-2002;
COMMENT        SHUNICHI SHIOZAWA,YOSHITAKE KONISHI
                OS Artificial Sequence
                PN WO 0234912-A/13
                PD 02-MAY-2002
                PF 24-OCT-2001 WO 2001JP009313
                PR 24-OCT-2000 JP ODP 324296,27-MAR-2001 JP O1P 090546 PR
                30-MAR-2001 JP O1P 099990
                PI SHUNICHI SHIOZAWA,YOSHITAKE KONISHI
                PC C12N15/12 C07K14/47 C12Q1/68 G01N33/50 A61K38/17 A61K48/00 CC
                Synthesized oligonucleotide
                FH key Location/Qualifiers
                FT source 1..30
                FT Location/Qualifiers
                FT 1..30 /organism='Artificial Sequence'.
FEATURES
  source
    Query Match 1..2%; Score 28.4; DB 1; Length 30;
    Best Local Similarity 96.7%; Pred. No. 4e+02;
    Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 2295 GATGCTCTCGATCTCTCGACCTCGTGATCC 2324
    |||||
    Db 30 GATGCTCTGATCTCTCGACCTCGTGATCC 1
RESULT 228
LOCUS          AR089907
DEFINITION     Sequence 27 from patent US 5994076.
ACCESSION      AR089907
VERSION        AR089907.1 GI:10016662
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE          Methods of assaying differential expression
JOURNAL        Patent: US 5994076-A 27 30-NOV-1999;
FEATURES
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    Query Match 1..2%; Score 28; DB 1; Length 28;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 920 GGAGATATGTTGTGAAAGACGAGTAGC 947
    |||||
    Db 1 GGAGATATGTTGTGAAAGACGAGTAGC 28
RESULT 229
LOCUS          AR089908/c
DEFINITION     Sequence 28 from patent US 5994076.
ACCESSION      AR089908
VERSION        AR089908.1 GI:10016663
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE          Methods of assaying differential expression
JOURNAL        Patent: US 5994076-A 27 30-NOV-1999;
FEATURES
  source
    Query Match 1..2%; Score 28; DB 1; Length 28;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 920 GGAGATATGTTGTGAAAGACGAGTAGC 947
    |||||
    Db 1 GGAGATATGTTGTGAAAGACGAGTAGC 28

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KEYWORDS       Unknown.
SOURCE         Unclassified.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE          Methods of assaying differential expression
JOURNAL        Patent: US 5994076-A 28 30-NOV-1999;
FEATURES
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    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1204 CCTAGCTGACTATTGGAAATGCATTC 1231
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    Db 28 CCTAGCTGACTATTGGAAATGCATTC 1
RESULT 230
LOCUS          AR196942
DEFINITION     Sequence 27 from patent US 6352829.
ACCESSION      AR196942
VERSION        AR196942.1 GI:20246791
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE          Methods of assaying differential expression
JOURNAL        Patent: US 6352829-A 27 05-MAR-2002;
FEATURES
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    Query Match 1..2%; Score 28; DB 1; Length 28;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 920 GGAGATATGTTGTGAAAGACGAGTAGC 947
    |||||
    Db 1 GGAGATATGTTGTGAAAGACGAGTAGC 28
RESULT 231
LOCUS          AR196943/c
DEFINITION     Sequence 28 from patent US 6352829.
ACCESSION      AR196943
VERSION        AR196943.1 GI:20246792
KEYWORDS       Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE          Methods of assaying differential expression
JOURNAL        Patent: US 6352829-A 28 05-MAR-2002;
FEATURES
  source
    Query Match 1..2%; Score 28; DB 1; Length 28;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1204 CCTTAGCTGACTATTGGAATGCACCTTC 1231
Db 28 CCTTAGCTGACTATTGGAATGCACCTTC 1

RESULT 232
AR208400
LOCUS AR208400 28 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 16 from patent US 6383752.
ACCESSION AR208400
VERSION AR208400.1 GI:21509544
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Agrawal,S. and Kandimala,E.R.
TITLE Pseudo-cyclic oligonucleobases
JOURNAL Patent: US 6383752-A 16 07-MAY-2002;
FEATURES
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        /organism="unknown"
        /mol_type="unassigned DNA"
    Query Match 1.2%; Score 28; DB 1; Length 28;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 671 ATCTGTGAGTGAGAACAGGTGTACCTT 698
Db 1 ATCTGTGAGTGAGAACAGGTGTACCTT 28

RESULT 233
AR259096
LOCUS AR259096 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 27 from patent US 6489455.
ACCESSION AR259096
VERSION AR259096.1 GI:27309607
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 27 03-DEC-2002;
FEATURES
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        /mol_type="genomic DNA"
    Query Match 1.2%; Score 28; DB 1; Length 28;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 920 GGAGATATGTTGTGAAGAGCAGCTAGC 947
Db 1 GGAGATATGTTGTGAAGAGCAGCTAGC 28

RESULT 234
AR259097/c
LOCUS AR259097 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 28 from patent US 6489455.
ACCESSION AR259097
VERSION AR259097.1 GI:27309608
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.

TITLE Methods of assaying differential expression
Patent: US 6489455-A 28 03-DEC-2002;
FEATURES
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        /organism="unknown"
        /mol_type="genomic DNA"
    Query Match 1.2%; Score 28; DB 1; Length 28;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1204 CCTTAGCTGACTATTGGAATGCACCTTC 1231
Db 28 CCTTAGCTGACTATTGGAATGCACCTTC 1

RESULT 235
AX184110/c
LOCUS AX184110 35 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1863 from Patent WO0142511.
ACCESSION AX184110
VERSION AX184110.1 GI:15135450
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1863 14-JUN-2001;
        WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
        Biotherapeutics Corporation (CA)
FEATURES
    source
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
    Query Match 1.2%; Score 27.6; DB 1; Length 35;
    Best Local Similarity 85.7%; Pred. No. 4.6e+02;
    Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2233 CCACCACACCTGGCTAATTTTGTACTTTAGTA 2267
Db 35 CCACAACGCCGCGCTAATTTTGTATTTTGTGTA 1

RESULT 236
A25214
LOCUS A25214 32 bp DNA linear PAT 11-APR-1995
DEFINITION Inter-Alu specific primer DNA (pdj33a) from patent WO9213101.
ACCESSION A25214
VERSION A25214.1 GI:904594
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 32)
AUTHORS
TITLE METHOD OF DETECTING DNA SEQUENCE VARIATION
JOURNAL Patent: WO 9213101-A 5 06-AUG-1992;
FEATURES
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
    Query Match 1.2%; Score 27.4; DB 1; Length 32;
    Best Local Similarity 96.8%; Pred. No. 4.5e+02;
    Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2332 TCGGCTCCCAAGAGTGTGGATTACAGG 2360

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Db      4 TCGGCTCCCAAGTCTGGGATTACAG 32
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E09142          32 bp      DNA      linear      PAT 29-SEP-1997
LOCUS          Synthetic DNA for Alu specific primer.
DEFINITION
ACCESSION
E09142
VERSION
E09142.1 GI:22025768
KEYWORDS
JP 1995115999-A/5.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Andreas,H.A. and Yan,P.
TITLE
DETECTING METHOD FOR DNA ARRANGEMENT VARIATION
JOURNAL
INGENII BV
COMMENT
OS None
OC Artificial sequences.
PN JP 1995115999-A/5
PD 09-MAY-1995
PF 22-MAY-1992 JP 1992130668
PI ANDOREASU HERARUDOUSU AITSUTERURINDEN, YAN FUEIKU PC
C12Q1/68.C12N15/00.G01N27/447.G01N27/447;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..32 /organism='Artificial sequences' FT
misc_feature 1..32 /notes='Alu specific primer'.
FT
FEATURES
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1..32
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 1.2%; Score 27.4; DB 1; Length 32;
Best Local Similarity 96.6%; Pred. No. 4.5e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2332 TCGGCTCCCAAGTCTGGGATTACAG 2360
|||||
Db      4 TCGGCTCCCAAGTCTGGGATTACAG 32
|||||
RESULT 237
E09142
LOCUS          26 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION
ACCESSION
AR208402
VERSION
AR208402.1 GI:21509547
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Agrawal,S. and Kandimalla,E.R.
TITLE
Pseudo-cyclic oligonucleobases
JOURNAL
Patent: US 6383752-A 18 07-MAY-2002;
FEATURES
source
1..26
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 1.1%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 622 ACAGGAAGTCTGGTAGTCAATCAG 647
|||||

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Db      1 ACAGGAAGTCTGGTAGTCAATCAG 26
|||||
RESULT 239
BD138344/c
LOCUS          26 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION
ACCESSION
BD138344
VERSION
BD138344.1 GI:23233289
KEYWORDS
JP 2002508944-A/270.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,T.L.M.
TITLE
Antisense modulation of human MDM2 expression
JOURNAL
Patent: JP 2002508944-A 270 26-MAR-2002;
ISIS PHARMACEUTICALS INC
COMMENT
OS Unidentified
PN JP 2002508944-A/270
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M
PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
FT source 1..26
/organism='Unidentified'.
FT Location/Qualifiers
1..26
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 1.1%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 415 TGAAGTTATTAAAGTCTGTTGGTGCA 440
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Db      26 TGAAGTTATTAAAGTCTGTTGGTGCA 1
|||||
RESULT 240
AR214391
LOCUS          30 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION
ACCESSION
AR214391
VERSION
AR214391.1 GI:23312044
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Sherr,C.J., Quelle,D., Roussel,M.F., Zindy,F. and Weber,J.D.
TITLE
ARF-P19, a novel regulator of the mammalian cell cycle
JOURNAL
Patent: US 6407062-A 35 18-JUN-2002;
FEATURES
source
1..30
/organism='unknown'
/mol_type='genomic DNA'
Query Match 1.1%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 5.1e+02;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Query Match      1.1%; Score 25.4; DB 1; Length 32;
Best Local Similarity 96.3%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/db_xref="taxon:32644"

QY 1764 ATGTGCTAACTTATTTCCCTAGTTG 1790
Db 32 ATGTGCTAACTTATTTCCCTAGCTG 6

RESULT 241
A72114/c
LOCUS AR228262
DEFINITION Sequence 69 from Patent WO9801467.
ACCESSION A72114
VERSION A72114.1 GI:4808071
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Lane,D., Boettger,V., Boettger,A., Picklesley,S., Hochkeppel,H.,
TITLE Garcia-Echeverria,C., Chene,P. and Furet,P.
JOURNAL INHIBITIONS OF THE INTERACTION BETWEEN P53 AND MDM2
FEATURES
source CIBA GEIGY AG (CH)
Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      1.1%; Score 25.4; DB 1; Length 32;
Best Local Similarity 96.3%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1764 ATGTGCTAACTTATTTCCCTAGTTG 1790
Db 32 ATGTGCTAACTTATTTCCCTAGCTG 6

RESULT 242
BD003106/c
LOCUS BD003106
DEFINITION Inhibitor of interaction between P53 and MDM2.
ACCESSION BD003106
VERSION BD003106.1 GI:18631067
KEYWORDS JP 2001500365-A/3.
SOURCE
ORGANISM
REFERENCE
AUTHORS Lane,D., Boettger,V., Boettger,A., Picklesley,S., Hochkeppel,H.K.,
TITLE Echeverria,C.G., Chene,P. and Furet,P.
JOURNAL Inhibitor of interaction between P53 and MDM2
COMMENT Patent: JP 2001500365-A 3 16-JAN-2001;
NOVARTIS AG,CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
OS Unidentified
PN JP 2001500365-A/3
PD 16-JAN-2001
PF 04-JUL-1997 JP 1998504775
PR 05-JUL-1996 GB 9614197.3,07-APR-1997 GB 9707041.1 PI
DAVID LANE,VOLKER BOTTGGER,ANGELIKA BOTTGGER,STEPHEN PICKSLEY, PI
HEINZ KURT HOCHKEPPEL,CARLOS GARCIA ECHEVERRIA,PATRICK CHENE, PI
PASCAL FURET
PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,C07K7/06,C07K7/08, PC
C12Q1/68.
PC G01N33/53//C07K14/82,C12N15/00,A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
FH Key 1..32 Location/Qualifiers
FT source 1..32 /organism='Unidentified'.
FEATURES
source Location/Qualifiers
1..32
/organism="unidentified"
/mol_type="genomic DNA"

Query Match      1.1%; Score 25.4; DB 1; Length 32;
Best Local Similarity 96.3%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1764 ATGTGCTAACTTATTTCCCTAGTTG 1790
Db 32 ATGTGCTAACTTATTTCCCTAGCTG 6

RESULT 243
AR228262
LOCUS AR228262
DEFINITION Sequence 4 from patent US 6448014.
ACCESSION AR228262
VERSION AR228262.1 GI:27267028
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Cloyd,M.W., Yen,C.-C. and Chen,J.
TITLE PCR-hybridization assays specific for integrated retroviruses
JOURNAL Patent: US 6448014-A 4 10-SEP-2002;
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAAGTCTGGATTACAG 2359
Db 1 GCCTCCCAAAGTCTGGATTACAG 25

RESULT 244
AX116120/c
LOCUS AX116120
DEFINITION Sequence 1243 from Patent WO0129262.
ACCESSION AX116120
VERSION AX116120.1 GI:14033062
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1243 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCTCCCAA 2209
Db 25 CCATTCTCTGCTCAGCTCCCAA 1

RESULT 245
AX693020
LOCUS AX693020
DEFINITION Sequence 25 bp DNA
PAT 31-MAR-2003

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DEFINITION Sequence 5752 from Patent EP1281758.  
ACCESSION AX693020  
VERSION AX693020.1 GI:29415983  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 5752 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES  
source  
1. .25  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred.No. 5.2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2274 GGGTTTCACCGTGTAGCCAGGATG 2298  
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Db 1 GGGTTTCACCGTGTAGCCAGGATG 25  
RESULT 246  
AX693021  
LOCUS AX693021 25 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5753 from Patent EP1281758.  
ACCESSION AX693021  
VERSION AX693021.1 GI:29415984  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 5753 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES  
source  
1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred.No. 5.2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2275 GGTTCACCGTGTAGCCAGGATGG 2299  
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Db 1 GGTTCACCGTGTAGCCAGGATGG 25  
RESULT 247  
AX693022  
LOCUS AX693022 25 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5754 from Patent EP1281758.  
ACCESSION AX693022  
VERSION AX693022.1 GI:29415985  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1

AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 5754 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES  
source  
1. .25  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred.No. 5.2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2276 GTTTCACCGTGTAGCCAGGATGGT 2300  
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Db 1 GTTTCACCGTGTAGCCAGGATGGT 25  
RESULT 248  
AX693023  
LOCUS AX693023 25 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5755 from Patent EP1281758.  
ACCESSION AX693023  
VERSION AX693023.1 GI:29415986  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 5755 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES  
source  
1. .25  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred.No. 5.2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2277 TTTCACCGTGTAGCCAGGATGGTC 2301  
|||||  
Db 1 TTTCACCGTGTAGCCAGGATGGTC 25  
RESULT 249  
AX693024  
LOCUS AX693024 25 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5756 from Patent EP1281758.  
ACCESSION AX693024  
VERSION AX693024.1 GI:29415987  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 5756 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES  
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1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTAGCCAGGATGGTCT 2302  
 |||||  
 Db 1 TTCACCGTGTAGCCAGGATGGTCT 25

RESULT 250  
 AX693025  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5757 from Patent EPI281758.  
 ACCESSION AX693025  
 VERSION AX693025.1 GI:29415988  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5757 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2279 TCACCGTGTAGCCAGGATGGTCTC 2303  
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 Db 1 TCACCGTGTAGCCAGGATGGTCTC 25

RESULT 251  
 AX693026  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5758 from Patent EPI281758.  
 ACCESSION AX693026  
 VERSION AX693026.1 GI:29415989  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5758 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCG 2304  
 |||||  
 Db 1 CACCGTGTAGCCAGGATGGTCTCG 25

RESULT 252  
 AX693027  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5759 from Patent EPI281758.  
 ACCESSION AX693027  
 VERSION AX693027.1 GI:29415990  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM

REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5759 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2281 ACCGTGTAGCCAGGATGGTCTCGA 2305  
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 Db 1 ACCGTGTAGCCAGGATGGTCTCGA 25

RESULT 253  
 AX693028  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5760 from Patent EPI281758.  
 ACCESSION AX693028  
 VERSION AX693028.1 GI:29415991  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5760 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2282 CCGTGTAGCCAGGATGGTCTCGAT 2306  
 |||||  
 Db 1 CCGTGTAGCCAGGATGGTCTCGAT 25

RESULT 254  
 AX693029  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5761 from Patent EPI281758.  
 ACCESSION AX693029  
 VERSION AX693029.1 GI:29415992  
 KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5761 05-FEB-2003;

FEATURES  
source Location/Qualifiers  
1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2283 CGGTAGCCAGGATGGTCTCGATC 2307  
|||||  
Db 1 CGGTAGCCAGGATGGTCTCGATC 25

RESULT 255  
AX693030  
LOCUS AX693030 25 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5762 from Patent EP1281758.  
ACCESSION AX693030  
VERSION AX693030.1 GI:29415993

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5762 05-FEB-2003;

FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2284 GTGTTAGCCAGGATGGTCTCGATCT 2308  
|||||  
Db 1 GTGTTAGCCAGGATGGTCTCGATCT 25

RESULT 256  
AX693031  
LOCUS AX693031 25 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5763 from Patent EP1281758.  
ACCESSION AX693031  
VERSION AX693031.1 GI:29415994

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5763 05-FEB-2003;

FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGGTCTCGATCTC 2309  
|||||  
Db 1 TGTAGCCAGGATGGTCTCGATCTC 25

RESULT 257  
AX693032  
LOCUS AX693032 25 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5764 from Patent EP1281758.  
ACCESSION AX693032  
VERSION AX693032.1 GI:29415995

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5764 05-FEB-2003;

FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGATCTCC 2310  
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Db 1 GTTAGCCAGGATGGTCTCGATCTCC 25

RESULT 258  
AX693033  
LOCUS AX693033 25 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5765 from Patent EP1281758.  
ACCESSION AX693033  
VERSION AX693033.1 GI:29415996

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5765 05-FEB-2003;

FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2287 TTAGCCAGGATGGTCTCGATCTCCT 2311

Db 1 TTAGCCAGGATGGTCTCGATCTCCT 25

RESULT 259

AX693034

LOCUS

DEFINITION

AX693034

ACCESSION

VERSION

AX693034.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .25

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match

Best Local Similarity

Matches 25; Conservative

1.1%; Score 25; DB 1; Length 25;

Pred. No. 5.2e+02;

Mismatches 0; Indels 0; Gaps 0;

QY 2288 TAGCCAGGATGGTCTCGATCTCCTG 2312

Db 1 TAGCCAGGATGGTCTCGATCTCCTG 25

RESULT 260

AX693035

LOCUS

DEFINITION

AX693035

ACCESSION

VERSION

AX693035.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .25

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match

Best Local Similarity

Matches 25; Conservative

1.1%; Score 25; DB 1; Length 25;

Pred. No. 5.2e+02;

Mismatches 0; Indels 0; Gaps 0;

QY 2289 AGCCAGGATGGTCTCGATCTCCTGA 2313

Db 1 AGCCAGGATGGTCTCGATCTCCTGA 25

RESULT 261

AX693036

LOCUS AX693036 25 bp DNA linear PAT 31-MAR-2003

DEFINITION Sequence 5768 from Patent EP1281758.

AX693036

ACCESSION

VERSION

AX693036.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .25

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match

Best Local Similarity

Matches 25; Conservative

1.1%; Score 25; DB 1; Length 25;

Pred. No. 5.2e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGGTCTCGATCTCCTGAC 2314

Db 1 GCCAGGATGGTCTCGATCTCCTGAC 25

RESULT 262

BD138345

LOCUS

DEFINITION

BD138345

ACCESSION

VERSION

BD138345.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS

PN

PD

PF

PR

PI

PC

PC

PC

CC

CC

CC

CC

FT

FT

Location/Qualifiers

1. .25

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

Query Match

Best Local Similarity

Matches 25; Conservative

1.1%; Score 25; DB 1; Length 25;

Pred. No. 5.2e+02; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCACCTCACAGATTCACGCTCGGA 379

Db 1 CCACCTCACAGATCCAGCTTCGGA 25  
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RESULT 263  
AX117259/c  
LOCUS AX117259 31 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 2382 from Patent WO0129262.  
ACCESSION AX117259  
VERSION AX117259.1 GI:14034210  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Picoult-Newburg,L. and Pohl,M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 2382 26-APR-2001;  
Orchid BioSciences, Inc. (US)  
FEATURES  
source  
1..31  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="caxon:32630"  
/note="Primer"  
Query Match 1.0%; Score 24.6; DB 1; Length 31;  
Best Local Similarity 87.1%; Pred. No. 5.9e+02;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTG 2286  
|||||  
Db 31 GTAGTTTAGTAGACAGAGGGTTTCATTATG 1  
|||||  
RESULT 264  
AX184256/c  
LOCUS AX184256 32 bp DNA linear PAT 06-AUG-2001  
DEFINITION Sequence 2009 from Patent WO0142511.  
ACCESSION AX184256  
VERSION AX184256.1 GI:15135601  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.  
TITLE Ibd-related polymorphisms  
JOURNAL Patent: WO 0142511-A 2009 14-JUN-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis  
Biotherapeutics Corporation (CA)  
FEATURES  
source  
1..32  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.0%; Score 24.6; DB 1; Length 32;  
Best Local Similarity 84.4%; Pred. No. 5.9e+02;  
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2300 TCTCGATCTCTGACCTCGTGATCGGCCACC 2331  
|||||  
Db 32 TCTCGATCTCTGACCTCGTGATCGGCCACC 1  
|||||  
RESULT 265  
AX117744  
LOCUS AX117744 27 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 2867 from Patent WO0129262.  
ACCESSION AX117744  
VERSION AX117744.1 GI:14034695

KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Picoult-Newburg,L. and Pohl,M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 2867 26-APR-2001;  
Orchid BioSciences, Inc. (US)  
FEATURES  
source  
1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"  
misc\_feature  
1..27  
/notes="n = C3 linker"  
Query Match 1.0%; Score 24.4; DB 1; Length 27;  
Best Local Similarity 92.8%; Pred. No. 5.7e+02;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2304 GATCTCTGACCTCGTGATCGGCCAC 2330  
|||||  
Db 1 GATCTCTGACCTCGTGATCGGCCAC 27  
|||||  
RESULT 266  
AR392160  
LOCUS AR392160 29 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1 from patent US 6613750.  
ACCESSION AR392160  
VERSION AR392160.1 GI:40116136  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Definho,R.A.  
TITLE Method of inhibiting cell proliferation using an anti-oncogene  
protein  
JOURNAL Patent: US 6613750-A 1 02-SEP-2003;  
FEATURES  
source  
1..29  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.0%; Score 24.2; DB 1; Length 29;  
Best Local Similarity 89.7%; Pred. No. 6e+02;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 964 CGCCATCGAATCCGGATCTTGATGCTGGT 992  
|||||  
Db 1 CGCCATCTAGACCGGATCTTGATGCTGGT 29  
|||||  
RESULT 267  
AR214384  
LOCUS AR214384 30 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 28 from patent US 6407062.  
ACCESSION AR214384  
VERSION AR214384.1 GI:23312037  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Sherr,C.J., Quelle,D., Rousset,M.F., Zindy,F. and Weber,J.D.  
TITLE ARF-p19, a novel regulator of the mammalian cell cycle  
JOURNAL Patent: US 6407062-A 28 18-JUN-2002;  
FEATURES  
source  
1..30  
/organism="unknown"



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Query Match      1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 89.7%; Pred. No. 6e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

/mol_type="genomic DNA"

QY 934 AAAGAAGCAGTAGCAGTGAATCTACAGG 962
Db 2 ATATGACGAGTAGCAGTGAATCTACAGG 30

RESULT 268
LOCUS AX184136/c
DEFINITION Sequence 1889 from Patent WO0142511.
ACCESSION AX184136
VERSION AX184136.1 GI:15135477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TOSHIKAWA, T. J., Lander, E. S., Rioux, J. and Siminovitch, K.
PI IBD-related polymorphisms
PATENT: WO 0142511-A 1889 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FH Key Location/Qualifiers
FEATURES
source
1..30
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 6e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2090 TATTTTTTTTGAGACCGAGTCTGCTCTGT 2119
Db 30 TTTTITTTTNGAGACCGAGTCTGCTCTGT 1

RESULT 269
LOCUS E40923
DEFINITION Method for measuring telomeric size.
ACCESSION E40923
VERSION E40923.1 GI:22553151
KEYWORDS JP 2001095586-A/1.
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TOSHIKAWA, T. J., Lander, E. S., Rioux, J. and Siminovitch, K.
PI IBD-related polymorphisms
PATENT: WO 0142511-A 1889 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FH Key Location/Qualifiers
FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 6e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2090 TATTTTTTTTGAGACCGAGTCTGCTCTGT 2119
Db 30 TTTTITTTTNGAGACCGAGTCTGCTCTGT 1

RESULT 269
LOCUS E40923
DEFINITION Method for measuring telomeric size.
ACCESSION E40923
VERSION E40923.1 GI:22553151
KEYWORDS JP 2001095586-A/1.
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TOSHIKAWA, T. J., Lander, E. S., Rioux, J. and Siminovitch, K.
PI IBD-related polymorphisms
PATENT: WO 0142511-A 1889 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FH Key Location/Qualifiers
FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACA 2358
Db 1 GCCTCCCAAGTCTGGGATTACA 24

RESULT 270
LOCUS E40925/c
DEFINITION Method for measuring telomeric size.
ACCESSION E40925
VERSION E40925.1 GI:22553153
KEYWORDS JP 2001095586-A/3.
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TOSHIKAWA, T. J., Lander, E. S., Rioux, J. and Siminovitch, K.
PI IBD-related polymorphisms
PATENT: WO 0142511-A 1889 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FH Key Location/Qualifiers
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACA 2358
Db 24 GCCTCCCAAGTCTGGGATTACA 1

RESULT 271
LOCUS AX693019
DEFINITION Sequence 5751 from Patent EP1281758.
ACCESSION AX693019
VERSION AX693019.1 GI:29415982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TOSHIKAWA, T. J., Lander, E. S., Rioux, J. and Siminovitch, K.
PI IBD-related polymorphisms
PATENT: WO 0142511-A 1889 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FH Key Location/Qualifiers
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GCGTTTTCACCGTGTAGCCAGGAT 2297
Db 1 GCGTTTTCACCGTGTAGCCAGGAT 2297

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Db      2  GGGTTTCACCGTGTTAGCCAGAT 25

RESULT 272
LOCUS   AX693037
DEFINITION Sequence 5769 from Patent EPI281758.
ACCESSION AX693037
VERSION   AX693037.1 GI:29416000
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
          mdz12
JOURNAL  Patent: EP 1281758-A 5769 05-FEB-2003;
          Acomica, Inc. (US)
FEATURES
source   1..25
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match 1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2291 CCAGGATGGTCTCGATCTCCTGAC 2314
      |||||
Db 1 CCAGGATGGTCTCGATCTCCTGAC 24

RESULT 273
LOCUS   A72116
DEFINITION Sequence 71 from Patent WO9801467.
ACCESSION A72116
VERSION   A72116.1 GI:4808073
KEYWORDS
SOURCE   unidentified
          unclassified.
REFERENCE
AUTHORS  Lane,D., Boettger,V., Boettger,A., Picksley,S., Hochkeppel,H.,
          Garcia-Echeverria,C., Chene,P. and Furet,P.
TITLE    INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
JOURNAL  Patent: WO 9801467-A 71 15-JAN-1998;
          CIBA GEIGY AG (CH)
FEATURES
source   1..27
          /organism="unidentified"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32644"

Query Match 1.0%; Score 24; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1191 GATCCTGAAATTCCTTAGCTGAC 1214
      |||||
Db 4 GATCCTGAAATTCCTTAGCTGAC 27

RESULT 274
LOCUS   BD003108
DEFINITION Inhibitor of interaction between P53 and MDM2.
ACCESSION BD003108
VERSION   BD003108.1 GI:18631069
KEYWORDS
SOURCE   JP 2001500365-A/5.

```

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```

SOURCE   unidentified
          unclassified.
          unclassified.
REFERENCE
AUTHORS  Lane,D., Boettger,V., Boettger,A., Picksley,S., Hochkeppel,H.K.,
          Echeverria,C.G., Chene,P. and Furet,P.
TITLE    Inhibitor of interaction between P53 and MDM2
JOURNAL  Patent: JP 2001500365-A 5 16-JAN-2001;
          NOVARTIS AG,CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
COMMENT  OS Unidentified
          PN JP 2001500365-A/5
          PD 16-JAN-2001
          PR 04-JUL-1997 JP 1998504775
          PR 05-JUL-1996 GB 9614197.3,07-APR-1997 GB 9707041.1 PI
          DAVID LANE,VOLKER BOETTGER,ANGELIKA ECHERRIA,STEPHEN PICKSLEY, PI
          HEINZ KURT HOCHKEPPEL,CARLOS GARCIA ECHERRIA,PATRICK CHENE, PI
          PASCAL FURET
          PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,C07K7/06,C07K7/08, PC
          C12Q1/68,
          PC G01N33/53//C07K14/82,C12N15/00,A61K37/02
          CC Strandedness: Single;
          CC Topology: Linear;
          PH Key Location/Qualifiers
          FT source 1..27
          FT /organism='Unidentified'.
FEATURES
source   1..27
          /organism="unidentified"
          /mol_type="genomic DNA"
          /db_xref="taxon:32644"

Query Match 1.0%; Score 24; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1191 GATCCTGAAATTCCTTAGCTGAC 1214
      |||||
Db 4 GATCCTGAAATTCCTTAGCTGAC 27

RESULT 275
LOCUS   A68624
DEFINITION Sequence 4 from Patent WO9801573.
ACCESSION A68624
VERSION   A68624.1 GI:4759651
KEYWORDS
SOURCE   unidentified
          unclassified.
REFERENCE
AUTHORS  Resnick,M.A., Lariouov,V.L., Kouprina,N.Y. and Perkins,E.L.
TITLE    TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING
JOURNAL  Patent: WO 9801573-A 4 15-JAN-1998;
          US HEALTH (US)
FEATURES
source   1..30
          /organism="unidentified"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32644"

Query Match 1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 6.4e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTGCTGTACCCAG 2126
      |||||
Db 1 TTTGAGACCGAGTCTGCTGTACCCAG 30

RESULT 276
LOCUS   AX118472

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```

DEFINITION Sequence 3595 from Patent WO0129262.
ACCESSION AX118472
VERSION AX118472.1 GI:14035423
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3595 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 6.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2343 AAGTCTGGGATTACAGCGTGACC 2367
Db 1 AAGTCTGGGATTACAGCGTGAGC 25

RESULT 277
AX548255
LOCUS AX548255 25 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 179 from Patent WO240716.
ACCESSION AX548255
VERSION AX548255.1 GI:25813289
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Palm,K.
TITLE Profiling tumor specific markers for the diagnosis and treatment of
JOURNAL neoplastic disease
Cemines, LLC (US)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 6.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGCGTGCA 2365
Db 1 CAAAGTCTGGGATTACAGCGTGA 25

RESULT 278
AX922581
LOCUS AX922581 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 921 from Patent WO2068649.
ACCESSION AX922581
VERSION AX922581.1 GI:40215504
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS
JOURNAL Patent: WO 02068649-A 921 06-SEP-2002;

DEFINITION Sequence 3595 from Patent WO0129262.
ACCESSION AX118472
VERSION AX118472.1 GI:14035423
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3595 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 6.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2302 TCGATCTCTGACCTCGTCGATCGGCC 2328
Db 1 TCGATCTCTGACCTCGTCGTCGTC 27

RESULT 280
AX118407
LOCUS AX118407 30 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3530 from Patent WO0129262.
ACCESSION AX118407
VERSION AX118407.1 GI:14035358
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3530 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.0%; Score 23.2; DB 1; Length 30;

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Best Local Similarity 89.3%; Pred. No. 6.6e+02;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2249 ATTCTTTCTACTTTAGTAGACAGGG 2276  
| | | | | | | | | | | | | | | | | | | | |  
Db 3 AATTTTCTATTTTGTAGTAGACGGGG 30

RESULT 281  
LOCUS CQ766174 23 bp DNA PAT 03-MAR-2004  
DEFINITION Sequence 135 from Patent WO2004/005547.  
ACCESSION CQ766174  
VERSION CQ766174.1 GI:44908434  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Weinzierl, R.  
TITLE Method  
JOURNAL  
FEATURES Location/Qualifiers  
source 1..23  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="HS consensus sequence"

Query Match 1.0%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2345 GTGCTGGGATTACAGGCATGAGC 2367  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 GTGCTGGGATTACAGGCATGAGC 23

RESULT 282  
LOCUS AR300897/c 23 bp DNA PAT 12-JUN-2003  
DEFINITION Sequence 4 from patent US 6537984.  
ACCESSION AR300897  
VERSION AR300897.1 GI:31688464  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Rosen, G.D., Lennox, E.S. and Musser, J.H.  
TITLE Uses of diterpenoid triepoxides as an anti-proliferative agent  
JOURNAL Patent: US 6537984-A 4 25-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..23  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.0%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1374 GAGGCTTTGATGTTCTCTGATTG 1396  
| | | | | | | | | | | | | | | | | | | | |  
Db 23 GAGGCTTTGATGTTCTCTGATTG 1

RESULT 283  
LOCUS AR361046/c 23 bp DNA PAT 17-AUG-2003  
DEFINITION Sequence 4 from patent US 6599499.  
ACCESSION AR361046  
VERSION AR361046.1 GI:33768613

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Rosen, G.D., Lennox, E.S. and Musser, J.H.  
TITLE Uses of diterpenoid triepoxides as an anti-proliferative agent  
JOURNAL Patent: US 6599499-A 4 29-JUL-2003;  
FEATURES Location/Qualifiers  
source 1..23  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.0%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1374 GAGGCTTTGATGTTCTCTGATTG 1396  
| | | | | | | | | | | | | | | | | | | | |  
Db 23 GAGGCTTTGATGTTCTCTGATTG 1

RESULT 284  
LOCUS AX693018 25 bp DNA PAT 31-MAR-2003  
DEFINITION Sequence 5750 from Patent EPI281758.  
ACCESSION AX693018  
VERSION AX693018.1 GI:29415981  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 5750 05-FEB-2003;  
FEATURES Location/Qualifiers  
source 1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.0%; Score 23; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGTTTCACCGTGTAGCCAGGA 2296  
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Db 3 GGTTTCACCGTGTAGCCAGGA 25

RESULT 285  
LOCUS AR089946 26 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 66 from patent US 5994076.  
ACCESSION AR089946  
VERSION AR089946.1 GI:10016701  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 66 30-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..26  
/organism="unknown"  
/mol\_type="unassigned DNA"

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Query Match      1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTGTGGGATTACAGGCATGAGC 2367
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Db 1 AAAGTGTAGGATTACAGGCGTGAGC 26

RESULT 286
AR196981
LOCUS AR196981 26 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 66 from patent US 6352829.
ACCESSION AR196981
VERSION AR196981.1 GI:20246830
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 26)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 66 05-MAR-2002;
FEATURES
  Location/Qualifiers
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTGTGGGATTACAGGCATGAGC 2367
||||| ||||||| ||||||| ||||||| |||||||
Db 1 AAAGTGTAGGATTACAGGCGTGAGC 26

RESULT 287
AR259135
LOCUS AR259135 26 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 66 from patent US 6489455.
ACCESSION AR259135
VERSION AR259135.1 GI:27309646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 26)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 66 03-DEC-2002;
FEATURES
  Location/Qualifiers
    source
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        /organism="unknown"
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Query Match      1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTGTGGGATTACAGGCATGAGC 2367
||||| ||||||| ||||||| ||||||| |||||||
Db 1 AAAGTGTAGGATTACAGGCGTGAGC 26

RESULT 288
AX116952
LOCUS AX116952 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2075 from Patent WO0129262.
ACCESSION AX116952
VERSION AX116952.1 GI:14033894
KEYWORDS
SOURCE synthetic construct

Query Match      1.0%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 6.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2344 AGTGCTGGGATTACAGGCATGAGCCAC 2370
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Db 1 AGTNCCTGGGATTACAGGCATGAGCCAC 27

RESULT 289
AX118160
LOCUS AX118160 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3283 from Patent WO0129262.
ACCESSION AX118160
VERSION AX118160.1 GI:14035111
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3283 26-APR-2001;
JOURNAL Orchard Biosciences, Inc. (US)
FEATURES
  Location/Qualifiers
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"
    misc_feature
      1..27
        /note="n = C3 linker"

Query Match      1.0%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 6.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAAGTGTCTGGGATTACA 2358
||||| ||||||| ||||||| ||||||| |||||||
Db 1 TTGGCCTCNCACAGTGTCTGGGATTACA 27

RESULT 290
AX116662
LOCUS AX116662 30 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1785 from Patent WO0129262.
ACCESSION AX116662
VERSION AX116662.1 GI:14033604
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1785 26-APR-2001;
JOURNAL Orchard Biosciences, Inc. (US)
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FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Primer"

Query Match
Best Local Similarity 1.0%; Score 22.8; DB 1; Length 30;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTGTGACTTTAGTAGACAGG 2275
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Db 5 TTTTGTGACTTTAGTAGACAGG 30

RESULT 291
AR051440/c
LOCUS AR051440 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5830670.
ACCESSION AR051440
VERSION AR051440.1 GI:5974804
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's
disease
JOURNAL Patent: US 5830670-A 6 03-NOV-1998;
FEATURES
source
  Location/Qualifiers
    1..30
      /organism="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 22.6; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTCGACCATTTCTGCTCAGCTCCC 2207
      |||||
Db 30 TTCAGCGATTCTCTGCTCAGCTCCC 2

RESULT 292
AR072580/c
LOCUS AR072580 30 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 6 from patent US 5948634.
ACCESSION AR072580
VERSION AR072580.1 GI:9999344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's
disease
JOURNAL Patent: US 5948634-A 6 07-SEP-1999;
FEATURES
source
  Location/Qualifiers
    1..30
      /organism="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 22.6; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTCGACCATTTCTGCTCAGCTCCC 2207
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Db 30 TTCAGCGATTCTCTGCTCAGCTCCC 2
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RESULT 293
AR073125/c
LOCUS AR073125 30 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 6 from patent US 5948888.
ACCESSION AR073125
VERSION AR073125.1 GI:9999888
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's
disease
JOURNAL Patent: US 5948888-A 6 07-SEP-1999;
FEATURES
source
  Location/Qualifiers
    1..30
      /organism="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 22.6; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTCGACCATTTCTGCTCAGCTCCC 2207
      |||||
Db 30 TTCAGCGATTCTCTGCTCAGCTCCC 2

RESULT 294
AR092647
LOCUS AX092647 24 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 59 from Patent WO0115676.
ACCESSION AX092647
VERSION AX092647.1 GI:13444704
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and
triglyceride levels
JOURNAL Patent: WO 0115676-A 59 08-MAR-2001;
FEATURES
source
  Location/Qualifiers
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      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 22.4; DB 1; Length 24;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTGATCC 2324
      |||||
Db 1 CTCGATTTCTGACCTCGTGATCC 24

RESULT 295
AR322085/c
LOCUS AR322085 25 bp mRNA linear PAT 17-AUG-2003
DEFINITION Sequence 10 from patent US 6566053.
ACCESSION AR322085
VERSION AR322085.1 GI:33707625
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS
TITLE
JOURNAL Patent: US 6566053-A 10 08-AUG-2003;
FEATURES
source
  Location/Qualifiers
    1..25
      /organism="unassigned DNA"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
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AUTHORS Perucho,M., Peinado,M.A., Ionov,Y., Malkhosyan,S., McClelland,M. and Welsh,J.  
 TITLE Identification of neoplasms by detection of genetic insertions and deletions  
 JOURNAL Patent: US 6566053-A 10 20-MAY-2003;  
 FEATURES Location/Qualifiers  
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 /organism="unknown"  
 /mol\_type="mRNA"

Query Match 0.9%; Score 22.4; DB 1; Length 25;  
 Best Local Similarity 95.8%; Pred. No. 6.7e+02;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGCTTTCACC 2283  
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 Db 24 TTTTAGTAGACAGAGGCTTTCACC 1

RESULT 296  
 AX184030/c  
 LOCUS AX184030 29 bp DNA linear PAT 06-AUG-2001  
 DEFINITION Sequence 1783 from Patent WO0142511.  
 ACCESSION AX184030  
 VERSION AX184030.1 GI:15135366  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.  
 TITLE Ibd-related polymorphisms  
 JOURNAL Patent: WO 0142511-A 1783 14-JUN-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis  
 Biotherapeutics Corporation (CA)  
 FEATURES Location/Qualifiers  
 source  
 1. .29  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 22.4; DB 1; Length 29;  
 Best Local Similarity 92.0%; Pred. No. 7.1e+02;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2230 CTGCCACCACACCTGGCTAATTTT 2254  
 |||||  
 Db 25 CTGCCACCACCTGGCTAATTTT 1

RESULT 297  
 AR044033  
 LOCUS AR044033 22 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 1 from patent US 5817462.  
 ACCESSION AR044033  
 VERSION AR044033.1 GI:5965498  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Garini,Y., Cabib,D., Buckwald,R.A., Ried,T. and Soenksen,D.G.  
 TITLE Method for simultaneous detection of multiple fluorophores for in situ hybridization and multicolor chromosome painting and banding  
 JOURNAL Patent: US 5817462-A 1 06-OCT-1998;  
 FEATURES Location/Qualifiers  
 source  
 1. .22  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;

AUTHORS Perucho,M., Peinado,M.A., Ionov,Y., Malkhosyan,S., McClelland,M. and Welsh,J.  
 TITLE Identification of neoplasms by detection of genetic insertions and deletions  
 JOURNAL Patent: US 6566053-A 10 20-MAY-2003;  
 FEATURES Location/Qualifiers  
 source  
 1. .25  
 /organism="unknown"  
 /mol\_type="mRNA"

Query Match 0.9%; Score 22.4; DB 1; Length 25;  
 Best Local Similarity 95.8%; Pred. No. 6.7e+02;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGCTTTCACC 2283  
 |||||  
 Db 24 TTTTAGTAGACAGAGGCTTTCACC 1

RESULT 296  
 AX184030/c  
 LOCUS AX184030 29 bp DNA linear PAT 06-AUG-2001  
 DEFINITION Sequence 1783 from Patent WO0142511.  
 ACCESSION AX184030  
 VERSION AX184030.1 GI:15135366  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.  
 TITLE Ibd-related polymorphisms  
 JOURNAL Patent: WO 0142511-A 1783 14-JUN-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis  
 Biotherapeutics Corporation (CA)  
 FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 22.4; DB 1; Length 29;  
 Best Local Similarity 92.0%; Pred. No. 7.1e+02;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2230 CTGCCACCACACCTGGCTAATTTT 2254  
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 Db 25 CTGCCACCACCTGGCTAATTTT 1

RESULT 297  
 AR044033  
 LOCUS AR044033 22 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 1 from patent US 5817462.  
 ACCESSION AR044033  
 VERSION AR044033.1 GI:5965498  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Garini,Y., Cabib,D., Buckwald,R.A., Ried,T. and Soenksen,D.G.  
 TITLE Method for simultaneous detection of multiple fluorophores for in situ hybridization and multicolor chromosome painting and banding  
 JOURNAL Patent: US 5817462-A 1 06-OCT-1998;  
 FEATURES Location/Qualifiers  
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 1. .22  
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 /mol\_type="unassigned DNA"

Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAAGTCTGGGATTACAG 2359  
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 Db 1 TCCCAAAGTCTGGGATTACAG 22

RESULT 298  
 AR208403/c  
 LOCUS AR208403 22 bp DNA linear PAT 20-JUN-2002  
 DEFINITION Sequence 19 from patent US 6383752.  
 ACCESSION AR208403  
 VERSION AR208403.1 GI:21509548  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Agrawal,S. and Kandimalia,E.R.  
 TITLE Pseudo-cyclic oligonucleobases  
 JOURNAL Patent: US 6383752-A 19 07-MAY-2002;  
 FEATURES Location/Qualifiers  
 source  
 1. .22  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 679 GTGAGAACAGGTGTCACTTGA 700  
 |||||  
 Db 22 GTGAGAACAGGTGTCACTTGA 1

RESULT 299  
 AR300896  
 LOCUS AR300896 22 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 3 from patent US 6537984.  
 ACCESSION AR300896  
 VERSION AR300896.1 GI:31688463  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Rosen,G.D., Lennox,E.S. and Musser,J.H.  
 TITLE Uses of diterpenoid triepoxides as an anti-proliferative agent  
 JOURNAL Patent: US 6537984-A 3 25-MAR-2003;  
 FEATURES Location/Qualifiers  
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 1. .22  
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Query Match 0.9%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 GTCATCAGCAGGAATCATCGG 660  
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 Db 1 GTCATCAGCAGGAATCATCGG 22

RESULT 300  
 AR361045  
 LOCUS AR361045 22 bp DNA linear PAT 17-AUG-2003  
 DEFINITION Sequence 3 from patent US 6599499.  
 ACCESSION AR361045  
 VERSION AR361045.1 GI:33768612  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 22)
AUTHORS Rosen,G.D., Lennox,E.S. and Musser,J.H.
TITLE Uses of diterpenoid triepoxides as an anti-proliferative agent
JOURNAL Patent: US 659499-A 3 29-JUL-2003;
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            /mol_type="genomic DNA"
Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 GTCATCAGCAGGATCATCGG 560
Db 1 GTCATCAGCAGGATCATCGG 22

RESULT 301
LOCUS AR393736/c 22 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 275 from patent US 6617122.
ACCESSION AR393736
VERSION AR393736.1 GI:40120580
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hayden,M.R., Brooks-Wilson,A.R. and Pimstone,S.N.
TITLE Process for identifying modulators of ABC1 activity
JOURNAL Patent: US 6617122-A 275 09-SEP-2003;
FEATURES
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            /mol_type="genomic DNA"
Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2188 TTCTCCTGCCTCAGCCTCCCAA 2209
Db 22 TTCTCCTGCCTCAGCCTCCCAA 1

RESULT 302
LOCUS AX693017 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5749 from Patent EPI281758.
ACCESSION AX693017
VERSION AX693017.1 GI:29415980
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5749 05-FEB-2003;
FEATURES
    source
        1..25
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match 0.9%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 2274 GGCTTTCACCGTGTAGCCAGG 2295
Db 4 GGCTTTCACCGTGTAGCCAGG 25

RESULT 303
LOCUS E50643/c 25 bp DNA linear PAT 31-JAN-2002
DEFINITION Simple detection method of drug-metabolizing synthetase gene polymorphism.
ACCESSION E50643
VERSION E50643.1 GI:18629424
KEYWORDS JP 2001017185-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Mizugaki,M. and Hiratauka,M.
TITLE Simple detection method of drug-metabolizing synthetase gene
JOURNAL Patent: JP 2001017185-A 7 23-JAN-2001;
COMMENT OTSUKA PHARMACEUT CO LTD
OS Unidentified
PN JP 2001017185-A/7
PD 23-JAN-2001
PE 10-DEC-1999 JP 1999351610
PR MICHINAO MIZUGAKI, MASAHIRO HIRATSUKA
PI C12N15/09,C12Q1/68,C12Q1/68,C12N15/00
PC C12N15/09,C12Q1/68,C12Q1/68,C12N15/00
FH Key Location/Qualifiers
FT source 1..25
FT /organism='Unidentified'.
FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 7.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2269 AGACAGGGTTTCACCGTGTAGCCA 2293
Db 25 AGACAGGGTTTCACCATGTGGCCA 1

RESULT 304
LOCUS AX614112 25 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 5137 from Patent WO02072882.
ACCESSION AX614112
VERSION AX614112.1 GI:28409541
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 5137 19-SEP-2002;
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 7.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```





TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5724 05-FEB-2003;

AEOMICA, INC. (US)

## FEATURES

source

1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 7.2e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2247 TAAATTTTGTACTTTTAGTAGAGA 2271

Db 1 TAAATTTTGTATTTTAGTAGAGA 25

## RESULT 310

AX692993

LOCUS

AX692993 Sequence 5725 from Patent EP1281758. linear PAT 31-MAR-2003

DEFINITION

AX692993

AX692993

AX692993.1 GI:29415956

KEYWORDS

source

1. .25

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 0.9%; Score 21.8; DB 1; Length 25;

Best Local Similarity 92.0%; Pred. No. 7.2e+02;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2248 AATTTTGTACTTTTAGTAGAGAC 2272

Db 1 AATATTTGTATTTTAGTAGAGAC 25

## RESULT 311

AX692997

LOCUS

AX692997 Sequence 5729 from Patent EP1281758. linear PAT 31-MAR-2003

DEFINITION

AX692997

AX692997

AX692997.1 GI:29415960

KEYWORDS

source

1. .25

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 0.9%; Score 21.6; DB 1; Length 28;

Best Local Similarity 85.7%; Pred. No. 7.6e+02;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2100 GAGACCGAGCTTGCTCTGTATCCAGG 2127

Query Match 0.9%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 7.2e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGG 2276

Db 1 TTTTGTATTTTAGTAGACAGGG 25

## RESULT 312

AX184125

LOCUS

AX184125 Sequence 1878 from Patent WO0142511. linear PAT 06-AUG-2001

DEFINITION

AX184125

AX184125

AX184125.1 GI:15135465

KEYWORDS

source

1. .27

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 0.9%; Score 21.8; DB 1; Length 27;

Best Local Similarity 88.5%; Pred. No. 7.3e+02;

Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTCGGATTACAGG 2360

Db 1 GCCTCCCAAGTCTCGGATTACAGG 26

## RESULT 313

AX49272

LOCUS

AX49272 Sequence 2 from Patent EP0714987. linear PAT 07-MAR-1997

DEFINITION

AX49272

AX49272

AX49272.1 GI:2302795

KEYWORDS

source

1 (bases 1 to 28)

/organism="unidentified"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32644"

Query Match 0.9%; Score 21.6; DB 1; Length 28;

Best Local Similarity 85.7%; Pred. No. 7.6e+02;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2100 GAGACCGAGCTTGCTCTGTATCCAGG 2127

```
||||| ||||| ||||| ||||| ||||| |||||
Db 1 GAGACAGAGTCTCGCTCTGTGCGCCAGG 28

RESULT 314
AR122136
LOCUS AR122136 28 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6165711.
ACCESSION AR122136
VERSION AR122136.1 GI:14106453
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dörner, F., Barrett, N. and Eibl, J.
TITLE Process for disintegrating nucleic acids and preparing biological
products of guaranteed quality
JOURNAL Patent: US 6165711-A 8 26-DEC-2000;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 21.6; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2100 GAGACGAGTCTGCTCTGTATCCAGG 2127
||||| ||||| ||||| ||||| |||||
Db 1 GAGACAGAGTCTCGCTCTGTGCGCCAGG 28

RESULT 315
AR345149/c
LOCUS AR345149 23 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 30 from patent US 6583112.
ACCESSION AR345149
VERSION AR345149.1 GI:33741785
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Fu, Y.-H., Yu, C.-E., Oshima, J., Mulligan, J.T. and Schellenberg, G.D.
TITLE Gene products related to werner's syndrome
JOURNAL Patent: US 6583112-A 30 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..23
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2336 CCTCCCAAGTGTGGGATTACA 2358
||||| ||||| ||||| ||||| |||||
Db 23 CCTCCCAAGTGTGGGATTACA 1

RESULT 316
AX823487
LOCUS AX823487 23 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 260 from Patent WO02068647.
ACCESSION AX823487
VERSION AX823487.1 GI:39749947
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS

JOURNAL Patent: WO 0200933-A 15 03-JAN-2002;
Interleukin Genetics, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

JOURNAL Patent: WO 02068647-A 260 06-SBP-2002;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: PCR Primer
Sequence"

Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 TTTGACGCGAGTCTTGCTCTGT 2119
||||| ||||| ||||| ||||| |||||
Db 1 TTTGACGCGAGTCTTGCTCTGT 23

RESULT 317
A82465
LOCUS A82465 25 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 3 from Patent WO9854359.
ACCESSION A82465
VERSION A82465.1 GI:67322209
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Duff, G. and Cox, A.
TITLE PREDICTION OF INFLAMMATORY DISEASE ASSOCIATED WITH IL-1 GENELOC1
JOURNAL Patent: WO 9854359-A 3 03-DEC-1998;
DUFF GORDON (GB); COX ANGELA (GB)
FEATURES Location/Qualifiers
source 1..25
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGAGCCACCG 2372
||||| ||||| ||||| ||||| |||||
Db 1 GGGATTACAGGCGTGAGCCACCG 23

RESULT 318
AX360029
LOCUS AX360029 25 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 15 from Patent WO0200933.
ACCESSION AX360029
VERSION AX360029.1 GI:18675655
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Duff, G.W. and Kornman, K.S.
TITLE Screening assays for identifying modulators of the inflammatory or
immune responses
JOURNAL Patent: WO 0200933-A 15 03-JAN-2002;
Interleukin Genetics, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
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Query Match
Best Local Similarity 0.9%; Score 21.4; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGCATGAGCCACCG 2372
|||||
Db 1 GGGATTACAGCGGTGAGCCACCG 23

RESULT 319
BD124526
LOCUS BD124526 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Prediction of inflammatory disease associated with IL-1 geneloci
polymorphisms.
ACCESSION BD124526
VERSION BD124526.1 GI:23219471
KEYWORDS JP 2002500513-A/3.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Duff,G., Cox,A., Camp,N.J. and Giovine,F.S.D.
TITLE Prediction of inflammatory disease associated with IL-1 geneloci
JOURNAL polymorphisms
Patent: JP 2002500513-A 3 08-JAN-2002;
COMMENT INTERLEUKIN GENETICS INC
OS Unidentified
FN JP 2002500513-A/3
PD 08-JAN-2002
PF 21-MAY-1998 JP 1999500358
PR 29-MAY-1997 GB 9711040.7
PI GORDON DUFF,ANGELA COX,NICOLA JANE CAMP,FRANCESCO SAVERIO DE
FI GIOVINE
PC C12Q1/68
CC Strandedness: Single;
CC Topology: linear;
CC Prediction of inflammatory disease associated with IL-1 CC
geneloci
CC polymorphisms
FH Key Location/Qualifiers
FT source 1..25
FT /organism='Unidentified'.
FEATURES
source
1..25
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match
Best Local Similarity 0.9%; Score 21.4; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGCATGAGCCACCG 2372
|||||
Db 1 GGGATTACAGCGGTGAGCCACCG 23

RESULT 320
AX115732/c
LOCUS AX115732 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 855 from Patent WO0129262.
ACCESSION AX115732
VERSION AX115732.1 GI:14032674
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 855 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source
Location/Qualifiers

Query Match
Best Local Similarity 0.9%; Score 21.4; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGCATGAGCCACCG 2372
|||||
Db 1 GGGATTACAGCGGTGAGCCACCG 23

RESULT 320
AX115732/c
LOCUS AX115732 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 855 from Patent WO0129262.
ACCESSION AX115732
VERSION AX115732.1 GI:14032674
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 855 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source
Location/Qualifiers
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source 1..27
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Primer'
misc_feature 1..27
/note='n = C3 linker'

Query Match
Best Local Similarity 0.9%; Score 21.2; DB 1; Length 27;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2142 GTGATCTTGCTCACTGCAAGCTCTGC 2168
|||||
Db 27 GTGATCTTAGTCACTGCAACCTCCGC 1

RESULT 321
AX117196
LOCUS AX117196 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2319 from Patent WO0129262.
ACCESSION AX117196
VERSION AX117196.1 GI:14034147
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2319 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source 1..27
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Primer'
misc_feature 1..27
/note='n = C3 linker'

Query Match
Best Local Similarity 0.9%; Score 21.2; DB 1; Length 27;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2257 TACTTTTAGTAGACAGGTTTCACC 2283
|||||
Db 1 TATTTTAGTAGAGATGGGNTTTCACC 27

RESULT 322
AX118476
LOCUS AX118476 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3599 from Patent WO0129262.
ACCESSION AX118476
VERSION AX118476.1 GI:14035427
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3599 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source 1..27
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Primer'
misc_feature 1..27
/note='n = C3 linker'
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Query Match      0.9%; Score 21.2; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 7.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2344 AGTGTGGGATTACAGGCATGAGCCAC 2370
      ||||| ||||| ||||| ||||| |||||
DB 1 AGTGCTGAATTACAGNCGTGAGCCAC 27

RESULT 323
LOCUS AR208405/c 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 21 from patent US 6383752.
ACCESSION AR208405
VERSION AR208405.1 GI:21509851
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Agrawal,S. and Kandimala,E.R.
TITLE Pseudo-cyclic oligonucleobases
JOURNAL Patent: US 6383752-A 21 07-MAY-2002;
FEATURES
    source
        1..21
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 726 GTACAAGAGCTTCAGGAAGAG 746
      ||||| ||||| ||||| ||||| |||||
DB 21 GTACAAGAGCTTCAGGAAGAG 1

RESULT 324
LOCUS AX117999 21 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3122 from Patent WO0129262.
ACCESSION AX117999
VERSION AX117999.1 GI:14034950
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3122 26-APR-2001;
FEATURES
    source
        1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGAT 2306
      ||||| ||||| ||||| ||||| |||||
DB 1 GTTAGCCAGGATGGTCTCGAT 21

RESULT 325
LOCUS AX190635/c 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 53 from Patent WO0144287.

ACCESSION AX190635
VERSION AX190635.1 GI:15143914
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Shimkets,R.A.
TITLE Novel polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0144287-A 53 21-JUN-2001;
FEATURES
    source
        1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="2826468 expression forward primer"

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGTG 2320
      ||||| ||||| ||||| ||||| |||||
DB 21 TCTCGATCTCTGACCTCGTG 1

RESULT 326
LOCUS AX800306 21 bp DNA linear PAT 13-OCT-2003
DEFINITION Sequence 68 from Patent WO0305595.
ACCESSION AX800306
VERSION AX800306.1 GI:37653543
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wen,X.Y., Stewart,A.K., Tsui,L.C. and Hegele,R.A.
TITLE Lipase genes and proteins
JOURNAL Patent: WO 0305595-A 68 10-JUL-2003;
FEATURES
    source
        1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGGATTACAGGCATGAG 2366
      ||||| ||||| ||||| ||||| |||||
DB 1 TGCTGGGATTACAGGCATGAG 21

RESULT 327
LOCUS BD073983 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073983
VERSION BD073983.1 GI:22619586
KEYWORDS JP 2001513996-A/22.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 22 11-SEP-2001;
```

```

COMMENT
OS Unidentified
PN JP 2001513996-A/22
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..21
FT /organism='Unidentified'.
FEATURES
source
1..21
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1007 AGGTGATTGGTTGGATCAGGA 1027
|||||
Db 1 AGGTGATTGGTTGGATCAGGA 21

RESULT 328
LOCUS BD074005 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074005
VERSION BD074005.1 GI:22619608
KEYWORDS JP 2001513996-A/44.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 44 11-SEP-2001;
COMMENT HYBRIDON INC
OS Unidentified
PN JP 2001513996-A/44
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..21
FT /organism='Unidentified'.
FEATURES
source
1..21
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1007 AGGTGATTGGTTGGATCAGGA 1027
|||||
Db 21 AGGTGATTGGTTGGATCAGGA 1

```

```

RESULT 329
LOCUS BD138343 21 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138343
VERSION BD138343.1 GI:23233288
KEYWORDS JP 2002508944-A/269.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 269 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/269
PD 26-MAR-2002 JP 2000538025
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M
PI COMSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..21
FT /organism='Unidentified'.
FEATURES
source
1..21
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAATGTGCAATACCAACA 327
|||||
Db 1 GGCAATGTGCAATACCAACA 21

RESULT 330
LOCUS AX092787/c 22 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 199 from Patent WO0115676.
ACCESSION AX092787
VERSION AX092787.1 GI:13444844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and
triglyceride levels
JOURNAL Patent: WO 0115676-A 199 08-MAR-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA) ; Xenon Genetics Inc. (CA)
FEATURES
source
1..22
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
variation 11
/note='N at position 11 is A or G.'

```



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)

Location/Qualifiers

1..24

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

/note="Sense primer for PSF promoter"

Query Match 0.9%; Score 20.8; DB 1; Length 24;

Best Local Similarity 91.7%; Pred. No. 7.8e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAGTGTCTGGGATTACAGGCGTGA 2365

Db 1 AAGTGTCTGGGATTACAGGCGTGA 24

## RESULT 336

## AX797527/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## source

1..24

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="Beschreibung der kuenstlichen Sequenz: Primer fur

PCR-Reaktion zur Amplifikation von M30 des Menschen"

Query Match 0.9%; Score 20.8; DB 1; Length 24;

Best Local Similarity 91.7%; Pred. No. 7.8e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTTACCCAGGCT 2129

Db 24 GAGTCTTGCTCTGTTACCCAGGCT 1

## RESULT 338

## AX115904

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

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## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

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## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

Schneider A., Hiemisch H., Rosener M., Klugmann M., Naim J.,

Eisenhardt G., Kner R., Lanahan A., Worley P., Spielvogel D. and

Scheek S.

The m30 gene family and the utilization thereof

Patent: WO 0221138-A 31 14-MAR-2002;

Axaron Bioscience AG (DE)

Location/Qualifiers



QY 2249 ATTTTGTACTTTTAGTAGAGAC 2272  
 Db 1 AATTTTGTATTTTAGTAGAGAC 24

RESULT 340  
 AX692917  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5649 from Patent EP1281758.  
 ACCESSION AX692917  
 VERSION AX692917.1 GI:29415880  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5649 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 CCGGGTTCGACCACTTCTCTGC 2196  
 Db 2 CCTGGGTTACACCACTTCTCTGC 25

RESULT 341  
 AX692918  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5650 from Patent EP1281758.  
 ACCESSION AX692918  
 VERSION AX692918.1 GI:29415881  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5650 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 CCGGGTTCGACCACTTCTCTGC 2196  
 Db 1 CCTGGGTTACACCACTTCTCTGC 24

RESULT 342  
 AX692920  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5652 from Patent EP1281758.

ACCESSION AX692920  
 VERSION AX692920.1 GI:29415883  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5652 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2176 GGGTTCGACCACTTCTCTGCCTC 2199  
 Db 2 GGGTTCACACCACTTCTCTGCCTC 25

RESULT 343  
 AX692923  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5655 from Patent EP1281758.  
 ACCESSION AX692923  
 VERSION AX692923.1 GI:29415886  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5655 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2178 GTTCGACCACTTCTCTGCCTCAG 2201  
 Db 1 GTTCACACCACTTCTCTGCCTCAG 24

RESULT 344  
 AX692927  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5659 from Patent EP1281758.  
 ACCESSION AX692927  
 VERSION AX692927.1 GI:29415890  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.

TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5659 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2183 CACCATTCCTCGCTCAGCTCC 2206  
 Db 2 CACCATTCCTCGCTCAGCTCC 25

RESULT 345  
 AX692929  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5661 from Patent EP1281758.  
 ACCESSION AX692929  
 VERSION AX692929.1 GI:29415892  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5661 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2184 ACCATTCTCCTCGCTCAGCTCCC 2207  
 Db 1 ACCATTCTCCTCGCTCAGCTCCC 24

RESULT 346  
 AX692990  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5722 from Patent EP1281758.  
 ACCESSION AX692990  
 VERSION AX692990.1 GI:29415953  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5722 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source  
 1..25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2246 CTAATTTTGTACTTTTAGTAGA 2269  
 Db 2 CTAATTTTGTACTTTTAGTAGA 25

RESULT 347  
 AX692994  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5726 from Patent EP1281758.  
 ACCESSION AX692994  
 VERSION AX692994.1 GI:29415957  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5726 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source  
 1..25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2249 ATTTTGTACTTTTAGTAGAGAC 2272  
 Db 1 ATTTTGTACTTTTAGTAGAGAC 24

RESULT 348  
 AX692996  
 LOCUS 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5728 from Patent EP1281758.  
 ACCESSION AX692996  
 VERSION AX692996.1 GI:29415959  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 5728 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source  
 1..25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2252 TTTTGTACTTTTAGTAGAGACGG 2275  
 Db 2 TTTTGTACTTTTAGTAGAGACGG 25

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RESULT 349
AX692998
LOCUS AX692998 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5730 from Patent EPI281758.
ACCESSION AX692998
VERSION AX692998.1 GI:29415961
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5730 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2253 TTGTACTTTTGTAGACAGGG 2276
Db 1 TTTGTATTTTGTAGACAGGG 24

RESULT 350
AR381743/C
LOCUS AR381743 27 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6610285.
ACCESSION AR381743
VERSION AR381743.1 GI:40089939
FEATURES
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hirata,Y.
TITLE Cytokine-like proteins that promote cell proliferation
JOURNAL Patent: US 6610285-A 18-26-AUG-2003;
FEATURES
source Location/Qualifiers
1..27
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 8.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2192 CTGTGCTCAGCTCCCAATTAGCT 2215
Db 27 CTGTGCTCAGCTCCCAAGCAGCT 4

RESULT 351
AX116940
LOCUS AX116940 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2063 from Patent WO0129262.
ACCESSION AX116940
VERSION AX116940.1 GI:14033882
FEATURES
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.

TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2063 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
misc_feature 1..27
/note="n = C3 linker"

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 8.1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2346 TGCTGGATTACAGGATGAGCCACC 2371
Db 1 TGCTGGATTATAGNCAGGCCACC 26

RESULT 352
AX183893/C
LOCUS AX183893 27 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1646 from Patent WO0142511.
ACCESSION AX183893
VERSION AX183893.1 GI:15135224
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1646 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
source Location/Qualifiers
1..27
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 8.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2185 CCATTCTCCTCGCTCAGCCTCCCAA 2209
Db 25 CGATTCTTCNGCCTCAGCCTCCCAA 1

RESULT 353
AX095325
LOCUS AX095325 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 503 from Patent WO0118250.
ACCESSION AX095325
VERSION AX095325.1 GI:13511528
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolck,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 503 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..21

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 1; Length 21;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2336 CCTCCCAAGTCTGGGATTA 2356
Db 1 CCTCCCAAGTCTGGGATTA 21

RESULT 354
AX709011 AX709011 27 bp DNA linear PAT 04-APR-2003
LOCUS AR242944/c
DEFINITION Sequence 35 from Patent WO03008443.
ACCESSION AR242944
VERSION AR242944.1 GI:29564684
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Averbach,P.A.
TITLE Peptides effective in the treatment of tumors and other conditions
JOURNAL requiring the removal or destruction of cells
JOURNAL Patent: WO 03008443-A 35 30-JAN-2003;
JOURNAL Nymox Corporation (CA)
FEATURES
source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 1; Length 27;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2331 CTCGCCTCCCAAGTCTGGGATTAC 2357
Db 1 CTCAGCCTCCCAAGCAGCTGGGATTAC 27

RESULT 355
E50641/c
LOCUS AR242948/c
DEFINITION Sequence 22 bp DNA linear PAT 31-JAN-2002
ACCESSION AR242948
VERSION AR242948.1 GI:18629422
KEYWORDS Simple detection method of drug-metabolizing synthetase gene
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 22)
AUTHORS Mizugaki,M. and Hiratsuka,M.
TITLE Simple detection method of drug-metabolizing synthetase gene
JOURNAL Patent: JP 2001017185-A 5 23-JAN-2001;
JOURNAL OTSUKA PHARMACEUT CO LTD
COMMENT
OS Unidentified
PN JP 2001017185-A/5
PD 23-JAN-2001
PF 10-DEC-1999 JP 1999351610
PR MICHINAO MIZUGAKI, MASAHIRO HIRATSUKA
PC C12N15/09,C12Q1/68,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..22
FT /organism="Unidentified".
FT Location/Qualifiers


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source 1..22
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.9%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2344 AGTGCTGGGATTACAGGCATGA 2365
Db 22 AATGCTGGGATTACAGGCATGA 1

RESULT 356
AR242944/c
LOCUS AR242944
DEFINITION Sequence 22 bp DNA linear PAT 20-DEC-2002
ACCESSION AR242944
VERSION AR242944.1 GI:27289606
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Brunkow,M.E., Proll,S., Paeper,B. and Staehling-Hampton,K.
TITLE Methods for identifying genomic deletions
JOURNAL Patent: US 6475739-A 90 05-NOV-2002;
JOURNAL Location/Qualifiers
FEATURES
source
1..22
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTCAGCTCCCA 2208
Db 22 ATTCTCTGCTCAGCTCCCA 1

RESULT 357
AR242948/c
LOCUS AR242948
DEFINITION Sequence 22 bp DNA linear PAT 20-DEC-2002
ACCESSION AR242948
VERSION AR242948.1 GI:27289610
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Brunkow,M.E., Proll,S., Paeper,B. and Staehling-Hampton,K.
TITLE Methods for identifying genomic deletions
JOURNAL Patent: US 6475739-A 94 05-NOV-2002;
JOURNAL Location/Qualifiers
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTCAGCTCCCA 2208
Db 22 ATTCTCTGCTCAGCTCCCA 1

RESULT 358
AR393735/c
LOCUS AR393735
DEFINITION Sequence 22 bp DNA linear PAT 18-DEC-2003
ACCESSION AR393735
VERSION AR393735.1 GI:29564684
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Averbach,P.A.
TITLE Peptides effective in the treatment of tumors and other conditions
JOURNAL requiring the removal or destruction of cells
JOURNAL Patent: WO 03008443-A 35 30-JAN-2003;
JOURNAL Nymox Corporation (CA)
FEATURES
source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 1; Length 27;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2331 CTCGCCTCCCAAGTCTGGGATTAC 2357
Db 1 CTCAGCCTCCCAAGCAGCTGGGATTAC 27

RESULT 355
E50641/c
LOCUS AR242948/c
DEFINITION Sequence 22 bp DNA linear PAT 31-JAN-2002
ACCESSION AR242948
VERSION AR242948.1 GI:18629422
KEYWORDS Simple detection method of drug-metabolizing synthetase gene
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 22)
AUTHORS Mizugaki,M. and Hiratsuka,M.
TITLE Simple detection method of drug-metabolizing synthetase gene
JOURNAL Patent: JP 2001017185-A 5 23-JAN-2001;
JOURNAL OTSUKA PHARMACEUT CO LTD
COMMENT
OS Unidentified
PN JP 2001017185-A/5
PD 23-JAN-2001
PF 10-DEC-1999 JP 1999351610
PR MICHINAO MIZUGAKI, MASAHIRO HIRATSUKA
PC C12N15/09,C12Q1/68,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..22
FT /organism="Unidentified".
FT Location/Qualifiers


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[illegible]

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2109 TCTTGCTCTGTACCAGGCTG 2130  
 Db 1 TCTTGCTCTGTACCAGGCTG 22

RESULT 363  
 AX115271  
 LOCUS AX115271 25 bp DNA linear PAT 11-MAY-2001  
 DEFINITION Sequence 394 from Patent WO0129262.  
 ACCESSION AX115271  
 VERSION AX115271.1 GI:14032213  
 KEYWORDS synthetic construct  
 ORGANISM synthetic construct  
 SOURCE artificial sequences.  
 REFERENCE 1  
 AUTHORS Picoult-Newburg, L. and Pohl, M.  
 TITLE Genotyping reagents, kits and methods of use thereof  
 JOURNAL Patent: WO 0129262-A 394 26-APR-2001;  
 Orchid Biosciences, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..25  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

Query Match 0.9%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2090 TATTTTTTTGAGCCGAGTCTTC 2114  
 Db 1 TTTTTTTTTCAGATGGAGTCTTC 25

RESULT 364  
 AX115532  
 LOCUS AX115532 25 bp DNA linear PAT 11-MAY-2001  
 DEFINITION Sequence 655 from Patent WO0129262.  
 ACCESSION AX115532  
 VERSION AX115532.1 GI:14032474  
 KEYWORDS synthetic construct  
 ORGANISM synthetic construct  
 SOURCE artificial sequences.  
 REFERENCE 1  
 AUTHORS Picoult-Newburg, L. and Pohl, M.  
 TITLE Genotyping reagents, kits and methods of use thereof  
 JOURNAL Patent: WO 0129262-A 655 26-APR-2001;  
 Orchid Biosciences, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..25  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

Query Match 0.9%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2339 CCCAAGTGTGGGATTACAGGCAT 2363  
 Db 1 CCCAATAGCTGGGATTACAGGAT 25

RESULT 365  
 AX116096  
 LOCUS AX116096 25 bp DNA linear PAT 11-MAY-2001  
 DEFINITION Sequence 1219 from Patent WO0129262.

ACCESSION AX116096  
 VERSION AX116096.1 GI:14033038  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Picoult-Newburg, L. and Pohl, M.  
 TITLE Genotyping reagents, kits and methods of use thereof  
 JOURNAL Patent: WO 0129262-A 1219 26-APR-2001;  
 Orchid Biosciences, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..25  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

Query Match 0.9%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCCTCCCAA 2209  
 Db 1 CAATTCTCTGCTCAGTCTCCCAA 25

RESULT 366  
 AX116664/c  
 LOCUS AX116664 25 bp DNA linear PAT 11-MAY-2001  
 DEFINITION Sequence 1787 from Patent WO0129262.  
 ACCESSION AX116664  
 VERSION AX116664.1 GI:14033606  
 KEYWORDS synthetic construct  
 ORGANISM synthetic construct  
 SOURCE artificial sequences.  
 REFERENCE 1  
 AUTHORS Picoult-Newburg, L. and Pohl, M.  
 TITLE Genotyping reagents, kits and methods of use thereof  
 JOURNAL Patent: WO 0129262-A 1787 26-APR-2001;  
 Orchid Biosciences, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..25  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

Query Match 0.9%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2326 CCCACCTCGCCCTCCCAAGTGCTG 2350  
 Db 25 CCCGCTTGACCTCCCAAGTGCTG 1

RESULT 367  
 AX117740/c  
 LOCUS AX117740 25 bp DNA linear PAT 11-MAY-2001  
 DEFINITION Sequence 2863 from Patent WO0129262.  
 ACCESSION AX117740  
 VERSION AX117740.1 GI:14034691  
 KEYWORDS synthetic construct  
 ORGANISM synthetic construct  
 SOURCE artificial sequences.  
 REFERENCE 1  
 AUTHORS Picoult-Newburg, L. and Pohl, M.  
 TITLE Genotyping reagents, kits and methods of use thereof  
 JOURNAL Patent: WO 0129262-A 2863 26-APR-2001;  
 Orchid Biosciences, Inc. (US)

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FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"

Query Match
  Best Local Similarity 0.9%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCCTGCCTCAGCCTCCCAATTA 2212
Db 25 TTCTCCTGCCTCAGCCTCCCGAGTA 1

RESULT 368
AX118236/c
LOCUS
  DEFINITION
    Sequence 3359 from Patent WO0129262.
  ACCESSION
    AX118236
  VERSION
    AX118236.1 GI:14035187
  KEYWORDS
    synthetic construct
  SOURCE
    synthetic construct
    artificial sequences.
  REFERENCE
    1
    Picoult-Newburg,L. and Pohl,M.
    Genotyping reagents, kits and methods of use thereof
    Patent: WO 0129262-A 3359 26-APR-2001;
    Orchid BioSciences, Inc. (US)
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        /db_xref="taxon:32630"
        /note="Primer"

Query Match
  Best Local Similarity 0.9%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCCTGCCTCAGCCTCCCAATTA 2212
Db 25 TTCTCCTGCCTCAGCCTCCCGAGTA 1

RESULT 369
AX692832
LOCUS
  DEFINITION
    Sequence 5564 from Patent EP1281758.
  ACCESSION
    AX692832
  VERSION
    AX692832.1 GI:29415795
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Shannon,M., Gu,Y. and Nguyen,C.T.
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
    Patent: EP 1281758-A 5564 05-FEB-2003;
    Aeomica, Inc. (US)
  FEATURES
    source
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.9%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCCTGCCTCAGCCTCCCAATTA 2212
Db 25 TTCTCCTGCCTCAGCCTCCCGAGTA 1

RESULT 370
AX692833
LOCUS
  DEFINITION
    Sequence 5565 from Patent EP1281758.
  ACCESSION
    AX692833
  VERSION
    AX692833.1 GI:29415796
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Shannon,M., Gu,Y. and Nguyen,C.T.
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
    Patent: EP 1281758-A 5565 05-FEB-2003;
    Aeomica, Inc. (US)
  FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.9%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2086 TTATTATTTTGTGACCGAGTCT 2110
Db 1 TTTTATTTTGTGACCGAGTCT 25

RESULT 371
AX692838
LOCUS
  DEFINITION
    Sequence 5570 from Patent EP1281758.
  ACCESSION
    AX692838
  VERSION
    AX692838.1 GI:29415801
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Shannon,M., Gu,Y. and Nguyen,C.T.
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
    Patent: EP 1281758-A 5570 05-FEB-2003;
    Aeomica, Inc. (US)
  FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.9%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2087 TATTATTTTGTGACCGAGTCT 2111
Db 1 TTTTATTTTGTGACCGAGTCT 25

RESULT 372
AX692839
LOCUS
  DEFINITION
    Sequence 5571 from Patent EP1281758.
  ACCESSION
    AX692839
  VERSION
    AX692839.1 GI:29415802
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Shannon,M., Gu,Y. and Nguyen,C.T.
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
    Patent: EP 1281758-A 5571 05-FEB-2003;
    Aeomica, Inc. (US)
  FEATURES
    source
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
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  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2092 TTTTATTTTGTGACCGAGTCTGTCTC 2116
Db 1 TTTTATTTTGTGACCGAGTCTGTCTC 25

RESULT 373
AX692840
LOCUS
  DEFINITION
    Sequence 5572 from Patent EP1281758.
  ACCESSION
    AX692840
  VERSION
    AX692840.1 GI:29415803
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Shannon,M., Gu,Y. and Nguyen,C.T.
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
    Patent: EP 1281758-A 5572 05-FEB-2003;
    Aeomica, Inc. (US)
  FEATURES
    source
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.9%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2093 TTTTATTTTGTGACCGAGTCTGTCTC 2117
Db 1 TTTTATTTTGTGACCGAGTCTGTCTC 25

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DEFINITION Sequence 5571 from Patent EP1281758.  
 ACCESSION AX692839  
 VERSION AX692839.1 GI:29415802  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5571 05-FEB-2003;  
 Aeomica, Inc. (US)

FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2093 TTTTGTGAGACCGAGTCTTGCTCT 2117  
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 Db 1 TTTTGTGAGACGAGTCTGCTCT 25

RESULT 373  
 AX692919  
 LOCUS AX692919 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5651 from Patent EP1281758.  
 ACCESSION AX692919  
 VERSION AX692919.1 GI:29415882  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5651 05-FEB-2003;  
 Aeomica, Inc. (US)

FEATURES  
 source Location/Qualifiers  
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 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2174 CCGGTTGCACCATTCCTGCTCT 2198  
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 Db 1 CTGGGTTACACCATTCCTGCTT 25

RESULT 374  
 AX692924  
 LOCUS AX692924 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5656 from Patent EP1281758.  
 ACCESSION AX692924  
 VERSION AX692924.1 GI:29415887  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5656 05-FEB-2003;  
 Aeomica, Inc. (US)

FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2179 TTCGACCATTCCTGCTCAGCC 2203  
 |||||  
 Db 1 TTCACACCATTCCTGCTTCAGTC 25

RESULT 375  
 AX692925  
 LOCUS AX692925 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5657 from Patent EP1281758.  
 ACCESSION AX692925  
 VERSION AX692925.1 GI:29415888  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5657 05-FEB-2003;  
 Aeomica, Inc. (US)

FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.9%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2180 TCGCACCATTCTCTGCTCAGCCT 2204  
 |||||  
 Db 1 TCACACCATTCCTGCTTCAGTCT 25

RESULT 376  
 AX692926  
 LOCUS AX692926 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 5658 from Patent EP1281758.  
 ACCESSION AX692926  
 VERSION AX692926.1 GI:29415889  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5658 05-FEB-2003;  
 Aeomica, Inc. (US)

FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"



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Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 8.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2250 TTTTTCGTACTTTTAGTAGAGACAG 2274
Db 1 TATTTTCGTATTTTAGTAGAGACGG 25

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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.  
AUTHORS Ibd-related polymorphisms  
TITLE Patent: WO 0142511-A 1371 14-JUN-2001;  
JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis  
Biotherapeutics Corporation (CA)  
FEATURES Location/Qualifiers  
source  
1..26  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.9%; Score 20.2; DB 1; Length 26;  
Best Local Similarity 84.6%; Pred. No. 8.4e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2345 GTGCTGGGATTACAGGCATGAGCCAC 2370  
Db 1 GTGCTGGGATTANAGGTGTGAACCAC 26  
AX183704/c  
LOCUS AX183704 26 bp DNA linear PAT 06-AUG-2001  
DEFINITION Sequence 1457 from Patent WO0142511.  
ACCESSION AX183704  
VERSION AX183704.1 GI:15135027  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.  
AUTHORS Ibd-related polymorphisms  
TITLE Patent: WO 0142511-A 1457 14-JUN-2001;  
JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis  
Biotherapeutics Corporation (CA)  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.9%; Score 20.2; DB 1; Length 26;  
Best Local Similarity 84.6%; Pred. No. 8.4e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2345 GTGCTGGGATTACAGGCATGAGCCAC 2370  
Db 26 GTGCTGGGATTGCANGTGTGAGCCAC 1  
AX154586/c  
LOCUS AX154586 20 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 3 from patent US 6238921.  
ACCESSION AX154586  
VERSION AX154586.1 GI:15122639  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.  
TITLE Antisense oligonucleotide modulation of human mdm2 expression  
JOURNAL Patent: US 6238921-A 3 29-MAY-2001;  
FEATURES Location/Qualifiers  
source  
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/organism="unknown"  
/mol\_type="unassigned DNA"

/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCACCGCGCGAGCTTGCGCTG 20  
Db 20 GCACCGCGCGAGCTTGCGCTG 1  
RESULT 384  
AX154587/c  
LOCUS AX154587 20 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 4 from patent US 6238921.  
ACCESSION AX154587  
VERSION AX154587.1 GI:15122640  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.  
TITLE Antisense oligonucleotide modulation of human mdm2 expression  
JOURNAL Patent: US 6238921-A 4 29-MAY-2001;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 37 GGCCCTGTGTGTCGGAAGA 56  
Db 20 GGCCCTGTGTGTCGGAAGA 1  
RESULT 385  
AX154588/c  
LOCUS AX154588 20 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 5 from patent US 6238921.  
ACCESSION AX154588  
VERSION AX154588.1 GI:15122641  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.  
TITLE Antisense oligonucleotide modulation of human mdm2 expression  
JOURNAL Patent: US 6238921-A 5 29-MAY-2001;  
FEATURES Location/Qualifiers  
source  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 95 CTCTGACCGAGATCCTGCTG 114  
Db 20 CTCTGACCGAGATCCTGCTG 1  
RESULT 386  
AX154589/c  
LOCUS AX154589 20 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 6 from patent US 6238921.  
ACCESSION AX154589

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VERSION AR154589.1 GI:15122642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 6 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 ATTAGTCGCTACGAGCGCCC 166
|||||
Db 20 ATTAGTCGCTACGAGCGCCC 1

RESULT 387
AR154590/c
LOCUS AR154590 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6238921.
ACCESSION AR154590
VERSION AR154590.1 GI:15122643
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 7 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 GAGAGTCGAATGATCCCCGA 200
|||||
Db 20 GAGAGTCGAATGATCCCCGA 1

RESULT 388
AR154591/c
LOCUS AR154591 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 8 from patent US 6238921.
ACCESSION AR154591
VERSION AR154591.1 GI:15122644
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 8 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 AGCAGGCAAAATGTGCAATAC 322
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Db 20 AGCAGGCAAAATGTGCAATAC 1

RESULT 391
AR154594/c
LOCUS AR154594 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6238921.
ACCESSION AR154594
VERSION AR154594.1 GI:15122647
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)

Qy 273 CTCCAAGCGCGAAACCCCG 292
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Db 20 CTCCAAGCGCGAAACCCCG 1

RESULT 389
AR154592/c
LOCUS AR154592 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6238921.
ACCESSION AR154592
VERSION AR154592.1 GI:15122645
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 9 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 295 TGGTGAGGAGCAGGCAAAATG 314
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Db 20 TGGTGAGGAGCAGGCAAAATG 1

RESULT 390
AR154593/c
LOCUS AR154593 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6238921.
ACCESSION AR154593
VERSION AR154593.1 GI:15122646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 10 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
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/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 393 AGCAGGCAAAATGTGCAATAC 322
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Db 20 AGCAGGCAAAATGTGCAATAC 1

RESULT 391
AR154594/c
LOCUS AR154594 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6238921.
ACCESSION AR154594
VERSION AR154594.1 GI:15122647
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
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AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.  
 TITLE Antisense oligonucleotide modulation of human mdm2 expression  
 JOURNAL Patent: US 6238921-A 11 29-MAY-2001;  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACCTACTGATGGTGCT 350  
 Db 20 CTGTACCTACTGATGGTGCT 1

RESULT 392  
 AR154595/c  
 LOCUS AR154595 20 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 12 from patent US 6238921.  
 ACCESSION AR154595  
 VERSION AR154595.1 GI:15122648  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.  
 TITLE Antisense oligonucleotide modulation of human mdm2 expression  
 JOURNAL Patent: US 6238921-A 12 29-MAY-2001;  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 GATCTACAGGAACCTTGGTAG 636  
 Db 20 GATCTACAGGAACCTTGGTAG 1

RESULT 393  
 AR154596/c  
 LOCUS AR154596 20 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 13 from patent US 6238921.  
 ACCESSION AR154596  
 VERSION AR154596.1 GI:15122649  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.  
 TITLE Antisense oligonucleotide modulation of human mdm2 expression  
 JOURNAL Patent: US 6238921-A 13 29-MAY-2001;  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1047 AGTGAGAAATTGAAGTTGA 1066  
 Db 20 AGTGAGAAATTGAAGTTGA 1

RESULT 394  
 AR154597/c  
 LOCUS AR154597 20 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 14 from patent US 6238921.  
 ACCESSION AR154597  
 VERSION AR154597.1 GI:15122650  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.  
 TITLE Antisense oligonucleotide modulation of human mdm2 expression  
 JOURNAL Patent: US 6238921-A 14 29-MAY-2001;  
 FEATURES Location/Qualifiers  
 source  
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 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTCTGATTGTAAA 1400  
 Db 20 TTGATGTTCTCTGATTGTAAA 1

RESULT 395  
 AR154598/c  
 LOCUS AR154598 20 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 15 from patent US 6238921.  
 ACCESSION AR154598  
 VERSION AR154598.1 GI:15122651  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.  
 TITLE Antisense oligonucleotide modulation of human mdm2 expression  
 JOURNAL Patent: US 6238921-A 15 29-MAY-2001;  
 FEATURES Location/Qualifiers  
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 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTACATGTGCAAGAAGCT 1714  
 Db 20 TTTACATGTGCAAGAAGCT 1

RESULT 396  
 AR154599/c  
 LOCUS AR154599 20 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 16 from patent US 6238921.  
 ACCESSION AR154599  
 VERSION AR154599.1 GI:15122652  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.  
 TITLE Antisense oligonucleotide modulation of human mdm2 expression  
 JOURNAL Patent: US 6238921-A 16 29-MAY-2001;  
 FEATURES Location/Qualifiers  
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Best Local Similarity 0.8%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1776 TATTTCCTCCAGTGTACCTG 1795					
Db 20 TATTTCCTCCAGTGTACCTG 1					
RESULT 397					
AR154600/c					
LOCUS AR154600 20 bp DNA linear PAT 08-AUG-2001					
DEFINITION Sequence 17 from patent US 6238921.					
ACCESSION AR154600					
VERSION AR154600.1 GI:15122653					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.					
TITLE Antisense oligonucleotide modulation of human mdm2 expression					
JOURNAL Patent: US 6238921-A 17 29-MAY-2001;					
FEATURES Location/Qualifiers					
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Query Match					
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1785 TAGTGACCTGTCTATAAGA 1804					
Db 20 TAGTGACCTGTCTATAAGA 1					
RESULT 398					
AR154601/c					
LOCUS AR154601 20 bp DNA linear PAT 08-AUG-2001					
DEFINITION Sequence 18 from patent US 6238921.					
ACCESSION AR154601					
VERSION AR154601.1 GI:15122654					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.					
TITLE Antisense oligonucleotide modulation of human mdm2 expression					
JOURNAL Patent: US 6238921-A 18 29-MAY-2001;					
FEATURES Location/Qualifiers					
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1785 TAGTGACCTGTCTATAAGA 1804					
Db 20 TAGTGACCTGTCTATAAGA 1					
RESULT 399					
AR154602/c					
LOCUS AR154602 20 bp DNA linear PAT 08-AUG-2001					
DEFINITION Sequence 19 from patent US 6238921.					
ACCESSION AR154602					
VERSION AR154602.1 GI:15122655					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.					
TITLE Antisense oligonucleotide modulation of human mdm2 expression					
JOURNAL Patent: US 6238921-A 19 29-MAY-2001;					
FEATURES Location/Qualifiers					
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Query Match					
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1818 CTAACCTATATACCCTAGGA 1837					
Db 20 CTAACCTATATACCCTAGGA 1					
RESULT 400					
AR154603/c					
LOCUS AR154603 20 bp DNA linear PAT 08-AUG-2001					
DEFINITION Sequence 20 from patent US 6238921.					
ACCESSION AR154603					
VERSION AR154603.1 GI:15122656					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.					
TITLE Antisense oligonucleotide modulation of human mdm2 expression					
JOURNAL Patent: US 6238921-A 20 29-MAY-2001;					
FEATURES Location/Qualifiers					
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/mol_type="unassigned DNA"					
Query Match					
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1934 TAGTGGAAATAGTGAATACTT 1953					
Db 20 TAGTGGAAATAGTGAATACTT 1					
RESULT 401					
AR154604/c					
LOCUS AR154604 20 bp DNA linear PAT 08-AUG-2001					
DEFINITION Sequence 21 from patent US 6238921.					
ACCESSION AR154604					
VERSION AR154604.1 GI:15122657					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.					
TITLE Antisense oligonucleotide modulation of human mdm2 expression					
JOURNAL Patent: US 6238921-A 21 29-MAY-2001;					
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Query Match					
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 2132 AGTGCAGTGGGTGATCTTGG 2151					
Db 20 AGTGCAGTGGGTGATCTTGG 1					
RESULT 402					
AR154605/c					
LOCUS AR154605 20 bp DNA linear PAT 08-AUG-2001					
DEFINITION Sequence 22 from patent US 6238921.					
ACCESSION AR154605					
VERSION AR154605.1 GI:15122658					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.					
TITLE Antisense oligonucleotide modulation of human mdm2 expression					
JOURNAL Patent: US 6238921-A 22 29-MAY-2001;					
FEATURES Location/Qualifiers					
source					
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Best Local Similarity 0.8%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 2132 AGTGCAGTGGGTGATCTTGG 2151					
Db 20 AGTGCAGTGGGTGATCTTGG 1					
RESULT 403					
AR154606/c					
LOCUS AR154606 20 bp DNA linear PAT 08-AUG-2001					
DEFINITION Sequence 23 from patent US 6238921.					
ACCESSION AR154606					
VERSION AR154606.1 GI:15122659					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.					
TITLE Antisense oligonucleotide modulation of human mdm2 expression					
JOURNAL Patent: US 6238921-A 23 29-MAY-2001;					
FEATURES Location/Qualifiers					
source					
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/organism="unknown"					
/mol_type="unassigned DNA"					
Query Match					

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QY 2224 AGTCATCTGCCACACACCT 2243
Db 20 AGTCATCTGCCACACACCT 1

RESULT 402
AR154605/c
LOCUS AR154605 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 22 from patent US 6238921.
ACCESSION AR154605
VERSION AR154605.1 GI:15122658
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 22 29-MAY-2001;
FEATURES
Location/Qualifiers
source 1..20
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/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGCAGG 2275
Db 20 GTACTTTTAGTAGACAGG 1

RESULT 403
AR154608/c
LOCUS AR154608 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 25 from patent US 6238921.
ACCESSION AR154608
VERSION AR154608.1 GI:15122661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 25 29-MAY-2001;
FEATURES
Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGCAGG 2275
Db 20 GTACTTTTAGTAGACAGG 1

RESULT 404
AR154605/c
LOCUS AR154605 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Fluorescent probe for chromosome painting.
ACCESSION BD233827
VERSION BD233827.1 GI:33043597
KEYWORDS JP 2002527077-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 20)
AUTHORS Cherif,D.

TITLE Fluorescent probe for chromosome painting
Patent: JP 2002527077-A 1 27-AUG-2002;
GENSET
OS Artificial Sequence
PN JP 2002527077-A/1
PD 27-AUG-2002
PF 15-OCT-1999 JP 2000576054
PR 15-OCT-1998 FR 98/12957
PI DORRA CHERIF
PC C12Q1/68,C12N15/09,C12N15/09,G01N33/58,C12N15/00, PC
C12N15/00
CC primer PCR Alu
FH Key Location/Qualifiers
FT primer bind 1..20.
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
Db 20 CCCAGGCTGGAGTGCAGTGG 1

RESULT 405
BD267626
LOCUS BD267626 20 bp DNA linear PAT 17-JUL-2003
DEFINITION UCPS.
ACCESSION BD267626
VERSION BD267626.1 GI:33077394
KEYWORDS JP 2002533062-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 20)
AUTHORS Adams,S. and Pan,J.
TITLE UCPS
JOURNAL Patent: JP 2002533062-A 22 08-OCT-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002533062-A/22
PD 08-OCT-2002
PF 03-NOV-1999 JP 2000585265
PR 30-NOV-1998 US 60/110286,16-APR-1999 US 60/129583 PR
15-JUL-1999 US 60/143886
PI SEAN ADAMS,JAMES PAN
PC C12N15/09,A61K31/7125,A61K45/00,A61K48/00,A61P3/04,A61P17/02,
PC A61P25/28.
PC A61P29/00,A61P31/04,A61P43/00,C07K14/47,C07K16/18,C07K16/46,
PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/02,G01N33/15,G01N33/50, PC
G01N33/53//
PC C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:865),(C12P21/
02,C12R1:91),
PC C12N15/00,C12N5/00
CC Artificial Sequence 1-20
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2349 TGGATTACAGGCATGAGCC 2368
Db      1 TGGATTACAGGCATGAGCC 20

RESULT 406
LOCUS   CQ784281/c
DEFINITION Sequence 4421 from Patent EP1396543.
ACCESSION CQ784281
VERSION   CQ784281.1 GI:45538769
KEYWORDS .
SOURCE   synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
        Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
        Koga,H.
TITLE   Primers for synthesizing full length cDNA clones and their use
JOURNAL Patent: EP 1396543-A 4421 10-MAR-2004;
        Research Association for Biotechnology (JP)
FEATURES
    source
        1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: an artificially
            synthesized primer se q uence"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2341 CAAAGTCTGGGATTACAGG 2360
Db      20 CAAAGTCTGGGATTACAGG 1

RESULT 407
LOCUS   CQ786097
DEFINITION Sequence 21 from Patent WO2004018711.
ACCESSION CQ786097
VERSION   CQ786097.1 GI:45721200
KEYWORDS .
SOURCE   synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Ming-Qing,D.
TITLE   Diagnostic test
JOURNAL Patent: WO 2004018711-A 21 04-MAR-2004;
        University College London (GB)
FEATURES
    source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer for amplification of D6S105"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2340 CCAAGTCTGGGATTACAG 2359
Db      1 CCAAGTCTGGGATTACAG 20

RESULT 408
LOCUS   E31877/c
DEFINITION Method for anticipating risk of Alzheimer's disease.
ACCESSION E31877
VERSION   E31877.1 GI:13017436
KEYWORDS .
SOURCE   unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Nario,O.
TITLE   Method for anticipating risk of Alzheimer's disease
JOURNAL Patent: JP 199908996-A 10 09-NOV-1999;
        SRL INC
COMMENT  OS Unidentified
        PN JP 1999308996-A/10
        PD 09-NOV-1999
        PF 28-APR-1998 JP 1998134578
        PR NARIO OTA
        PC C12N15/09,C12Q1/68,C12N15/00
        CC Key Location/Qualifiers
        FH Key 1..20
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        FT Location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="taxon:32644"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2263 TAGTAGAGACAGGTTTCAC 2282
Db      20 TAGTAGAGACAGGTTTCAC 1

RESULT 409
LOCUS   AR208406/c
DEFINITION Sequence 22 from patent US 6383752.
ACCESSION AR208406
VERSION   AR208406.1 GI:21509552
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Agrawal,S. and Kandimalla,E.R.
TITLE   Pseudo-cyclic oligonucleobases
JOURNAL Patent: US 6383752-A 22 07-MAY-2002;
        Location/Qualifiers
FEATURES
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      675 GTGAGTGAGACAGGTGTCA 694
Db      20 GTGAGTGAGACAGGTGTCA 1

RESULT 410
LOCUS   AR236783/c
DEFINITION Sequence 3 from patent US 6465247.
ACCESSION AR236783
VERSION   AR236783.1 GI:27280976

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KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weissman,I.L., Traver,D.J. and Akashi,K.
TITLE Mammalian myeloid progenitor cell subsets
JOURNAL Patent: US 6465247-A 3 15-OCT-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTCTGGGATTACAGGCAT 2363
Db 20 AGTCTGGGATTACAGGCAT 1

RESULT 413
AR310706/c
LOCUS AR310706 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2 from patent US 6559279.
ACCESSION AR310706
VERSION AR310706.1 GI:31703861
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M. and Guzaev,A.P.
TITLE Process for preparing peptide derivatized oligomeric compounds
JOURNAL Patent: US 6559279-A 2 06-MAY-2003;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTCATGTGCAAGAAGCT 1714
Db 20 TTTCATGTGCAAGAAGCT 1

RESULT 414
AR321577/c
LOCUS AR321577 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6562959.
ACCESSION AR321577
VERSION AR321577.1 GI:33706806
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cherif,D.
TITLE Detection of altered expression of genes regulating cell proliferation
JOURNAL Patent: US 6562959-A 1 13-MAY-2003;
FEATURES Location/Qualifiers
source
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/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCAGGCTGGAGTCAGTGG 2141
Db 20 CCAGGCTGGAGTCAGTGG 1

RESULT 415
AR337145
LOCUS AR337145 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 70 from patent US 6566135.
ACCESSION AR337145
VERSION AR337145.1 GI:33722999
KEYWORDS
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KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weissman,I.L., Traver,D.J. and Akashi,K.
TITLE Mammalian myeloid progenitor cell subsets
JOURNAL Patent: US 6465247-A 3 15-OCT-2002;
FEATURES Location/Qualifiers
source
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/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTCTGGGATTACAGGCAT 2363
Db 20 AGTCTGGGATTACAGGCAT 1

RESULT 411
AR305303/c
LOCUS AR305303 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 257 from patent US 6545137.
ACCESSION AR305303
VERSION AR305303.1 GI:31694613
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
TITLE Receptor
JOURNAL Patent: US 6545137-A 257 08-APR-2003;
FEATURES Location/Qualifiers
source
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/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTCTGGGATTACAGGCAT 2363
Db 20 AGTCTGGGATTACAGGCAT 1

RESULT 412
AR309407/c
LOCUS AR309407 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 257 from patent US 6555654.
ACCESSION AR309407
VERSION AR309407.1 GI:31701412
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
TITLE LDL-receptor
JOURNAL Patent: US 6555654-A 257 29-APR-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
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SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Watt,A.T.  
TITLE Antisense modulation of caspase 6 expression  
JOURNAL Patent: US 6566135-A 70 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2340 CCAAAGTCTGGGATTACAG 2359  
Db 1 CCAAAGTCTGGGATTACAG 20  
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RESULT 416  
AR370250/c  
LOCUS AR370250 20 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 71 from patent US 6300132.  
ACCESSION AR370250  
VERSION AR370250.1 GI:34606756  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Cowseart,L.M.  
TITLE Antisense inhibition of telomeric repeat binding factor 2  
JOURNAL expression  
FEATURES Patent: US 6300132-A 71 09-OCT-2001;  
source Location/Qualifiers  
1..20  
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Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTCGATCTCCT 2311  
Db 20 CAGGATGGTCTCGATCTCCT 1  
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RESULT 417  
AR370252/c  
LOCUS AR370252 20 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 73 from patent US 6300132.  
ACCESSION AR370252  
VERSION AR370252.1 GI:34606758  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Cowseart,L.M.  
TITLE Antisense inhibition of telomeric repeat binding factor 2  
JOURNAL expression  
FEATURES Patent: US 6300132-A 73 09-OCT-2001;  
source Location/Qualifiers  
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/mol\_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGATTACAGCATGA 2365  
Db 20 TGCTGGATTACAGCATGA 1  
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RESULT 418  
AR435741/c  
LOCUS AR435741 20 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 7 from patent US 6656730.  
ACCESSION AR435741  
VERSION AR435741.1 GI:40198823  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Manoharan,M.  
TITLE Oligonucleotides conjugated to protein-binding drugs  
JOURNAL Patent: US 6656730-A 7 02-DEC-2003;  
FEATURES Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTACATGTGCAAGAAGCT 1714  
Db 20 TTTACATGTGCAAGAAGCT 1  
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RESULT 419  
AX115919  
LOCUS AX115919 20 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 1042 from Patent WO0129262.  
ACCESSION AX115919  
VERSION AX115919.1 GI:14032861  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Picoult-Newburg,L. and Pohl,M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 1042 26-APR-2001;  
FEATURES Orchid Biosciences, Inc. (US)  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAAGTCTGGGATTAC 2357  
Db 1 TCCCAAAGTCTGGGATTAC 20  
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RESULT 420  
AX116275  
LOCUS AX116275 20 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 1398 from Patent WO0129262.  
ACCESSION AX116275  
VERSION AX116275.1 GI:14033217  
KEYWORDS  
SOURCE synthetic construct

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ORGANISM      synthetic construct
               artificial sequences.
REFERENCE
AUTHORS      Picoult-Newburg,L. and Pohl,M.
JOURNAL      Genotyping reagents, kits and methods of use thereof
              Patent: WO 0129262-A 1398 26-APR-2001;
              Orchid Biosciences, Inc. (US)
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source
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2352 GATTACAGGCATGAGCCACC 2371
Db      1 GATTACAGGCATGAGCCACC 20

RESULT 421
AX146647/c
LOCUS      AX146647      20 bp      DNA      linear      PAT 31-MAY-2001
DEFINITION      Sequence 1 from Patent WO0134093.
ACCESSION      AX146647
VERSION      AX146647.1 GI:14285040
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE
AUTHORS      Agrawal,S.
TITLE      Potentiation of prodrug efficacy
JOURNAL      Patent: WO 0134093-A 1 17-MAY-2001;
            HYBRIDON, INC. (US)
FEATURES
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/db_xref="taxon:32630"
/notes="oligonucleotide sequence"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      675 GTGAGTGAGAACAGGTGTCA 694
Db      20 GTGAGTGAGAACAGGTGTCA 1

RESULT 422
AX657359
LOCUS      AX657359      20 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION      Sequence 72 from Patent WO02100896.
ACCESSION      AX657359
VERSION      AX657359.1 GI:29160099
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE
AUTHORS      dalla Venezia,N.L., Magnard,C.M., Lenoir,G.M. and
            Sinilnikova-Brard,O.
TITLE      Method for diagnosing cancer susceptibility
JOURNAL      Patent: WO 02100896-A 72 19-DEC-2002;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR);
            UNIVERSITE CLAUDE BERNARD - LYON 1 (FR)
FEATURES
source
1..20

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="amorce PCR"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2338 TCCCAAAGTCTGGGATTAC 2357
Db      1 TCCCAAAGTCTGGGATTAC 20

RESULT 423
BD073963
LOCUS      BD073963      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073963
VERSION      BD073963.1 GI:22619566
KEYWORDS      JP 2001513996-A/2.
SOURCE      unidentified
            unidentified
            unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 2 11-SEP-2001;
            HYBRIDON INC
COMMENT      OS Unidentified
            PN JP 2001513996-A/2
            PD 11-SEP-2001
            PF 18-AUG-1998 JP 2000507794
            PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
            JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
            PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
            PC C12N15/00
            CC Strandedness: Both;
            CC Topology: Linear;
            CC Antisense oligonucleotide specific to MDM2
            FH Key      Location/Qualifiers
            FT source      1..20
            FT      /organism='Unidentified'.
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source
1..20
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/mol_type="genomic DNA"
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      481 TTGGCCAGTATATTATGACT 500
Db      1 TTGGCCAGTATATTATGACT 20

RESULT 424
BD073964
LOCUS      BD073964      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073964
VERSION      BD073964.1 GI:22619567
KEYWORDS      JP 2001513996-A/3.
SOURCE      unidentified
            unidentified
            unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 3 11-SEP-2001;
            HYBRIDON INC

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COMMENT OS Unidentified
PN JP 2001513996-A/3
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
/organism='Unidentified'.
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 695 CCTGAAGGTGGGAGTGATC 714
|||||
Db 1 CCTGAAGGTGGGAGTGATC 20

RESULT 425
BD073965
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073965
VERSION BD073965.1 GI:22619568
KEYWORDS JP 2001513996-A/4.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 4 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/4
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
/organism='Unidentified'.
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source
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1018 TGGATCAGGATTCAGTTTCA 1037
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Db 1 TGGATCAGGATTCAGTTTCA 20

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RESULT 426
BD073968
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073968
VERSION BD073968.1 GI:22619571
KEYWORDS JP 2001513996-A/7.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 7 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/7
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
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/db_xref='taxon:32644'
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 357 ACCTCAGATTCACGCTTC 376
|||||
Db 1 ACCTCAGATTCACGCTTC 20

RESULT 427
BD073969
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073969
VERSION BD073969.1 GI:22619572
KEYWORDS JP 2001513996-A/8.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 8 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/8
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
/organism='Unidentified'.

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    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 CCAGCTTCGGACACAGAC 388
Db 1 CCAGCTTCGGACACAGAC 20

RESULT 428
LOCUS BD073970 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073970
VERSION BD073970.1 GI:22619573
KEYWORDS JP 2001513996-A/9.
SOURCE unidentified
ORGANISM unidentified

REFERENCE
  1 (bases 1 to 20)
  Chen,J., Agrawal,S. and Zhang,R.
  Antisense oligonucleotide specific to MDM2
  TITLE Antisense oligonucleotide specific to MDM2
  JOURNAL Patent: JP 2001513996-A 9 11-SEP-2001;
  HYBRIDON INC

COMMENT
  OS Unidentified
  PN JP 2001513996-A/9
  PD 11-SEP-2001
  PF 18-AUG-1998 JP 2000507794
  PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
  JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
  PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
  CC C12N15/00
  CC Strandedness: Both;
  CC Topology: Linear;
  CC Antisense oligonucleotide specific to MDM2
  FH Key Location/Qualifiers
  FT source 1..20
  /organism="unidentified".

FEATURES
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    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Query Match
  Best Local Similarity 100.0%; Pred. No. 7.9e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 TCCTTAGCTGACTATTGGAA 1222
Db 1 TCCTTAGCTGACTATTGGAA 20

RESULT 430
LOCUS BD073972 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073972
VERSION BD073972.1 GI:22619575
KEYWORDS JP 2001513996-A/11.
SOURCE unidentified
ORGANISM unidentified

REFERENCE
  1 (bases 1 to 20)
  Chen,J., Agrawal,S. and Zhang,R.
  Antisense oligonucleotide specific to MDM2
  TITLE Antisense oligonucleotide specific to MDM2
  JOURNAL Patent: JP 2001513996-A 11 11-SEP-2001;
  HYBRIDON INC

COMMENT
  OS Unidentified
  PN JP 2001513996-A/11
  PD 11-SEP-2001
  PF 18-AUG-1998 JP 2000507794
  PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
  JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
  PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
  CC C12N15/00
  CC Strandedness: Both;
  CC Topology: Linear;
  CC Antisense oligonucleotide specific to MDM2
  FH Key Location/Qualifiers
  FT source 1..20
  /organism="unidentified".

FEATURES
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    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Query Match
  Best Local Similarity 100.0%; Pred. No. 7.9e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 TCTACCTCATCTAGAGGAG 799
Db 1 TCTACCTCATCTAGAGGAG 20

RESULT 429
LOCUS BD073971 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073971
VERSION BD073971.1 GI:22619574
KEYWORDS JP 2001513996-A/10.
SOURCE unidentified
ORGANISM unidentified

REFERENCE
  1 (bases 1 to 20)
  Chen,J., Agrawal,S. and Zhang,R.
  Antisense oligonucleotide specific to MDM2
  TITLE Antisense oligonucleotide specific to MDM2
  JOURNAL Patent: JP 2001513996-A 10 11-SEP-2001;
  HYBRIDON INC

COMMENT
  OS Unidentified
  PN JP 2001513996-A/10
  PD 11-SEP-2001
  PF 18-AUG-1998 JP 2000507794
  PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
  JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
  PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
  CC C12N15/00
  CC Strandedness: Both;
  CC Topology: Linear;
  CC Antisense oligonucleotide specific to MDM2
  FH Key Location/Qualifiers
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Query Match
  Best Local Similarity 100.0%; Pred. No. 7.9e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249
Db 1 TCATGCAATGAATGAATCC 20

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RESULT 431
BD073974
LOCUS          BD073974          20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073974
VERSION        BD073974.1 GI:22619577
KEYWORDS       JP 2001513996-A/13.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2
JOURNAL       Patent: JP 2001513996-A 13 11-SEP-2001;
              HYBRIDON INC
COMMENT       OS Unidentified
              PN JP 2001513996-A/13
              PD 11-SEP-2001
              PF 18-AUG-1998 JP 2000507794
              PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              JT JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
              PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
              PC C12N15/00
              CC Strandedness: Both;
              CC Topology: Linear;
              CC Antisense oligonucleotide specific to MDM2
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.

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            /db_xref='taxon:32644'

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGACAG 688
Db 1 ACATCTGTGAGTGAGACAG 20

RESULT 432
BD073975
LOCUS          BD073975          20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073975
VERSION        BD073975.1 GI:22619578
KEYWORDS       JP 2001513996-A/14.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2
JOURNAL       Patent: JP 2001513996-A 14 11-SEP-2001;
              HYBRIDON INC
COMMENT       OS Unidentified
              PN JP 2001513996-A/14
              PD 11-SEP-2001
              PF 18-AUG-1998 JP 2000507794
              PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              JT JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
              PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
              PC C12N15/00
              CC Strandedness: Both;
              CC Topology: Linear;
              CC Antisense oligonucleotide specific to MDM2
              FH Key Location/Qualifiers
              FT source 1..20

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGACAG 688
Db 1 ACATCTGTGAGTGAGACAG 20

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FT          Location/Qualifiers
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              /mol_type='genomic DNA'
              /db_xref='taxon:32644'

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
Db 1 GTGAGTGAGAACAGGTGTCA 20

RESULT 433
BD073976
LOCUS          BD073976          20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073976
VERSION        BD073976.1 GI:22619579
KEYWORDS       JP 2001513996-A/15.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2
JOURNAL       Patent: JP 2001513996-A 15 11-SEP-2001;
              HYBRIDON INC
COMMENT       OS Unidentified
              PN JP 2001513996-A/15
              PD 11-SEP-2001
              PF 18-AUG-1998 JP 2000507794
              PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              JT JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
              PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
              PC C12N15/00
              CC Strandedness: Both;
              CC Topology: Linear;
              CC Antisense oligonucleotide specific to MDM2
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.

FEATURES
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            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGAACAGGTGTCACTTG 699
Db 1 TGAGAACAGGTGTCACTTG 20

RESULT 434
BD073977
LOCUS          BD073977          20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073977
VERSION        BD073977.1 GI:22619580
KEYWORDS       JP 2001513996-A/16.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2

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JOURNAL      Patent: JP 2001513996-A 16 11-SEP-2001;
HYBRIDON INC
COMMENT      OS Unidentified
PN          JP 2001513996-A/16
PD          11-SEP-2001
PF          18-AUG-1998 JP 2000507794
PR          22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIAN DONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC          C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC          C12N15/00
CC          Strandedness: Both;
CC          Topology: Linear;
CC          Antisense oligonucleotide specific to MDM2
FH          Key Location/Qualifiers
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          Location/Qualifiers
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          685 ACAGGTGTCACCTGAGGT 704
          |||||
          1 ACAGGTGTCACCTGAGGT 20

RESULT 435
BD073978
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073978
VERSION   BD073978.1 GI:22619581
KEYWORDS  JP 2001513996-A/17.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE     Antisense oligonucleotide specific to MDM2
JOURNAL   Patent: JP 2001513996-A 17 11-SEP-2001;
          HYBRIDON INC
COMMENT    OS Unidentified
          PN JP 2001513996-A/17
          PD 11-SEP-2001
          PF 18-AUG-1998 JP 2000507794
          PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
          JIAN DONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
          PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
          PC C12N15/00
          CC Strandedness: Both;
          CC Topology: Linear;
          CC Antisense oligonucleotide specific to MDM2
          FH Key Location/Qualifiers
          FT source 1..20
          FT /organism='Unidentified'.
          Location/Qualifiers
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          704 TGGGAGTGATCAAAAGGACC 723
          |||||
          1 TGGGAGTGATCAAAAGGACC 20

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/organism='unidentified'
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Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          704 TGGGAGTGATCAAAAGGACC 723
          |||||
          1 TGGGAGTGATCAAAAGGACC 20

FEATURES
source
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

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RESULT 436
BD073979
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073979
VERSION   BD073979.1 GI:22619582
KEYWORDS  JP 2001513996-A/18.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE     Antisense oligonucleotide specific to MDM2
JOURNAL   Patent: JP 2001513996-A 18 11-SEP-2001;
          HYBRIDON INC
COMMENT    OS Unidentified
          PN JP 2001513996-A/18
          PD 11-SEP-2001
          PF 18-AUG-1998 JP 2000507794
          PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
          JIAN DONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
          PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
          PC C12N15/00
          CC Strandedness: Both;
          CC Topology: Linear;
          CC Antisense oligonucleotide specific to MDM2
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          Location/Qualifiers
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          709 GTGATCAAAAGGACCTTGTA 728
          |||||
          1 GTGATCAAAAGGACCTTGTA 20

FEATURES
source
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          709 GTGATCAAAAGGACCTTGTA 728
          |||||
          1 GTGATCAAAAGGACCTTGTA 20

RESULT 437
BD073980
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073980
VERSION   BD073980.1 GI:22619583
KEYWORDS  JP 2001513996-A/19.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE     Antisense oligonucleotide specific to MDM2
JOURNAL   Patent: JP 2001513996-A 19 11-SEP-2001;
          HYBRIDON INC
COMMENT    OS Unidentified
          PN JP 2001513996-A/19
          PD 11-SEP-2001
          PF 18-AUG-1998 JP 2000507794
          PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
          JIAN DONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
          PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
          PC C12N15/00
          CC Strandedness: Both;
          CC Topology: Linear;
          CC Antisense oligonucleotide specific to MDM2
          FH Key Location/Qualifiers
          FT source 1..20
          FT /organism='Unidentified'.
          Location/Qualifiers
          1..20
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          /mol_type='genomic DNA'
          /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          704 TGGGAGTGATCAAAAGGACC 723
          |||||
          1 TGGGAGTGATCAAAAGGACC 20

FEATURES
source
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

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FT source 1..20 /organism='Unidentified'.
FT Location/Qualifiers
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  /mol_type='genomic DNA'
  /db_xref='taxon:32644'

Query Match
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 717 AAGGACCTTGACAGAGCT 736
    |||||
Db 1 AAGGACCTTGACAGAGCT 20

RESULT 438
LOCUS BD073981 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073981
VERSION BD073981.1 GI:22619584
KEYWORDS JP 2001513996-A/20.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 20 11-SEP-2001;
COMMENT HYBRIDON INC
OS Unidentified
PN JP 2001513996-A/20
PD 11-SEP-2001
PR 18-AUG-1998 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

Query Match
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1003 ATTCAGGTGATTGGTGGAT 1022
    |||||
Db 1 ATTCAGGTGATTGGTGGAT 20

RESULT 440
LOCUS BD073984 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073984
VERSION BD073984.1 GI:22619587
KEYWORDS JP 2001513996-A/23.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 23 11-SEP-2001;
COMMENT HYBRIDON INC
OS Unidentified
PN JP 2001513996-A/23
PD 11-SEP-2001
PR 18-AUG-1998 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

Query Match
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 998 TGAACATTCAGGTGATTGGT 1017
    |||||
Db 1 TGAACATTCAGGTGATTGGT 20

RESULT 439
LOCUS BD073982 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073982
VERSION BD073982.1 GI:22619585
KEYWORDS JP 2001513996-A/21.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.

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TITLE Antisense oligonucleotide specific to MDM2
JOURNAL HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/21
PD 11-SEP-2001
PR 18-AUG-1998 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

Query Match
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1003 ATTCAGGTGATTGGTGGAT 1022
    |||||
Db 1 ATTCAGGTGATTGGTGGAT 20

RESULT 440
LOCUS BD073984 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073984
VERSION BD073984.1 GI:22619587
KEYWORDS JP 2001513996-A/23.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 23 11-SEP-2001;
COMMENT HYBRIDON INC
OS Unidentified
PN JP 2001513996-A/23
PD 11-SEP-2001
PR 18-AUG-1998 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

Query Match
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1027 ATTCAGTTTCAGATCAGTTT 1046
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Db      1  ATTGAGTTTCAGATCAGTTT 20

RESULT 441
LOCUS   BD073985
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073985
VERSION   BD073985.1 GI:22619588
KEYWORDS  JP 2001513996-A/24.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 24 11-SEP-2001;
HYBRIDON INC
COMMENT   OS Unidentified
          PN JP 2001513996-A/24
          PD 11-SEP-2001
          PF 18-AUG-1998 JP 2000507794
          PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
          PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
          PC C12N15/00
          CC Strandedness: Both;
          CC Topology: Linear;
          CC Antisense oligonucleotide specific to MDM2
          FH Key Location/Qualifiers
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          FT Location/Qualifiers
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTTAGTGTAGAAATT 1057
Db      1  GATCAGTTTAGTGTAGAAATT 20

RESULT 442
LOCUS   BD073988/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073988
VERSION   BD073988.1 GI:22619591
KEYWORDS  JP 2001513996-A/27.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 27 11-SEP-2001;
HYBRIDON INC
COMMENT   OS Unidentified
          PN JP 2001513996-A/27
          PD 11-SEP-2001
          PF 18-AUG-1998 JP 2000507794
          PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
          PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
          PC C12N15/00
          CC Strandedness: Both;
          CC Topology: Linear;
          CC Antisense oligonucleotide specific to MDM2
          FH Key Location/Qualifiers
          FT source 1..20
          FT /organism='Unidentified'.
          FT Location/Qualifiers
          FT 1..20
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          FT /mol_type='genomic DNA'
          FT /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTTAGTGTAGAAATT 1057
Db      1  GATCAGTTTAGTGTAGAAATT 20

RESULT 443
LOCUS   BD073989/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073989
VERSION   BD073989.1 GI:22619592
KEYWORDS  JP 2001513996-A/28.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 28 11-SEP-2001;
HYBRIDON INC
COMMENT   OS Unidentified
          PN JP 2001513996-A/28
          PD 11-SEP-2001
          PF 18-AUG-1998 JP 2000507794
          PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
          PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
          PC C12N15/00
          CC Strandedness: Both;
          CC Topology: Linear;
          CC Antisense oligonucleotide specific to MDM2
          FH Key Location/Qualifiers
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          FT /organism='Unidentified'.
          FT Location/Qualifiers
          FT 1..20
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          FT /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 695 CCTTGAAGGTGGAGTGATC 714
Db      20  CCTTGAAGGTGGAGTGATC 1

RESULT 444
LOCUS   BD073990/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073990
VERSION   BD073990.1 GI:22619593
KEYWORDS  JP 2001513996-A/29.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 20)

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AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE        Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 29 11-SEP-2001;
COMMENT      HYBRIDON INC
OS           Unidentified
PN           JP 2001513996-A/29
PD           11-SEP-2001
PF           18-AUG-1998 JP 2000507794
PR           22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANFONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC           C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC           C12N15/00
CC           Strandedness: Both;
CC           Topology: Linear;
CC           Antisense oligonucleotide specific to MDM2
FH           Key Location/Qualifiers
FT           1..20 /organism='Unidentified'.
FEATURES
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1018 TGGATCAGGATTCAGTTTCA 1037
Db      20 TGGATCAGGATTCAGTTTCA 1

RESULT 445
LOCUS      BD073991/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION  BD073991
VERSION     BD073991.1 GI:22619594
KEYWORDS   JP 2001513996-A/30.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 30 11-SEP-2001;
COMMENT    HYBRIDON INC
OS         Unidentified
PN         JP 2001513996-A/30
PD         11-SEP-2001
PF         18-AUG-1998 JP 2000507794
PR         22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANFONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC         C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC         C12N15/00
CC         Strandedness: Both;
CC         Topology: Linear;
CC         Antisense oligonucleotide specific to MDM2
FH         Key Location/Qualifiers
FT         1..20
    /organism='unidentified'
    /mol_type='genomic DNA'
    /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 ACCTCACAGATTCAGCTTC 376
Db      20 ACCTCACAGATTCAGCTTC 1

RESULT 446
LOCUS      BD073992/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION  BD073992
VERSION     BD073992.1 GI:22619595
KEYWORDS   JP 2001513996-A/31.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 31 11-SEP-2001;
COMMENT    HYBRIDON INC
OS         Unidentified
PN         JP 2001513996-A/31
PD         11-SEP-2001
PF         18-AUG-1998 JP 2000507794
PR         22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANFONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC         C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC         C12N15/00
CC         Strandedness: Both;
CC         Topology: Linear;
CC         Antisense oligonucleotide specific to MDM2
FH         Key Location/Qualifiers
FT         1..20
    /organism='unidentified'
    /mol_type='genomic DNA'
    /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      369 CCAGCTTCGACACAGAGAC 388
Db      20 CCAGCTTCGACACAGAGAC 1

RESULT 447
LOCUS      BD073993/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION  BD073993
VERSION     BD073993.1 GI:22619596
KEYWORDS   JP 2001513996-A/32.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 32 11-SEP-2001;
COMMENT    HYBRIDON INC
OS         Unidentified
PN         JP 2001513996-A/32
PD         11-SEP-2001
PF         18-AUG-1998 JP 2000507794
PR         22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANFONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC         C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC         C12N15/00
CC         Strandedness: Both;
CC         Topology: Linear;
CC         Antisense oligonucleotide specific to MDM2
FH         Key Location/Qualifiers
FT         1..20
    /organism='unidentified'
    /mol_type='genomic DNA'
    /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 ACCTCACAGATTCAGCTTC 376
Db      20 ACCTCACAGATTCAGCTTC 1

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[illegible][illegible]

Qy 669 ACATCTGTGAGTGAGAACAG 688  
 |||||  
 Db 20 ACATCTGTGAGTGAGAACAG 1

## RESULT 451

BD073997/c  
 LOCUS BD073997 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antisense oligonucleotide specific to MDM2.  
 ACCESSION BD073997

VERSION BD073997.1 GI:22619600  
 KEYWORDS JP 2001513996-A/36.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Chen,J., Agrawal,S. and Zhang,R.  
 TITLE Antisense oligonucleotide specific to MDM2  
 JOURNAL Patent: JP 2001513996-A 36 11-SEP-2001;  
 HYBRIDON INC

COMMENT OS Unidentified  
 PN JP 2001513996-A/36  
 PD 11-SEP-2001  
 PF 18-AUG-1998 JP 2000507794  
 PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI  
 PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,  
 PC C12N15/00  
 CC Strandedness: Both;  
 CC Topology: Linear;  
 CC Antisense oligonucleotide specific to MDM2  
 FH Key Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.  
 FT Location/Qualifiers

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 source

1..20  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 675 GTGAGTGAGAACAGGTGTCA 694  
 |||||  
 Db 20 GTGAGTGAGAACAGGTGTCA 1

## RESULT 452

BD073998/c  
 LOCUS BD073998 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antisense oligonucleotide specific to MDM2.  
 ACCESSION BD073998

VERSION BD073998.1 GI:22619601  
 KEYWORDS JP 2001513996-A/37.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Chen,J., Agrawal,S. and Zhang,R.  
 TITLE Antisense oligonucleotide specific to MDM2  
 JOURNAL Patent: JP 2001513996-A 37 11-SEP-2001;  
 HYBRIDON INC

COMMENT OS Unidentified  
 PN JP 2001513996-A/37  
 PD 11-SEP-2001  
 PF 18-AUG-1998 JP 2000507794  
 PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI  
 PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,  
 PC C12N15/00  
 CC Strandedness: Both;

CC Topology: Linear;  
 CC Antisense oligonucleotide specific to MDM2  
 FH Key Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.  
 FT Location/Qualifiers

FEATURES  
 source

1..20  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 680 TGAGAACAGGTGTCACTTG 699  
 |||||  
 Db 20 TGAGAACAGGTGTCACTTG 1

## RESULT 453

BD073999/c  
 LOCUS BD073999 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antisense oligonucleotide specific to MDM2.  
 ACCESSION BD073999

VERSION BD073999.1 GI:22619602  
 KEYWORDS JP 2001513996-A/38.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Chen,J., Agrawal,S. and Zhang,R.  
 TITLE Antisense oligonucleotide specific to MDM2  
 JOURNAL Patent: JP 2001513996-A 38 11-SEP-2001;  
 HYBRIDON INC

COMMENT

OS Unidentified  
 PN JP 2001513996-A/38  
 PD 11-SEP-2001  
 PF 18-AUG-1998 JP 2000507794  
 PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI

PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,  
 PC C12N15/00  
 CC Strandedness: Both;  
 CC Topology: Linear;  
 CC Antisense oligonucleotide specific to MDM2  
 FH Key Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.  
 FT Location/Qualifiers

FEATURES  
 source

1..20  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 685 ACAGGTGTCACTTGAAGGT 704  
 |||||  
 Db 20 ACAGGTGTCACTTGAAGGT 1

## RESULT 454

BD074000/c  
 LOCUS BD074000 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antisense oligonucleotide specific to MDM2.  
 ACCESSION BD074000

VERSION BD074000.1 GI:22619603  
 KEYWORDS JP 2001513996-A/39.  
 SOURCE unidentified  
 ORGANISM unclassified.

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unclassified.
1 (bases 1 to 20)
Chen,J., Agrawal,S. and Zhang,R.
Antisense oligonucleotide specific to MDM2
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 2001513996-A/39
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20 /organism='Unidentified'.
FT Location/Qualifiers
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/organism='unidentified'
/mol_type='genomic DNA'
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723
|||||
Db 20 TGGGAGTGATCAAAAGGACC 1

RESULT 455
BD074001/c
LOCUS
DEFINITION
Antisense oligonucleotide specific to MDM2.
ACCESSION
BD074001
VERSION
BD074001.1 GI:22619604
KEYWORDS
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 20)
Chen,J., Agrawal,S. and Zhang,R.
Antisense oligonucleotide specific to MDM2
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 2001513996-A/40
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
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FT Location/Qualifiers
1..20
/organism='unidentified'
/mol_type='genomic DNA'
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723
|||||
Db 20 TGGGAGTGATCAAAAGGACC 1

RESULT 455
BD074001/c
LOCUS
DEFINITION
Antisense oligonucleotide specific to MDM2.
ACCESSION
BD074001
VERSION
BD074001.1 GI:22619604
KEYWORDS
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 20)
Chen,J., Agrawal,S. and Zhang,R.
Antisense oligonucleotide specific to MDM2
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 2001513996-A/40
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20 /organism='Unidentified'.
FT Location/Qualifiers
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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unclassified.
1 (bases 1 to 20)
Chen,J., Agrawal,S. and Zhang,R.
Antisense oligonucleotide specific to MDM2
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 2001513996-A/39
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
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FT Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 AAGGACCTTGTCACAGAGCT 736
|||||
Db 20 AAGGACCTTGTCACAGAGCT 1

RESULT 457
BD074003/c
LOCUS
DEFINITION
Antisense oligonucleotide specific to MDM2.
ACCESSION
BD074003
VERSION
BD074003.1 GI:22619606
KEYWORDS
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 20)
Chen,J., Agrawal,S. and Zhang,R.
Antisense oligonucleotide specific to MDM2
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 2001513996-A/42
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00

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CC Strandedness: Both;  
 CC Topology: Linear;  
 CC Antisense oligonucleotide specific to MDM2  
 PH Key Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.  
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 source Location/Qualifiers  
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 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 998 TGAACATTCAGGTGATTGGT 1017  
 |||||  
 Db 20 TGAACATTCAGGTGATTGGT 1

RESULT 458  
 BD074004/c  
 LOCUS BD074004 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antisense oligonucleotide specific to MDM2.  
 ACCESSION BD074004  
 VERSION BD074004.1 GI:22619607  
 KEYWORDS JP 2001513996-A/43.  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.  
 1 (bases 1 to 20)  
 Chen,J., Agrawal,S. and Zhang,R.  
 Antisense oligonucleotide specific to MDM2  
 TITLE Antisense oligonucleotide specific to MDM2  
 JOURNAL Patent: JP 2001513996-A 43 11-SEP-2001;  
 HYBRIDON INC  
 COMMENT OS Unidentified  
 PN JP 2001513996-A/43  
 PD 11-SEP-2001  
 PR 18-AUG-1998 JP 2000507794  
 PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI  
 JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG  
 PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,  
 PC C12N15/00  
 CC Strandedness: Both;  
 CC Topology: Linear;  
 CC Antisense oligonucleotide specific to MDM2  
 PH Key Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.

FEATURES  
 source Location/Qualifiers  
 1..20  
 /organism='unidentified'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 ATTCAGGTGATTGGTTGGAT 1022  
 |||||  
 Db 20 ATTCAGGTGATTGGTTGGAT 1

RESULT 459  
 BD074006/c  
 LOCUS BD074006 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antisense oligonucleotide specific to MDM2.  
 ACCESSION BD074006  
 VERSION BD074006.1 GI:22619609  
 KEYWORDS JP 2001513996-A/45.  
 SOURCE unidentified

ORGANISM unidentified  
 unclassified.  
 1 (bases 1 to 20)  
 Chen,J., Agrawal,S. and Zhang,R.  
 Antisense oligonucleotide specific to MDM2  
 TITLE Antisense oligonucleotide specific to MDM2  
 JOURNAL Patent: JP 2001513996-A 45 11-SEP-2001;  
 HYBRIDON INC  
 COMMENT OS Unidentified  
 PN JP 2001513996-A/45  
 PD 11-SEP-2001  
 PR 18-AUG-1998 JP 2000507794  
 PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI  
 JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG  
 PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,  
 PC C12N15/00  
 CC Strandedness: Both;  
 CC Topology: Linear;  
 CC Antisense oligonucleotide specific to MDM2  
 PH Key Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.

FEATURES  
 source Location/Qualifiers  
 1..20  
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 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATTCAGTTTCAGATCAGTTT 1046  
 |||||  
 Db 20 ATTCAGTTTCAGATCAGTTT 1

RESULT 460  
 BD074007/c  
 LOCUS BD074007 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antisense oligonucleotide specific to MDM2.  
 ACCESSION BD074007  
 VERSION BD074007.1 GI:22619610  
 KEYWORDS JP 2001513996-A/46.  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.  
 1 (bases 1 to 20)  
 Chen,J., Agrawal,S. and Zhang,R.  
 Antisense oligonucleotide specific to MDM2  
 TITLE Antisense oligonucleotide specific to MDM2  
 JOURNAL Patent: JP 2001513996-A 46 11-SEP-2001;  
 HYBRIDON INC  
 COMMENT OS Unidentified  
 PN JP 2001513996-A/46  
 PD 11-SEP-2001  
 PR 18-AUG-1998 JP 2000507794  
 PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI  
 JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG  
 PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,  
 PC C12N15/00  
 CC Strandedness: Both;  
 CC Topology: Linear;  
 CC Antisense oligonucleotide specific to MDM2  
 PH Key Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.

FEATURES  
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Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 ATTCAGGTGATTGGTTGGAT 1022  
 |||||  
 Db 20 ATTCAGGTGATTGGTTGGAT 1

RESULT 459  
 BD074006/c  
 LOCUS BD074006 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antisense oligonucleotide specific to MDM2.  
 ACCESSION BD074006  
 VERSION BD074006.1 GI:22619609  
 KEYWORDS JP 2001513996-A/45.  
 SOURCE unidentified

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTTACGTAGTAATT 1057
Db 20 GATCAGTTTACGTAGTAATT 1

RESULT 461
BD074008/c
LOCUS BD074008 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074008
VERSION BD074008.1 GI:22619611
KEYWORDS JP 2001513996-A/47.
SOURCE unidentified
ORGANISM unidentified
unclassified.
1 (bases 1 to 20)
Chen,J., Agrawal,S. and Zhang,R.
Antisense oligonucleotide specific to MDM2
Patent: JP 2001513996-A 47 11-SEP-2001;
HYBRIDON INC.
COMMENT OS Unidentified
PN JP 2001513996-A/47
PD 11-SEP-2001
PF 18-SEP-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANQONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7086,A61K48/00,A61P35/00,C07H21/00,
C12N15/00
CC Strandedness: Both;
CC Topology: linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
/organism='Unidentified'.
FEATURES
source
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGACAGGTGTCA 694
Db 20 GTGAGTGAGACAGGTGTCA 1

RESULT 462
BD088804/c
LOCUS BD088804 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088804
VERSION BD088804.1 GI:22634414
KEYWORDS JP 2001321190-A/1048.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 20)
Soeda,E.
A method of arraying genome clone
Patent: JP 2001321190-A 1048 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1048
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGACAGGTGTCA 694
Db 20 GTGAGTGAGACAGGTGTCA 1

RESULT 461
BD074008/c
LOCUS BD074008 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074008
VERSION BD074008.1 GI:22619611
KEYWORDS JP 2001513996-A/47.
SOURCE unidentified
ORGANISM unidentified
unclassified.
1 (bases 1 to 20)
Chen,J., Agrawal,S. and Zhang,R.
Antisense oligonucleotide specific to MDM2
Patent: JP 2001513996-A 47 11-SEP-2001;
HYBRIDON INC.
COMMENT OS Unidentified
PN JP 2001513996-A/47
PD 11-SEP-2001
PF 18-SEP-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANQONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7086,A61K48/00,A61P35/00,C07H21/00,
C12N15/00
CC Strandedness: Both;
CC Topology: linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
/organism='Unidentified'.
FEATURES
source
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGACAGGTGTCA 694
Db 20 GTGAGTGAGACAGGTGTCA 1

RESULT 462
BD088804/c
LOCUS BD088804 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088804
VERSION BD088804.1 GI:22634414
KEYWORDS JP 2001321190-A/1048.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 20)
Soeda,E.
A method of arraying genome clone
Patent: JP 2001321190-A 1048 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1048
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC

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C12N15/00.
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
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1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTCTGGGATTA 2356
Db 1 CTCCCAAAGTCTGGGATTA 20

RESULT 463
BD089238/c
LOCUS BD089238 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD089238
VERSION BD089238.1 GI:22634848
KEYWORDS JP 2001321190-A/1482.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 20)
Soeda,E.
A method of arraying genome clone
Patent: JP 2001321190-A 1482 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1482
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00.
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
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FEATURES
source
1..20
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2142 GTGATCTTGGCTCAGTCGCA 2161
Db 20 GTGATCTTGGCTCAGTCGCA 1

RESULT 464
BD106214/c
LOCUS BD106214 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel LDL-receptor.
ACCESSION BD106214
VERSION BD106214.1 GI:23201032
KEYWORDS JP 2002501376-A/229.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.

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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 1 (bases 1 to 20)  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

REFERENCE  
 AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D., Hammond, H. and Hey, P.  
 TITLE Novel LDL-receptor  
 JOURNAL Patent: JP 2002501376-A 229 15-JAN-2002;  
 THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO INC

COMMENT  
 PN JP 2002501376-A/229  
 PD 15-JAN-2002  
 PE 15-APR-1998 JP 1998543635  
 PR 15-APR-1997 US 60/043553, 05-JUN-1997 US 60/048740 PI  
 JOHN ANDREW TODD, JOHN WILFRED HESS, CHARLES THOMAS CASKEY, ROGER  
 PI DAVID COX,  
 PI DAVID GERHOLD, HOLLY HAMMOND, PATRICIA HEY  
 PC C12N15/12, C12N15/11, C12Q1/68, C07K14/705, C07K16/28, A61K38/17,  
 PC A61K39/395,  
 PC A61K48/00  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.

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 : /mol\_type="genomic DNA"  
 : /db\_xref="taxon:35827"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTGCTGGGATTACAGGCAT 2363  
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 Db 20 AGTGCTGGGATTACAGGCAT 1

RESULT 465  
 BD128205/c  
 LOCUS 20 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
 ACCESSION BD128205  
 VERSION BD128205.1 GI:232233150  
 KEYWORDS JP 2002017375-A/3636.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE  
 AUTHORS Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and Koga, H.  
 TITLE Primer for synthesizing full-length cDNA and use thereof  
 JOURNAL Patent: JP 2002017375-A 3636 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 OS Unidentified  
 PN JP 2002017375-A/3636  
 PD 22-JAN-2002  
 PE 07-JUL-2000 JP 2000253172  
 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO  
 PI ISHII,  
 PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIMA,  
 PI TETSUJI OTSUKI, HISASHI KOGA  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68/C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
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 FH key Location/Qualifiers  
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 /organism="Unidentified".

FEATURES  
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 : /mol\_type="genomic DNA"  
 : /db\_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360  
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 Db 20 CAAAGTCTGGGATTACAGG 1

RESULT 466  
 BD138077/c  
 LOCUS 20 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Antisense modulation of human MDM2 expression.  
 ACCESSION BD138077  
 VERSION BD138077.1 GI:23233022  
 KEYWORDS JP 2002508944-A/3.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE  
 AUTHORS Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsett, L.M.  
 TITLE Antisense modulation of human MDM2 expression  
 JOURNAL Patent: JP 2002508944-A 3 26-MAR-2002;  
 ISIS PHARMACEUTICALS INC  
 OS Unidentified  
 PN JP 2002508944-A/3  
 PD 26-MAR-2002  
 PE 26-MAR-1999 JP 2000538025  
 PR 26-MAR-1998 US 09/048810  
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M COWSETT

PI C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04///  
 PC C12Q1/68,  
 PC C12N15/00  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 CC Antisense modulation of human MDM2 expression FH Key  
 Location/Qualifiers  
 FT source 1..20  
 /organism="Unidentified".

FEATURES  
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Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTG 20  
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 Db 20 GCACCGCGGAGCTTGGCTG 1

RESULT 467  
 BD138078/c  
 LOCUS 20 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Antisense modulation of human MDM2 expression.  
 ACCESSION BD138078  
 VERSION BD138078.1 GI:23233023  
 KEYWORDS JP 2002508944-A/4.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE  
 1 (bases 1 to 20)

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AUTHORS      Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE        Antisense modulation of human MDM2 expression
JOURNAL      Patent: JP 2002508944-A 4 26-MAR-2002;
              ISIS PHARMACEUTICALS INC
COMMENT      OS Unidentified
              PN JP 2002508944-A/4
              PD 26-MAR-2002
              PF 26-MAR-1999 JP 2000538025
              PR 26-MAR-1998 US 09/048810
              PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
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   /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCTGTGTGTCGGAAGA 56
Db 20 GGCCTGTGTGTCGGAAGA 1

RESULT 468
BD138079/c
LOCUS      BD138079
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138079
VERSION     JP 2002508944-A/5.
KEYWORDS   JP 2002508944-A/5.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 5 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified
            PN JP 2002508944-A/5
            PD 26-MAR-2002
            PF 26-MAR-1999 JP 2000538025
            PR 26-MAR-1998 US 09/048810
            PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
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   1..20
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   /mol_type='genomic DNA'
   /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCTGTGTGTCGGAAGA 56
Db 20 GGCCTGTGTGTCGGAAGA 1

RESULT 468
BD138079/c
LOCUS      BD138079
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138079
VERSION     JP 2002508944-A/5.
KEYWORDS   JP 2002508944-A/5.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 5 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified
            PN JP 2002508944-A/5
            PD 26-MAR-2002
            PF 26-MAR-1999 JP 2000538025
            PR 26-MAR-1998 US 09/048810
            PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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   /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATTAGTGGGTACGAGCGCCC 166
Db 20 ATTAGTGGGTACGAGCGCCC 1

RESULT 470
BD138081/c
LOCUS      BD138081
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138081
VERSION     BD138081.1 GI:23233026
KEYWORDS   JP 2002508944-A/7.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 7 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified

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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCGTACCGAGATCCTGCTG 114
Db 20 CTCGTACCGAGATCCTGCTG 1

RESULT 469
BD138080/c
LOCUS      BD138080
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138080
VERSION     BD138080.1 GI:23233025
KEYWORDS   JP 2002508944-A/6.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 6 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified
            PN JP 2002508944-A/6
            PD 26-MAR-2002
            PF 26-MAR-1999 JP 2000538025
            PR 26-MAR-1998 US 09/048810
            PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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FT Location/Qualifiers
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   /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATTAGTGGGTACGAGCGCCC 166
Db 20 ATTAGTGGGTACGAGCGCCC 1

RESULT 470
BD138081/c
LOCUS      BD138081
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138081
VERSION     BD138081.1 GI:23233026
KEYWORDS   JP 2002508944-A/7.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 7 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified

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PN JP 2002508944-A/7
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI CONSENT
PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
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   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GAGAGTGGATGATCCCCGA 200
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DB 20 GAGAGTGGATGATCCCCGA 1

RESULT 471
BD138082/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 8 26-MAR-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/8
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI CONSENT
PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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FT Location/Qualifiers
   /organism='Unidentified'.
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   1..20
   /organism="unidentified"
   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PN JP 2002508944-A/7
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI CONSENT
PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
   /organism='Unidentified'.
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   /db_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 273 CTCGAAGCGCGAAAACCCCG 292
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DB 20 CTCGAAGCGCGAAAACCCCG 1

RESULT 472
BD138083/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 9 26-MAR-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/9
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI CONSENT
PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
   /organism='Unidentified'.
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   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 TGGTGAGGAGCGCAAAATG 314
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DB 20 TGGTGAGGAGCGCAAAATG 1

RESULT 473
BD138084/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 10 26-MAR-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/10
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

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PI COWSERT  
 PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//  
 PC C12Q1/68,  
 PC C12N15/00  
 CC Strandedness: Single;  
 CC Topology: linear;  
 CC Antisense modulation of human MDM2 expression FH Key  
 CC Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.  
 FEATURES  
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 Location/Qualifiers  
 1..20  
 /organism='unidentified'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 303 ACCAGGCAATGTGCAATAC 322  
 DB 20 ACCAGGCAATGTGCAATAC 1  
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RESULT 474  
 BDI38085/c  
 LOCUS  
 DEFINITION Antisense modulation of human MDM2 expression.  
 ACCESSION BDI38085  
 VERSION BDI38085.1 GI:23233030  
 KEYWORDS JP 2002508944-A/11.  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.  
 TITLE Antisense modulation of human MDM2 expression  
 JOURNAL Patent: JP 2002508944-A 11 26-MAR-2002;  
 ISIS PHARMACEUTICALS INC  
 COMMENT OS Unidentified  
 PN JP 2002508944-A/11  
 PD 26-MAR-2002  
 PF 26-MAR-1999 JP 2000538025  
 PR 26-MAR-1998 US 09/048810  
 PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT  
 PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//  
 PC C12Q1/68,  
 PC C12N15/00  
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 DB 20 CTGTACTACTGATGCTGCT 1  
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RESULT 475  
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 LOCUS  
 DEFINITION Antisense modulation of human MDM2 expression.  
 ACCESSION BDI38086  
 VERSION BDI38086.1 GI:23233031  
 KEYWORDS JP 2002508944-A/12.  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.  
 TITLE Antisense modulation of human MDM2 expression  
 JOURNAL Patent: JP 2002508944-A 12 26-MAR-2002;  
 ISIS PHARMACEUTICALS INC  
 COMMENT OS Unidentified  
 PN JP 2002508944-A/12  
 PD 26-MAR-2002  
 PF 26-MAR-1999 JP 2000538025  
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 PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT  
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RESULT 476  
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 LOCUS  
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 ACCESSION BDI38087  
 VERSION BDI38087.1 GI:23233032  
 KEYWORDS JP 2002508944-A/13.  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.  
 TITLE Antisense modulation of human MDM2 expression  
 JOURNAL Patent: JP 2002508944-A 13 26-MAR-2002;  
 ISIS PHARMACEUTICALS INC  
 COMMENT OS Unidentified  
 PN JP 2002508944-A/13  
 PD 26-MAR-2002  
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 PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT  
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LOCUS BD138088 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138088
VERSION BD138088.1 GI:23233033
KEYWORDS JP 2002508944-A/14.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 14 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/14
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M
PI COWSETT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
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PC C12N15/00
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LOCUS BD138089 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138089

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VERSION BD138089.1 GI:23233034
KEYWORDS JP 2002508944-A/15.
SOURCE unidentified
ORGANISM unidentified
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REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 15 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
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PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M
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LOCUS BD138090 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138090
VERSION BD138090.1 GI:23233035
KEYWORDS JP 2002508944-A/16.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 16 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/16
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M
PI COWSETT
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PC C12Q1/68,
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CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138099
VERSION BD138099.1 GI:23233044
KEYWORDS JP 2002508944-A/25.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 25 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/25
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
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QY 4 CCGCGCGAGCTTGGCTGCTT 23
Db 20 CCGCGCGAGCTTGGCTGCTT 1

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LOCUS BD138108 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138108
VERSION BD138108.1 GI:23233053
KEYWORDS JP 2002508944-A/34.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 34 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/34
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
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Db 20 GGCCCTGTGTGCGAAGA 1

RESULT 487
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138107
VERSION BD138107.1 GI:23233052
KEYWORDS JP 2002508944-A/33.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 33 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/33
PD 26-MAR-2002
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PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCGAGCTTGGCTGCTT 23
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RESULT 488
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LOCUS BD138108 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138108
VERSION BD138108.1 GI:23233053
KEYWORDS JP 2002508944-A/34.
SOURCE unidentified
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REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 34 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
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PN JP 2002508944-A/34
PD 26-MAR-2002
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PI COWSEERT
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QY 14 TTGGCTGCTTCTGGGCGCTG 33
Db 20 TTGGCTGCTTCTGGGCGCTG 1

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RESULT 489
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138109
VERSION     BD138109.1 GI:23233054
KEYWORDS   JP 2002508944-A/35.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 35 26-MAR-2002;
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COMMENT   PN JP 2002508944-A/35
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          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI  COWSERT
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Db  20 GCTTCTGGGGCCTGTGTGGC 1

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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138110
VERSION     BD138110.1 GI:23233055
KEYWORDS   JP 2002508944-A/36.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 36 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
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          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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PC  C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC  C12Q1/68,
PC  C12N15/00
CC  Strandedness: Single;
CC  Topology: Linear;
CC  Antisense modulation of human MDM2 expression FH Key
CC  Location/Qualifiers
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RESULT 491
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LOCUS      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138111
VERSION     BD138111.1 GI:23233056
KEYWORDS   JP 2002508944-A/37.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 37 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   PN JP 2002508944-A/37
          PD 26-MAR-2002
          PF 26-MAR-1999 JP 2000538025
          PR 26-MAR-1998 US 09/048810
          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI  COWSERT
PC  C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
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PC  C12N15/00
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QY  29 GCCTGTGTGGCCCTGTGTGT 48
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Db  20 GCCTGTGTGGCCCTGTGTGT 1

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LOCUS      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138112
VERSION     BD138112.1 GI:23233057
KEYWORDS   JP 2002508944-A/38.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 38 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   PN JP 2002508944-A/38
          PD 26-MAR-2002
          PF 26-MAR-1999 JP 2000538025
          PR 26-MAR-1998 US 09/048810
          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI  COWSERT
PC  C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC  C12Q1/68,
PC  C12N15/00
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CC  Topology: Linear;
CC  Antisense modulation of human MDM2 expression FH Key
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  34 TGTGGCCCTGTGTGTGTGGAA 53
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Db  20 TGTGGCCCTGTGTGTGTGGAA 1

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CC  Strandedness: Single;
CC  Topology: Linear;
CC  Antisense modulation of human MDM2 expression FH Key
CC  Location/Qualifiers
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  29 GCCTGTGTGGCCCTGTGTGT 48
    |||||
Db  20 GCCTGTGTGGCCCTGTGTGT 1

RESULT 491
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LOCUS      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138111
VERSION     BD138111.1 GI:23233056
KEYWORDS   JP 2002508944-A/37.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 37 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   PN JP 2002508944-A/37
          PD 26-MAR-2002
          PF 26-MAR-1999 JP 2000538025
          PR 26-MAR-1998 US 09/048810
          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI  COWSERT
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PC  C12Q1/68,
PC  C12N15/00
CC  Strandedness: Single;
CC  Topology: Linear;
CC  Antisense modulation of human MDM2 expression FH Key
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FT  source      1..20
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  34 TGTGGCCCTGTGTGTGTGGAA 53
    |||||
Db  20 TGTGGCCCTGTGTGTGTGGAA 1

RESULT 492
BD138112/c
LOCUS      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138112
VERSION     BD138112.1 GI:23233057
KEYWORDS   JP 2002508944-A/38.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 38 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   PN JP 2002508944-A/38
          PD 26-MAR-2002
          PF 26-MAR-1999 JP 2000538025
          PR 26-MAR-1998 US 09/048810
          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI  COWSERT
PC  C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC  C12Q1/68,
PC  C12N15/00
CC  Strandedness: Single;
CC  Topology: Linear;
CC  Antisense modulation of human MDM2 expression FH Key
CC  Location/Qualifiers
FT  source      1..20
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  34 TGTGGCCCTGTGTGTGTGGAA 53
    |||||
Db  20 TGTGGCCCTGTGTGTGTGGAA 1

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ACCESSION      BD138112
VERSION        BD138112.1  GI:23233057
KEYWORDS       JP 2002508944-A/38.
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 20)
AUTHORS       Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE         Antisense modulation of human MDM2 expression
JOURNAL       Patent: JP 2002508944-A 38 26-MAR-2002;
              ISIS PHARMACEUTICALS INC
COMMENT       OS Unidentified
              PN JP 2002508944-A/38
              PD 26-MAR-2002
              PF 26-MAR-1999 JP 2000538025
              PR 26-MAR-1998 US 09/048810
              PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSBERT
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PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred.No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GTGTGTCGGAAGATGGAGC 62
DB 20 GTGTGTCGGAAGATGGAGC 1

RESULT 493
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LOCUS          BD138113
DEFINITION     Antisense modulation of human MDM2 expression.
ACCESSION      BD138113
VERSION        BD138113.1  GI:23233058
KEYWORDS       JP 2002508944-A/39.
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 20)
AUTHORS       Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE         Antisense modulation of human MDM2 expression
JOURNAL       Patent: JP 2002508944-A 39 26-MAR-2002;
              ISIS PHARMACEUTICALS INC
COMMENT       OS Unidentified
              PN JP 2002508944-A/39
              PD 26-MAR-2002
              PF 26-MAR-1999 JP 2000538025
              PR 26-MAR-1998 US 09/048810
              PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSBERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
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Best Local Similarity 100.0%; Pred.No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 GTGTGTCGGAAGATGGAGC 1

RESULT 493
BD138113/C
LOCUS          BD138113
DEFINITION     Antisense modulation of human MDM2 expression.
ACCESSION      BD138113
VERSION        BD138113.1  GI:23233058
KEYWORDS       JP 2002508944-A/39.
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 20)
AUTHORS       Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE         Antisense modulation of human MDM2 expression
JOURNAL       Patent: JP 2002508944-A 39 26-MAR-2002;
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              PD 26-MAR-2002
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              PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSBERT
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PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
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Query Match      0.8%; Score 20; DB 1; Length 20;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 GGAAGATGGAGCAAGAAGC 1

RESULT 494
BD138114/C
LOCUS          BD138114
DEFINITION     Antisense modulation of human MDM2 expression.
ACCESSION      BD138114
VERSION        BD138114.1  GI:23233059
KEYWORDS       JP 2002508944-A/40.
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 20)
AUTHORS       Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE         Antisense modulation of human MDM2 expression
JOURNAL       Patent: JP 2002508944-A 40 26-MAR-2002;
              ISIS PHARMACEUTICALS INC
COMMENT       OS Unidentified
              PN JP 2002508944-A/40
              PD 26-MAR-2002
              PF 26-MAR-1999 JP 2000538025
              PR 26-MAR-1998 US 09/048810
              PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSBERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
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Query Match      0.8%; Score 20; DB 1; Length 20;
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QY 62 CAAGAAGCCGAGCCGAGGG 81
DB 20 CAAGAAGCCGAGCCGAGGG 1

RESULT 495
BD138115/C
LOCUS          BD138115
DEFINITION     Antisense modulation of human MDM2 expression.
ACCESSION      BD138115
VERSION        BD138115.1  GI:23233060
KEYWORDS       JP 2002508944-A/41.
SOURCE         unidentified
ORGANISM       unidentified

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Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 41 26-MAR-2002;
ISIS PHARMACEUTICALS INC
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PN JP 2002508944-A/41
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGAGCCCGAGGGGGCGCCG 89
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DB 20 CGAGCCCGAGGGGGCGCCG 1

RESULT 496
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LOCUS
DEFINITION
Antisense modulation of human MDM2 expression.
ACCESSION
BD138116
VERSION
BD138116.1 GI:23233061
KEYWORDS
JP 2002508944-A/42.
SOURCE
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ORGANISM
unclassified.
1 (bases 1 to 20)
Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 42 26-MAR-2002;
ISIS PHARMACEUTICALS INC
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PN JP 2002508944-A/42
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
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Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGAGCCCGAGGGGGCGCCG 89
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DB 20 CGAGCCCGAGGGGGCGCCG 1

RESULT 497
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LOCUS
DEFINITION
Antisense modulation of human MDM2 expression.
ACCESSION
BD138117
VERSION
BD138117.1 GI:23233062
KEYWORDS
JP 2002508944-A/43.
SOURCE
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ORGANISM
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1 (bases 1 to 20)
Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 43 26-MAR-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/43
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 GATCCTGCTGCTTTCGCAGC 124
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DB 20 GATCCTGCTGCTTTCGCAGC 1

RESULT 498
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LOCUS
DEFINITION
Antisense modulation of human MDM2 expression.
ACCESSION
BD138118
VERSION
BD138118.1 GI:23233063
KEYWORDS
JP 2002508944-A/44.
SOURCE
unidentified
ORGANISM
unclassified.
1 (bases 1 to 20)
Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 44 26-MAR-2002;

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COMMENT
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PN JP 2002508944-A/44
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
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PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TCGTTTCGAGCAGGAGCA 132
DB 20 TCGTTTCGAGCAGGAGCA 1

RESULT 499
BD138119/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.
TITLE
Antisense modulation of human MDM2 expression
JOURNAL
Patent: JP 2002508944-A 45 26-MAR-2002;
ISIS PHARMACEUTICALS INC
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OS Unidentified
PN JP 2002508944-A/45
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

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PC C12Q1/68,
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CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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FT Location/Qualifiers
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 GCAGCCGAGGAGCAGCGTCCC 139
DB 20 GCAGCCGAGGAGCAGCGTCCC 1

RESULT 500
BD138120/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.
TITLE
Antisense modulation of human MDM2 expression
JOURNAL
Patent: JP 2002508944-A 46 26-MAR-2002;
ISIS PHARMACEUTICALS INC
COMMENT
OS Unidentified
PN JP 2002508944-A/46
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSERT
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PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
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Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 AGTGGCTACGAGCGCCAGT 169
DB 20 AGTGGCTACGAGCGCCAGT 1

RESULT 501
BD138121/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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1 (bases 1 to 20)
AUTHORS
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.
TITLE
Antisense modulation of human MDM2 expression
JOURNAL
Patent: JP 2002508944-A 47 26-MAR-2002;
ISIS PHARMACEUTICALS INC
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PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025

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PR 26-MAR-1998 US 09/048810  
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 CC Antisense modulation of human MDM2 expression FH Key  
 CC Location/Qualifiers  
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source  
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 /db\_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 CGAGCGCCAGTGCCTGGC 177  
 Db 20 CGAGCGCCAGTGCCTGGC 1

## RESULT 502

BD138122/c  
 LOCUS 20 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Antisense modulation of human MDM2 expression.  
 ACCESSION BD138122

VERSION BD138122.1 GI:232333067  
 KEYWORDS JP 2002508944-A/48.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.  
 TITLE Antisense modulation of human MDM2 expression  
 JOURNAL Patent: JP 2002508944-A 48 26-MAR-2002;  
 ISIS PHARMACEUTICALS INC  
 COMMENT OS Unidentified  
 PN JP 2002508944-A/48  
 PD 26-MAR-2002  
 PF 26-MAR-1999 JP 2000538025  
 PR 26-MAR-1998 US 09/048810  
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSERT  
 PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//  
 PC C12Q1/68,  
 PC C12N15/00  
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 CC Topology: Linear;  
 CC Antisense modulation of human MDM2 expression FH Key  
 CC Location/Qualifiers  
 FT source 1..20  
 FT /organism='Unidentified'.

## FEATURES

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 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 CCACTGCCCTGGCCCGAGA 184  
 Db 20 CCACTGCCCTGGCCCGAGA 1

## RESULT 503

BD138123/c  
 LOCUS 20 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Antisense modulation of human MDM2 expression.  
 ACCESSION BD138123  
 VERSION BD138123.1 GI:232333068  
 KEYWORDS JP 2002508944-A/49.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.  
 TITLE Antisense modulation of human MDM2 expression  
 JOURNAL Patent: JP 2002508944-A 49 26-MAR-2002;  
 ISIS PHARMACEUTICALS INC  
 COMMENT OS Unidentified  
 PN JP 2002508944-A/49  
 PD 26-MAR-2002  
 PF 26-MAR-1999 JP 2000538025  
 PR 26-MAR-1998 US 09/048810  
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

## COMMENT

OS Unidentified  
 PN JP 2002508944-A/49  
 PD 26-MAR-2002  
 PF 26-MAR-1999 JP 2000538025  
 PR 26-MAR-1998 US 09/048810  
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M  
 COWSERT  
 PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//  
 PC C12Q1/68,  
 PC C12N15/00  
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 CC Topology: Linear;  
 CC Antisense modulation of human MDM2 expression FH Key  
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 FT source 1..20  
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 /Location/Qualifiers  
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 /db\_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 174 TGGCCCGAGAGTGGGAATGA 193  
 Db 20 TGGCCCGAGAGTGGGAATGA 1

## RESULT 504

BD138124/c  
 LOCUS 20 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Antisense modulation of human MDM2 expression.  
 ACCESSION BD138124  
 VERSION BD138124.1 GI:232333069  
 KEYWORDS JP 2002508944-A/50.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.  
 TITLE Antisense modulation of human MDM2 expression  
 JOURNAL Patent: JP 2002508944-A 50 26-MAR-2002;  
 ISIS PHARMACEUTICALS INC  
 COMMENT OS Unidentified  
 PN JP 2002508944-A/50  
 PD 26-MAR-2002  
 PF 26-MAR-1999 JP 2000538025  
 PR 26-MAR-1998 US 09/048810  
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

## COMMENT

OS Unidentified  
 PN JP 2002508944-A/50  
 PD 26-MAR-2002  
 PF 26-MAR-1999 JP 2000538025  
 PR 26-MAR-1998 US 09/048810  
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M  
 COWSERT  
 PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//

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PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.
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                /mol_type='genomic DNA'
                /db_xref='taxon:32644'
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 GCCCAGGGCGTGTCTTCC 221
Db |||||
20 GCCCAGGGCGTGTCTTCC 1

RESULT 505
BD138125/c
LOCUS BD138125 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138125
VERSION BD138125.1 GI:23233070
KEYWORDS JP 2002508944-A/51.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 51 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/51
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.
FEATURES
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                /db_xref='taxon:32644'
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GCGTCGTGTCTTCCGAGTA 227
Db |||||
20 GCGTCGTGTCTTCCGAGTA 1

RESULT 506
BD138126/c
LOCUS BD138126 20'bp DNA linear PAT 18-SEP-2002

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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138126
VERSION BD138126.1 GI:23233071
KEYWORDS JP 2002508944-A/52.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 52 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/52
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CTTCCGCGAGTAGTCAGTCCC 236
Db |||||
20 CTTCCGCGAGTAGTCAGTCCC 1

RESULT 507
BD138127/c
LOCUS BD138127 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138127
VERSION BD138127.1 GI:23233072
KEYWORDS JP 2002508944-A/53.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 53 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/53
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key

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Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TGAGGAGCAGGCAAAATGTGC 317  
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Db 20 TGAGGAGCAGGCAAAATGTGC 1

## RESULT 514

BD138134/c  
LOCUS BD138134 20 bp DNA linear PAT 18-SEP-2002  
DEFINITION Antisense modulation of human MDM2 expression.  
ACCESSION BD138134

VERSION BD138134.1 GI:23233079  
KEYWORDS JP 2002508944-A/60.  
SOURCE unidentified

ORGANISM  
unclassified.

REFERENCE 1. (bases 1 to 20)  
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.

TITLE Antisense modulation of human MDM2 expression  
JOURNAL Patent: JP 2002508944-A 60 26-MAR-2002;

COMMENT ISIS PHARMACEUTICALS INC  
OS Unidentified

PN JP 2002508944-A/60  
PD 26-MAR-2002

PF 26-MAR-1999 JP 2000538025  
PI 26-MAR-1998 US 09/048810

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## PI COWSERT

PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//

PC C12Q1/68,

PC C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

CC Antisense modulation of human MDM2 expression FH Key

Location/Qualifiers

FT source 1. .20 /organism='Unidentified'.

## FEATURES

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/db\_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 GAGGAGCAGGCAAAATGTGCA 318  
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Db 20 GAGGAGCAGGCAAAATGTGCA 1

## RESULT 515

BD138135/c  
LOCUS BD138135 20 bp DNA linear PAT 18-SEP-2002  
DEFINITION Antisense modulation of human MDM2 expression.  
ACCESSION BD138135

VERSION BD138135.1 GI:23233080  
KEYWORDS JP 2002508944-A/61.  
SOURCE unidentified

ORGANISM  
unclassified.

1. (bases 1 to 20)

REFERENCE Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.

TITLE Antisense modulation of human MDM2 expression

JOURNAL Patent: JP 2002508944-A 61 26-MAR-2002;

COMMENT ISIS PHARMACEUTICALS INC

OS Unidentified

PN JP 2002508944-A/61

PD 26-MAR-2002

PF 26-MAR-1999 JP 2000538025  
PR 26-MAR-1998 US 09/048810  
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

## PI COWSERT

PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//

PC C12Q1/68,

PC C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

CC Antisense modulation of human MDM2 expression FH Key

Location/Qualifiers

FT source 1. .20 /organism='Unidentified'.

## FEATURES

source

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/mol\_type='genomic DNA'

/db\_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 AGGAGCAGGCAAAATGTGCA 319  
|||||

Db 20 AGGAGCAGGCAAAATGTGCA 1

## RESULT 516

BD138136/c

LOCUS BD138136 20 bp DNA linear PAT 18-SEP-2002

DEFINITION Antisense modulation of human MDM2 expression.

ACCESSION BD138136

VERSION BD138136.1 GI:23233081

KEYWORDS JP 2002508944-A/62.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1. (bases 1 to 20)

AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.

TITLE Antisense modulation of human MDM2 expression

JOURNAL Patent: JP 2002508944-A 62 26-MAR-2002;

COMMENT ISIS PHARMACEUTICALS INC

OS Unidentified

PN JP 2002508944-A/62

PD 26-MAR-2002

PF 26-MAR-1999 JP 2000538025

PI 26-MAR-1998 US 09/048810

PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

## PI COWSERT

PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//

PC C12Q1/68,

PC C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

CC Antisense modulation of human MDM2 expression FH Key

Location/Qualifiers

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## FEATURES

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Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GGAGCAGGCAAAATGTGCAAT 320  
|||||

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Db      20 GGAGCAGCAAAATGTGCAAT 1

RESULT 517
BD138137/c
LOCUS      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138137
VERSION     BD138137.1 GI:23233082
KEYWORDS   JP 2002508944-A/63.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 63 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   OS Unidentified
          PN JP 2002508944-A/63
          PD 26-MAR-2002
          PF 26-MAR-1999 JP 2000538025
          PR 26-MAR-1998 US 09/048810
          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
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FEATURES
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Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAAAATGTGCAATACC 323
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Db      20 GCAGGCAAAATGTGCAATACC 1

RESULT 519
BD138139/c
LOCUS      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138139
VERSION     BD138139.1 GI:23233084
KEYWORDS   JP 2002508944-A/65.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 65 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   OS Unidentified
          PN JP 2002508944-A/65
          PD 26-MAR-2002
          PF 26-MAR-1999 JP 2000538025
          PR 26-MAR-1998 US 09/048810
          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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FEATURES
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GAGCAGCAAAATGTGCAATA 321
      |||||
Db      20 GAGCAGCAAAATGTGCAATA 1

RESULT 518
BD138138/c
LOCUS      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138138
VERSION     BD138138.1 GI:23233083
KEYWORDS   JP 2002508944-A/64.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 64 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   OS Unidentified
          PN JP 2002508944-A/64
          PD 26-MAR-2002
          PF 26-MAR-1999 JP 2000538025
          PR 26-MAR-1998 US 09/048810
          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT

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PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
FT source 1..20
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          Location/Qualifiers
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FEATURES
source
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAAAATGTGCAATACC 323
      |||||
Db      20 GCAGGCAAAATGTGCAATACC 1

RESULT 519
BD138139/c
LOCUS      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138139
VERSION     BD138139.1 GI:23233084
KEYWORDS   JP 2002508944-A/65.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 20)
AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE     Antisense modulation of human MDM2 expression
JOURNAL   Patent: JP 2002508944-A 65 26-MAR-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   OS Unidentified
          PN JP 2002508944-A/65
          PD 26-MAR-2002
          PF 26-MAR-1999 JP 2000538025
          PR 26-MAR-1998 US 09/048810
          PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
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PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
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FEATURES
source
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGCAAAATGTGCAATACCA 324
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Db      20 CAGGCAAAATGTGCAATACCA 1

RESULT 520
BD138140/c

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CC	Antisense modulation of human MDM2 expression	PH	Key
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FT	Location/Qualifiers		
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FT	/db_xref="taxon:32644"		
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source			
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Best Local Similarity	100.0%; Pred. No. 7.9e+02;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	307 GCGAAATGTGCAATACCAAC 326		
Db	20 GCGAAATGTGCAATACCAAC 1		
RESULT 522			
BD138142/c			
LOCUS	20 bp DNA linear	PAT 18-SEP-2002	
DEFINITION	Antisense modulation of human MDM2 expression.		
ACCESSION	BD138142		
VERSION	BD138142.1 GI:23233087		
KEYWORDS	JP 2002508944-A/68.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1. (bases 1 to 20)		
AUTHORS	Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.		
TITLE	Antisense modulation of human MDM2 expression		
JOURNAL	Patent: JP 2002508944-A 68 26-MAR-2002;		
COMMENT	ISIS PHARMACEUTICALS INC		
OS	Unidentified		
PN	JP 2002508944-A/68		
PD	26-MAR-2002		
PF	26-MAR-1999 JP 2000538025		
PR	26-MAR-1998 US 05/048810		
PI	LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M		
PI	CONSORT		
PC	C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//		
PC	C12Q1/68,		
PC	C12N15/00		
CC	Strandedness: Single;		
CC	Topology: Linear;		
CC	Antisense modulation of human MDM2 expression	PH	Key
FT	Location/Qualifiers		
FT	source		
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FT	Location/Qualifiers		
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source			
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Best Local Similarity	100.0%; Pred. No. 7.9e+02;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	20 GCGAAATGTGCAATACCAAC 1		
RESULT 523			
BD138143/c			
LOCUS	20 bp DNA linear	PAT 18-SEP-2002	
DEFINITION	Antisense modulation of human MDM2 expression.		
ACCESSION	BD138143		
VERSION	BD138143.1 GI:23233088		
KEYWORDS	JP 2002508944-A/69.		

